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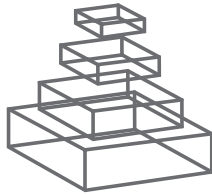
MODULATORS OF HYPOTHALAMIC- PITUITARY-GONADAL AXIS FOR THE CONTROL OF SPERMATOGENESIS AND SPERM QUALITY IN VERTEBRATES

Topic Editors

Rosaria Meccariello, Silvia Fasano,
Riccardo Pierantoni and Gilda Cobellis



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MODULATORS OF HYPOTHALAMIC-PITUITARY-GONADAL AXIS FOR THE CONTROL OF SPERMATOGENESIS AND SPERM QUALITY IN VERTEBRATES

Topic Editors:

Rosaria Meccariello, University of Naples Parthenope, Italy

Silvia Fasano, Second University of Naples, Italy

Riccardo Pierantoni, Second University of Naples, Italia

Gilda Cobellis, Second University of Naples, Italy

Spermatogenesis is a process highly conserved throughout vertebrate species and is mainly under hypothalamic-pituitary control. It occurs in the testis in a stepwise fashion so that committed spermatogonia develop into spermatocytes and enter meiosis to produce round spermatids. These undergo a morphological transformation (spermiogenesis) into mature spermatids (i.e.: spermatozoa), which are differentially released from Sertoli cells (spermiation) depending on the species. In mammals, further transformations are necessary to form mature spermatozoa, suitable for fertilization. Gonadotropins, mainly responsive to gonadotropin-releasing hormone, control spermatogenesis through specific receptors located at the gonadal level. However, besides the endocrine route, the chemical mediators may also act locally in the gonad. Indeed, it is documented that testis physiology, including steroidogenesis and spermatogenesis, does not fully account for traditional endocrine control but an intragonadal network of autocrine and/or paracrine regulators also exists, whose activity, via cell-to-cell communication, regulates germ cell progression and development of qualitatively mature spermatozoa. Of note, a number of testicular modulators, such as gonadotropin releasing hormone, Kiss-peptin, endocannabinoids, has been early isolated in the brain and latest in the gonads. To fully understand precise mechanisms underlying the functional interaction of this intricate network, needless to say, it is crucially required to have detailed information about modulators and target cells.

Through synergy between the respective specializations of all the authors, this topic reviewed emerging knowledge about neuroendocrine and local mediators controlling germ cell progression and maturation.

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Modulators of hypothalamic–pituitary–gonadal axis for the control of spermatogenesis and sperm quality in vertebrates

Rosaria Meccariello¹, Silvia Fasano², Riccardo Pierantoni^{2*} and Gilda Cobellis²

¹ Dipartimento di Scienze Motorie e del Benessere (DiSMEB), Parthenope University of Naples, Naples, Italy

² Department of Experimental Medicine, Second University of Naples, Naples, Italy

*Correspondence: riccardo.pierantoni@unina2.it

Edited by:

Cunming Duan, University of Michigan, USA

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In both male and female, gametogenesis is regulated by hypothalamus–pituitary–gonadal axis (HPG) that corresponds to the hormonal axis, gonadotropin-releasing hormone (GnRH)–gonadotropins–steroids. Indeed, the main target of GnRH is the gonadotrope cells, located in the adenohypophysis. These, in turn, release two gonadotropin hormones, the follicle stimulating hormone (FSH) and the luteinizing hormone (LH), that through the main circulation reach gonads to regulate gametogenesis via the synthesis of steroid hormones. It is now accepted that further non-steroid factors support germ cell progression via intragonadal action (1).

The first evidence of relationships between pituitary and gonad came out in 1905 from a study on castrated animals, which showed hypertrophy of the pituitary gland (2). Later in 1910, Homans and co-workers (3) showed that the “experimental hypophysectomy” in prepubertal animals induced persistence of gonadal infantilism. Surprisingly, only in 1930 the reciprocal relationship between gonads and pituitary via feedbacks was elucidated (4). Later in 1954, the long feedback connecting the hypothalamus and the gonad was described (5), but only in the 1970s did the picture become complete through the description of the short- and ultrashort-feedback mechanisms. It was at the end of the 1970s that paracrine and autocrine communications were described as being carried out also by “classic” hormones (6). In particular, it was observed that chemical messengers acting through the bloodstream could be produced in multiple tissues, not necessarily including any of the traditional ductless glands. This observation led to the new definition of what constitutes a hormone by considering its function (ὄρμῶν, to excite) rather than its source (ductless glands). A hormone may now be considered as a chemical messenger acting through endocrine (bloodstream), paracrine, and/or autocrine (local) routes. Furthermore, any chemical mediators, not only hormones, besides the endocrine route may also act locally in the gonad (7, 8).

In the testis, it has been demonstrated that a network of intragonadal endocrine, paracrine, and autocrine factors converge in a complex stage-specific multi-factorial control of spermatogenesis (6). Indeed, it has been documented that traditional endocrine control does not fully account for testis physiology, including

steroidogenesis and spermatogenesis, and an intragonadal network of autocrine and/or paracrine regulators also exist, which regulates germ cell progression and development of qualitatively mature spermatozoa via cell-to-cell communication (9, 10).

The aim of this Research Topic is to give a comparative track on HPG axis activity for the control of spermatogenesis and quality sperm production. Through synergy between the respective specializations of all the authors, this Research Topic reviews the emerging knowledge about neuroendocrine and local mediators controlling progression and maturation of germ cells in male vertebrates.

The Research Topic firstly reports the description of a primitive HPG in hagfish, one of the only two extant members of the class of agnathans – the most primitive vertebrates known, living or extinct – providing evidence that there are neuroendocrine–pituitary hormones that share common structure and functional features compared to later evolved vertebrates (11). A complex set of neuronal network converges information concerning environmental, stressors, and metabolic cues onto the centers governing the reproductive axis. In this respect, the most recent discoveries in the central pathways integrating metabolism and reproduction in teleost fish have been reviewed here (12). However, the list of central and local modulators of HPG is growing up and currently comprises gonadotropin-inhibiting hormone, firstly identified in Japanese quail in 2000 (13) as an inhibitor of gonadotropin synthesis and release but subsequently identified in all vertebrates (14); classical female hormone such as estrogens that elicit their activity through genomic and non-genomic mechanisms (15); lastly endocannabinoids (16), a set of lipid mediators that share some of the effects with delta-9-tetrahydrocannabinol (Δ^9 -THC), the active principle of marijuana plant, *Cannabis sativa*. The middle part of this Research Topic comprises a set of four review articles dedicated to the control of fetal and postnatal development of both Leydig and germ cells and to the intragonadal networks controlling the progression of the spermatogenesis (17–20); two original research articles point out the discussed involvement of new players such as kisspeptins in the local control of testis physiology (21) and the difficulties to reproduce the testicular environment *in vitro* to get a successful spermatogenesis (22). Lastly, in order

to gain the production of high quality sperm, the importance of antioxidant defenses (23), GnRH, kisspeptins, estradiol (24), and endocannabinoids (25) has been reported.

The last part of this Research Topic is focused on disease models such as Kallmann Syndrome (26), blindness (27), lysosomal storage disease (28), and cryptorchidism (29).

We hope that this contribution published in *Frontiers in Endocrinology* may represent a comprehensive guide in the plethora of data concerning the control of male reproductive activity and that readers might find new insights for the building of general models.

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Endocannabinoids as markers of sperm quality: hot spots

Mauro Maccarrone^{1,2}*

¹ Center of Integrated Research, Campus Bio-Medico University of Rome, Rome, Italy

² European Center for Brain Research/Santa Lucia Foundation, Rome, Italy

*Correspondence: m.maccarrone@unicampus.it

Edited by:

Riccardo Pierantoni, Seconda Università di Napoli, Italy

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Male reproductive health is under threat from a range of environmental and lifestyle assaults, including endocrine disruptors, toxic pollutants, and ionizing radiations, as well as lifestyle factors such as sexually transmitted infections, alcoholism, smoking, and anabolic steroid use. The latest potential hazard in our modern lifestyle is the use of plant-derived cannabinoids present in hashish and marijuana as recreational drugs, and more recently as therapeutic agents (1). In the last decade, a highly sophisticated endogenous cannabinoid system (ECS) has been discovered in mammals, where it regulates many physiological functions including human male reproduction (2–5). Here, I shall briefly discuss the activity of distinct ECS elements that can be useful to assess sperm function, and hence to potentially monitor sperm quality. Among others, these include the effect of type-1 cannabinoid receptor (CB₁) in regulating energy metabolism and motility of human sperm, and that of transient receptor potential vanilloid 1 (TRPV1) channels in controlling their fertilizing ability. Remarkably, both receptors share a common natural agonist, that is the endocannabinoid (eCB) *N*-arachidonylethanolamine (anandamide, AEA); instead, another major eCB like 2-arachidonoylglycerol (2-AG) can activate CB₁, but is ineffective at TRPV1 receptors (6). The potential therapeutic exploitation of these ECS elements for the treatment of human infertility will be also addressed.

Human sperm express CB₁, and its activation by AEA affects motility and acrosome reaction (AR). Both processes require energy, and a major role for glycolysis in supplying ATP for sperm motility has been recognized. Recently, human sperm exposure to methanandamide, a

non-hydrolyzable analog of AEA, has been shown to significantly decrease mitochondrial transmembrane potential without triggering any mitochondria-dependent apoptotic death, and such an effect was prevented by the CB₁ antagonist SR141716, but not by the CB₂ antagonist SR144528, nor by the TRPV1 antagonist iodoresiniferatoxin (7). Interestingly, in the presence of glucose human sperm exposure to methanandamide for up to 18 h failed to affect sperm motility, that instead was dramatically reduced by the same substance under glycolysis blockage; again, the latter effect was prevented by SR141716 (7). Overall, CB₁ activation induced a non-apoptotic decrease of mitochondrial potential, whose detrimental reflection on sperm motility could be revealed only when blocking glycolysis. These findings contribute to elucidate the relationship between CB₁, energetic metabolism and mitochondria, an issue that appears relevant well beyond sperm biology. Indeed, mitochondrial CB₁ activation has been recently reported to control energy metabolism in neurons (8), though the actual receptor localization on mitochondria remains controversial (9).

Another hot spot is the involvement of the AEA-binding TRPV1 receptor in human sperm fertilizing ability. Immunoreactivity for CB₁ has been localized in the post-acrosomal region and in the midpiece of human sperm, whereas for TRPV1 it was restricted to the post-acrosomal region (10). Capsazepine (CPZ), a selective antagonist of TRPV1, was shown to inhibit progesterone (P)-enhanced sperm/oocyte fusion, as evaluated by the hamster egg penetration test. This inhibition was due to a reduction of the P-induced AR rate

above that of spontaneous AR, which was instead increased (10). Altogether, these data demonstrate that TRPV1 plays a key-role in the human sperm fertilizing ability, by impacting on its fusion with the oocyte membrane. In line with this, a marked decrease of the ability of TRPV1 to bind its ligands has been shown in infertile versus fertile sperm, again supporting a major role for this ion channel in sperm functionality (11). On this basis, one might speculate that the reduction of AEA causes infertile sperm to lose their quiescent state and with that, the ability to prevent premature capacitation. This could then precipitate a premature AR, rendering that sperm infertile because of a reduced ability to penetrate an oocyte *in vivo*, or in assisted conception such as in *in vitro* fertilization (IVF) protocols. This hypothesis has recently found grounds through a clinical study performed on men affected by asthenozoospermia and oligoasthenoteratozoospermia (12). Indeed, AEA levels in seminal plasma were found to be halved in patients with respect to normal subjects (~0.08 versus ~0.20 nM). Remarkably, these differences in AEA content in men with different pathological semen subtypes were associated with poor semen quality, such as decreased sperm count and abnormal sperm motility, as well as with alterations of CB₁ at transcriptional level (12). Therefore, evaluation of eCBs content in human sperm and/or in seminal plasma could be proposed as a novel diagnostic tool in reproductive medicine. In line with this, a marked reduction (down to ~25%) of both AEA and 2-AG content in seminal plasma from infertile men has been recently documented (11). Instead, no significant alterations were found in sperm from infertile versus fertile men, neither for AEA nor for 2-AG (11). Collectively,

these data pinpoint eCBs (and AEA in particular) as new biomarkers to determine semen quality, thus opening new avenues for the treatment of infertility in humans.

Further points of interest in the regulation of sperm quality by ECS are related to the role of membrane properties and epigenetic control of chromatin activity.

Mammalian sperm become fertile after completing capacitation, a process associated with cholesterol loss and changes in the biophysical properties of the membranes, e.g., at the level of cholesterol-rich microdomains termed lipid rafts (13). Membrane raft dynamics prepares the sperm to undergo AR, and in addition it may have a role in sperm-egg membrane interaction (14). Interestingly, CB₁ and TRPV1 are affected by sperm membrane properties (15), and CB₁ signal transduction is enhanced by lipid raft disruption in different neuronal and immune cells (16). In addition, the AEA congener *N*-palmitoylethanolamine (PEA), that has been shown in the male reproductive tract, modulates plasma membrane polarity with an effect on Ca²⁺ influx during the capacitation process (17). Remarkably, PEA might also affect some physiological sperm kinematic parameters (like sperm motility), thus impacting on the development of hyperactivation during capacitation, ultimately leading to idiopathic infertility (18). Taken together, further investigations into the contribution of sperm membrane lipid composition to the control of eCB signaling, and hence to its relevance for sperm quality and fertilizing ability, hold promise for a better design of preventive and/or therapeutic strategies against infertility. In this context, it remains to be assessed whether (and to what extent) sperm functionality might be affected by accumulation of AEA and congeners in intracellular stores called adiposomes (or lipid droplets), that are present in sperm (19), and are important for eCB signaling in different cell types (20, 21).

The last hot spot that I would like to address concerns chromatin remodeling and epigenetic regulation of sperm functions. Because CB₁ activation plays a pivotal role in spermiogenesis (that is the developmental stage where DNA is remodeled), it has been recently hypothesized that

regulation of the CB₁ gene (*Cnr1*) might also influence chromatin quality in sperm (22). By using *Cnr1* null mutant (*Cnr1*^{-/-}) mice, CB₁ activation was demonstrated to regulate indeed chromatin remodeling of spermatids, *via* either increasing the levels of the *Tnp2* gene (encoding for the transition protein 2, that stimulates DNA nick repair *in vitro*), or enhancing histone displacement. Comparative analysis of wild-type, *Cnr1*^{+/-} and *Cnr1*^{-/-} animals suggested the possible occurrence of haploinsufficiency for *Tnp2* turnover under CB₁ control, whereas histone displacement was disrupted in *Cnr1*^{+/-} and *Cnr1*^{-/-} mice to a lesser extent. Furthermore, flow cytometry analysis demonstrated that the genetic loss of *Cnr1* decreased sperm chromatin quality and was associated with sperm DNA fragmentation. Of note, this damage increased during epididymal transit, from caput to cauda (22). Collectively, these results demonstrate that the expression (and expectedly the activity) of CB₁ controls the physiological alterations of DNA packaging during spermiogenesis and epididymal transit, which might have major implications for male fertility, given the deleterious effects of sperm DNA damage (22). On a final note, it should be recalled that the epigenetic regulation of target genes by eCBs, and conversely that of ECS genes (in particular CB₁) by pathological conditions, are emerging as a major issue to understand the fine tuning of eCB signaling in human health and disease (23). Therefore, it can be anticipated that epigenetic studies on sperm quality and fertilizing capacity will open new avenues for preventing or curing (e.g., through a correct lifestyle) human infertility with innovative therapeutics.

In conclusion, distinct ECS elements like CB₁ and TRPV1, along with the endogenous levels of their common ligand and AEA, hold the promise to represent useful diagnostic biomarkers and therapeutic targets of male fertility defects. It seems noteworthy that, while CB₁ has major effects also on female reproductive events (from oocyte development, to ovarian transport, and embryo implantation), apparently TRPV1 does not impact on female fertility (24), apart from generating hyperalgesia via primary sensory neurons during endometriosis (25). Therefore, the latter ion channel seems to represent an

ideal target to specifically combat reproductive dysfunctions in males.

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Paracrine mechanisms involved in the control of early stages of mammalian spermatogenesis

Pellegrino Rossi* and Susanna Dolci

Dipartimento di Biomedicina e Prevenzione, Università degli Studi di Roma Tor Vergata, Rome, Italy

Edited by:

Gilda Cobellis, Second University of Naples, Italy

Reviewed by:

Riccardo Pierantoni, Second University of Naples, Italy

Francisco Prat, Consejo Superior de Investigaciones Científicas, Spain

***Correspondence:**

Pellegrino Rossi, Dipartimento di Biomedicina e Prevenzione, Università degli Studi di Roma Tor Vergata, Via Montpellier 1, Rome 00133, Italy
e-mail: pellegrino.rossi@med.uniroma2.it

Within the testis, Sertoli-cell is the primary target of pituitary FSH. Several growth factors have been described to be produced specifically by Sertoli cells and modulate male germ cell development through paracrine mechanisms. Some have been shown to act directly on spermatogonia such as GDNF, which acts on self-renewal of spermatogonial stem cells (SSCs) while inhibiting their differentiation; BMP4, which has both a proliferative and differentiative effect on these cells, and KIT ligand (KL), which stimulates the KIT tyrosine-kinase receptor expressed by differentiating spermatogonia (but not by SSCs). KL not only controls the proliferative cycles of KIT-positive spermatogonia, but it also stimulates the expression of genes that are specific of the early phases of meiosis, whereas the expression of typical spermatogonial markers is down-regulated. On the contrary, FGF9 acts as a meiotic inhibiting substance both in fetal gonocytes and in post-natal spermatogonia through the induction of the RNA-binding protein NANOS2. Vitamin A, which is metabolized to Retinoic Acid in Sertoli cells, controls both SSCs differentiation through KIT induction and NANOS2 inhibition, and meiotic entry of differentiating spermatogonia through STRA8 upregulation.

Keywords: primordial germ cells, spermatogonial stem cells, spermatogenesis, meiosis, growth factors, paracrine control, signal transduction, gene expression

BRIEF INTRODUCTION: PARACRINE CONTROL OF FETAL MALE GERM CELL DEVELOPMENT

The control of the germ cell fate by paracrine factors secreted by the surrounding somatic environment already starts in the fetal life in the period of germ cell specification, independently from the influence of the hypothalamic-pituitary axis. Bone Morphogenetic Protein 4 (BMP4) has been shown to induce primordial germ cell (PGC) formation, to act as a PGC survival and localization factor within the allantois (1) and as a mitogen in *in vitro* cultured PGCs (2). During PGC specification in the extraembryonic mesoderm, SOX2 induction is required for the transcriptional regulation of KIT expression in PGCs (3). KIT is a tyrosine-kinase receptor, which is activated by KIT Ligand (KL), a growth factor expressed by the surrounding somatic environment. KL/KIT interaction is essential in the fetal period both during the specification of PGCs and for their proliferation and migration [(3–7), and references therein]. KIT expression is then down-regulated both in fetal oocytes undergoing meiosis and in gonocytes, which stop to proliferate after germ cell sex determination. Sertoli cells can prevent meiotic entry of gonocytes through the production of paracrine factors acting as meiotic inhibiting substances. The best characterized meiotic inhibiting substance produced by fetal Sertoli cells is Fibroblast Growth factor 9 (FGF9). FGF9 is a SRY/SOX9-dependent growth factor crucial for male sex differentiation acting on the somatic compartment of the fetal testis (8, 9). However, FGF9 also acts directly on male fetal gonocytes by upregulating levels of the RNA-binding protein NANOS2 (10, 11). NANOS2 prevents meiosis through the post-transcriptional regulation of key genes involved in the meiotic program (10, 12, 13). Recently, it has been shown that the meiosis-preventing activity of

FGF9 in the fetal testis is mediated, at least in part, by NODAL, a member of the TGF- β family, and its partner Cripto (14–16).

In the same period in which FGF9 is expressed during testis determination, Sertoli cells produce an enzyme, CYP26B1, which degrades Retinoic Acid (RA) of mesonephric origin, in order to block Stimulated by Retinoic Acid 8 (STRA8) expression, and, as a consequence, to prevent premature gonocyte entry into meiosis (17–20). Although the identification of RA as the CYP26B1 substrate in the fetal testis (required for STRA8 induction and meiosis initiation in the fetal ovary) has been questioned (21), most of the available data in the literature support the role of RA as a master inducer of the mitotic-meiotic switch in germ cells (22). In line with this evidence is the finding that RA treatment down-regulates NANOS2 expression in fetal gonocytes (10).

PARACRINE CONTROL OF POST-NATAL MALE GERM CELL DEVELOPMENT

Pituitary gonadotropins, FSH, and LH, were originally identified for their essential role in ovarian function, as the stimulator of follicular activity and the inducer of follicular luteinization, respectively (23). Later on, it became clear that the same hormones play important roles also in testicular function, FSH being involved in the induction of spermatogenesis at puberty, and LH being the main inducer of androgen production (24). Spermatogenesis is a highly ordered differentiative process that occurs under FSH and androgen control. Sertoli cells, the only known targets for these hormones in the seminiferous tubules, mediate hormone action on spermatogenesis by controlling the germinal stem cell niche and by creating a suitable environment for the complex developmental events of germ cell proliferation and differentiation. Sertoli

cells directly orchestrate these complex events through both membrane intercellular communications and the production of growth factors and cytokines that act directly on the germ cell compartment. In the following paragraphs we will focus on the better characterized Sertoli-cell controlled paracrine mechanisms acting on the early stages of mammalian spermatogenesis, which are schematically summarized in **Figure 1**.

MAINTENANCE OF THE GERM STEM CELL NICHE

Spermatogonial stem cells (SSCs) are the direct descendants of fetal gonocytes. In the testis, SSCs are a subpopulation of undifferentiated spermatogonia residing in the basal layer of the seminiferous epithelium. Their mitotic expansion allows continuous production of germ cells committed to differentiation. One of the specific properties of SSCs and other undifferentiated spermatogonia that distinguishes them from differentiating spermatogonia is the expression of the Glial cell line-derived neurotrophic factor (GDNF)-family receptor $\alpha 1$ (GFR $\alpha 1$) and the c-Ret receptor

tyrosine-kinase, which are both required for signaling in response to the Sertoli-cell-derived GDNF (25–28). GDNF has been shown to be essential for fate determination of SSCs, since in aging males heterozygotes for GDNF deletion, testes appear devoided of germ cells and show a phenotype similar to Sertoli-cell-only syndrome (25). Furthermore, overexpression of GDNF in mouse testes appeared to stimulate self-renewal of stem cells and block spermatogonial differentiation, inducing a seminomatous phenotype (25, 27). GDNF-induced activation of AKT and MEK signaling pathways in SSCs leads to increased generation of reactive oxygen species (ROS) generated by NAPDH oxidase 1, and apparently (contrary to their alleged detrimental role for spermatogenesis) ROS stimulate proliferation and self-renewal of SSCs through the activation of p38 and JNK MAPKs (29). Thus, GDNF is important for SSCs self-renewal, and, at the same time negatively controls their differentiation. This notion has been recently challenged by the finding that GFR $\alpha 1$ -positive chained spermatogonia (A paired and A aligned) are more numerous than GFR $\alpha 1$ -positive

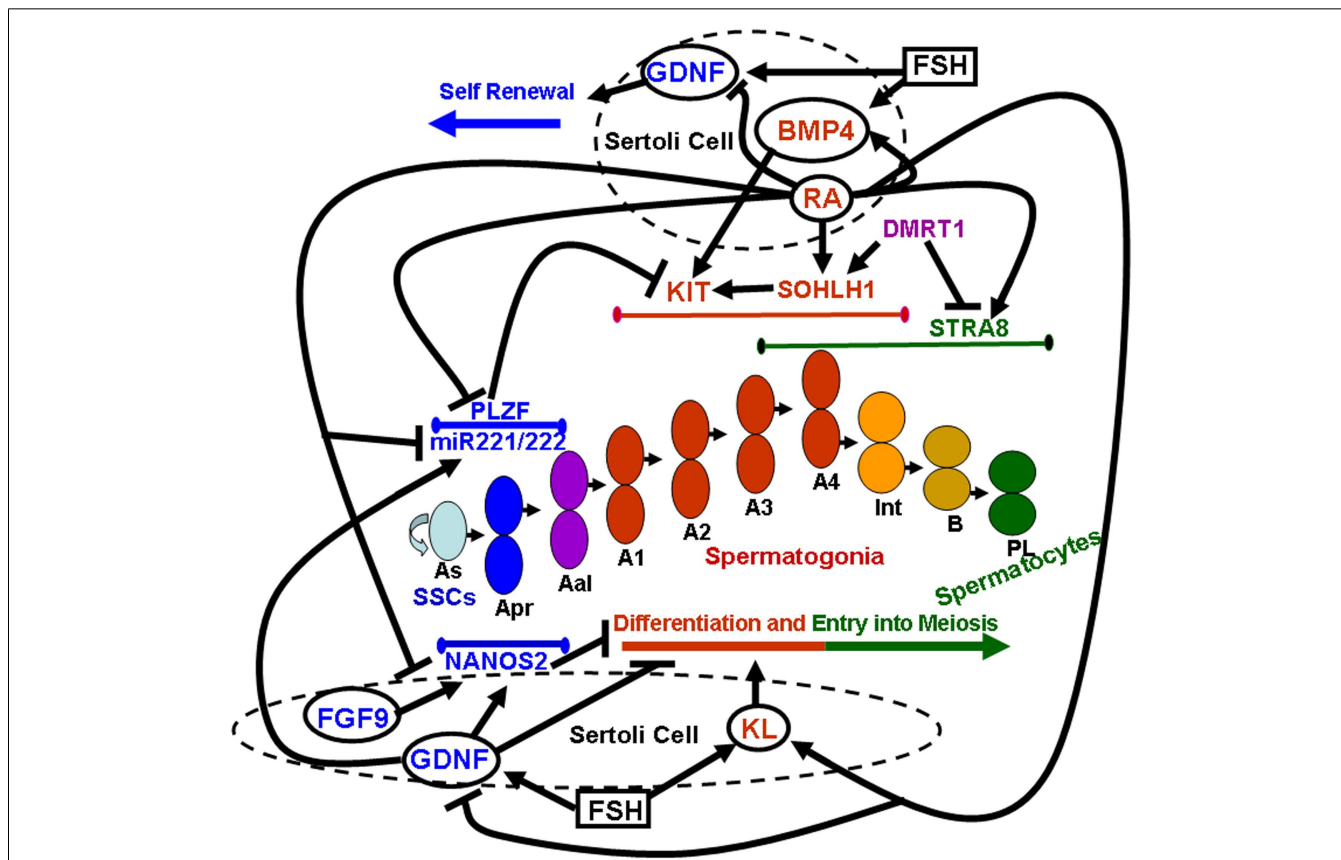


FIGURE 1 | Sertoli-cell controlled paracrine mechanisms acting on the early stages of mammalian spermatogenesis. Paracrine factors secreted by Sertoli cells (whose membrane is represented by dashed circles) are enclosed within solid line circles. Follicle stimulating hormone (FSH) is enclosed within a solid line square. Endogenous factors expressed by germ cells are represented by non-enclosed words. Blue colors refer to paracrine and endogenous factors that promote self-renewal of spermatogonial stem cells (SSCs) and inhibit spermatogonial differentiation and/or meiotic entry. Red colors refer to paracrine and endogenous factors that promote spermatogonial differentiation. Purple colors refer to endogenous factors which promote

spermatogonial differentiation but at the same time inhibit meiotic entry. Green colors refer to endogenous factors that drive entry into meiosis. Lines delimited by small ellipsoids refer to the stage of expression of the germ cell endogenous factors involved in either self-renewal of SSCs and inhibition of differentiation (blue colors) or in differentiation (red colors) and meiotic entry (green colors). The succession of the various types of germ cells during the earliest stages of mouse spermatogenesis is represented in the center of the image: As, a single spermatogonia; Apr, a paired spermatogonia; Aal, a aligned spermatogonia; A1, A2, A3, A4, type A1–A4 spermatogonia; Int, intermediate spermatogonia; B, type B spermatogonia; PL, pre-leptotene spermatocytes.

A single spermatogonia, which are thought to represent the major SSCs reservoir in the mouse testis (30). However, GDNF signaling is essential to maintain NANOS2 expression in SSCs, and it has been proposed that this RNA-binding protein, besides its well-established role in preventing meiosis in fetal gonocytes, is also important to prevent spermatogonial differentiation in the post-natal testis (31). Overall, it is clear that GDNF mainly acts in positively regulating the proliferation of SSCs and maintenance of their undifferentiated state. Importantly, FSH and its second messenger cyclic AMP (cAMP) have been reported to stimulate GDNF expression in Sertoli cells (32, 33), which is instead down-regulated by RA treatment (33). These evidences suggest that GDNF might be one of the paracrine factors that influences SSCs proliferation and population size under the control of the hypothalamic-pituitary axis.

CONTROL OF SPERMATOGONIAL DIFFERENTIATION

Undifferentiated SSCs (A single spermatogonia) have been described as single cells that are able both to renew themselves and to produce more differentiated A paired spermatogonia. The A paired cells then divide into A aligned spermatogonia that further differentiate into A1 spermatogonia (34). Appearance of A1 (differentiating) spermatogonia coincides with regain of the expression of KIT, encoding the receptor for KL (35–38). KIT mediates proliferation, survival, and differentiation in type A spermatogonia (33, 39–41). Upon KIT expression, spermatogonia become sensitive to KL produced by Sertoli cells (39, 42) and undergo a definite number of proliferative cycles, forming the A2–A4, intermediate, and B spermatogonia, before entering meiosis. The temporal appearance of KIT expression and of KL sensitivity in mouse spermatogonia, between 4 and 7 days postpartum (dpp) (33, 35, 36, 40), marks the switch from the A aligned spermatogonia to the A1–B differentiating cell types. Indeed, KIT is universally considered the most important marker that distinguishes differentiating spermatogonia from their undifferentiated precursors, including SSCs. Thus, paracrine factors in the testicular environment that stimulate KIT expression in mitotic germ cells play an essential role for the start of spermatogenesis at puberty. One of the paracrine signals involved in this event is BMP4, which is produced by Sertoli cells very early in the post-natal life, and whose expression is positively regulated by cAMP and RA (33, 43). Its receptor ALK3 and the SMAD5 transducer are expressed in undifferentiated spermatogonia, and *in vitro* treatment of these cells with BMP4 exerts both mitogenic and differentiative effects, inducing [³H]thymidine incorporation and KIT expression both at the RNA and protein levels (43). As a result of the latter event, KIT-negative spermatogonia acquire sensitivity to KL (43). Since SSCs are able to renew themselves and at the same time to progress through differentiation (i.e., to the KIT-dependent stages of proliferation), BMP4 could be one of the factors that regulates such process. Alternatively, BMP4 could act on a subset of undifferentiated spermatogonia that have lost SSC features, i.e., that have entered the differentiative stage but are not yet KIT-positive. In agreement with the first possibility, BMP4 addition, on the opposite of GDNF, was shown to impair *in vitro* maintenance of mouse primary SSCs (44). Moreover, more recently BMP4 was shown to induce differentiation and KIT expression in a rat SSC cell

line (45). In the adult testis, BMP4 has been reported to be produced by spermatogonia, but not by Sertoli cells (46), suggesting that it might work as a paracrine-autocrine factor modulating the establishment of the cycle of the seminiferous epithelium.

Another well-established paracrine factor involved in spermatogonial differentiation is the Vitamin A derivative RA. Mice kept on a diet deficient on vitamin A (VAD mice) or lacking vitamin A derivatives are sterile because the seminiferous tubules contain only undifferentiated KIT-negative spermatogonia, indicating a role of vitamin A in spermatogonia differentiation (38, 47). RA functions inside the nucleus recognizing two different classes of retinoid receptors. Both classes (RARs and RXRs) consist of three types of receptors, α , β , and γ , encoded by distinct genes and transduce RA signal by binding directly to RA-responsive elements. During post-natal development, each RAR is detected predominantly in a specific cell type of the seminiferous epithelium: RAR α in Sertoli cells, RAR β in round spermatids and RAR γ in type A spermatogonia (48). RAR α conditional ablation in Sertoli cells showed germ cell apoptosis and seminiferous epithelium dysfunctions related to the disruption of Sertoli cells cyclical gene expression, which preceded testis degeneration (49). It has been reported that during the first, prepubertal, spermatogenic cycle RALDH-dependent synthesis of RA by Sertoli cells is indispensable to initiate differentiation of A aligned into A1 spermatogonia, and that this effect is mainly mediated by autocrine action of RA through RAR α in the somatic compartment (50). However, RA (either the all-trans or the 9-cis Retinoic isomers) treatment *in vitro* exerts a direct effect on the differentiation of mitotic germ cell compartment by promoting KIT expression in undifferentiated spermatogonia (33, 51). This effect has been confirmed *in vivo* by the observation that targeted ablation of RAR γ impairs the A aligned to A1 transition in the course of some of the seminiferous epithelium cycles (52). Altogether these data indicate that RA favors spermatogonial differentiation through a direct action on spermatogonia and an indirect action mediated by changes in the expression pattern of paracrine factors such as KL, BMP4, and GDNF secreted by Sertoli cells (33).

Due to its importance for promoting expansion of differentiating spermatogonia, KIT expression in SSCs is subjected to a very tight transcriptional control. Promyelocytic Leukemia Zinc Finger (PLZF, also known as ZFP145, or ZBTB16) is a DNA sequence-specific transcriptional repressor that can exert local and long-range chromatin remodeling activity through the recruitment of DNA histone deacetylases and through the action of several nuclear corepressors (53). PLZF is specifically expressed in SSCs, and male PLZF knock-out (KO) mice show progressive spermatogonia depletion due to the deregulated expression of genes controlling the switch between self-renewal and differentiation (54–56). PLZF represses both endogenous KIT expression and expression of a reporter gene under the control of KIT regulatory elements (57). A discrete sequence of the KIT promoter, required for PLZF-mediated KIT transcriptional repression, was demonstrated to be bound by PLZF *in vitro* and also *in vivo*, by using chromatin immunoprecipitation (ChIP) of spermatogonia. Moreover, a 3-bp mutation in this PLZF binding site abolishes the responsiveness of the KIT promoter to PLZF repression. In agreement with these findings, a significant increase in KIT expression

was found in the undifferentiated spermatogonia isolated from PLZF KO mice (57). Thus, one mechanism by which PLZF maintains the pool of SSCs is through a direct repression of KIT transcription, thus acting as a gatekeeper of spermatogonial differentiation. RA was shown to trigger downregulation of PLZF in SSCs (58), which might be part of the mechanisms which triggers up-regulation of KIT during spermatogonial differentiation.

Positive regulators of KIT transcription in spermatogonia are two b-Helix-Loop-Helix (HLH) transcription factors specifically expressed in germ cells, SOHLH1 (Spermatogenesis and Oogenesis HLH1), and SOHLH2. Both SOHLHs have been involved in the differentiation of spermatogonia and oocytes (59–64). In the male, deletion of each transcription factor leads to the disappearance of KIT-expressing spermatogonia in the prepuberal testis. An expression study of SOHLH1 and SOHLH2 during fetal and post-natal development showed a strong positive correlation between KIT and the two transcription factors in post-natal spermatogonia (65). SOHLH2 was found enriched mainly in undifferentiated spermatogonia, whereas SOHLH1 expression was maximal in KIT-dependent stages. Reporter gene expression driven by sequences contained within the KIT promoter and first intron was strongly up-regulated in transfection experiments overexpressing either SOHLH1 or SOHLH2, and co-transfection of both factors showed a cooperative effect (65). *In vivo*, co-immunoprecipitation results evidenced that the two proteins interact and overexpression of both factors increased endogenous KIT expression. Using ChIP analysis, SOHLH1 was found to occupy discrete bHLH binding site containing regions within the KIT promoter in spermatogonia chromatin (64, 65). Interestingly, expression of SOHLH1 was increased in post-natal mitotic germ cells by treatment with All-trans RA (65), which might be another mechanisms through which vitamin A derivatives triggers KIT up-regulation and spermatogonial differentiation. Using conditional gene targeting, it has been shown that loss of the Doublesex-related transcription factor DMRT1 in spermatogonia causes a precocious exit from the spermatogonial program and entry into meiosis (66). Apparently, DMRT1 acts in differentiating spermatogonia by restricting RA responsiveness, directly repressing transcription of the meiotic inducer STRA8, and activating transcription of SOHLH1, thereby preventing meiosis and promoting spermatogonial development (66). In agreement with the direct role played by SOHLH1 in regulating KIT transcription (65), a drastic reduction of KIT expression in spermatogonia was evident in testes from DMRT1 conditional KO mice (66).

Retinoic acid can up-regulate KIT expression in spermatogonia also at the post-transcriptional level, by interfering with the action of two X-linked microRNAs, miR-221 and miR-222 (67). Since miR-221/222 negatively regulate both KIT mRNA and KIT protein abundance in spermatogonia, impaired expression of these microRNAs in mouse undifferentiated spermatogonia induces transition from a KIT-negative to a KIT-positive state and loss of stem cell capacity to regenerate spermatogenesis. Undifferentiated spermatogonia overexpressing miR-221/222 were found to be resistant to RA-induced transition to a KIT-positive state and incapable of differentiation *in vivo* (67). Moreover, growth factors that promote maintenance of undifferentiated spermatogonia, such as GDNF, were found to up-regulate miR-221/222 expression. On

the contrary, exposure to RA down-regulates miR-221/222 abundance (67). In conclusion, RA promotes progression of SSCs to differentiating spermatogonia through different mechanisms, all of which positively influence KIT expression: downregulation of PLZF and of miR-221/222, and up-regulation of SOHLH1.

CONTROL OF SPERMATOGONIAL EXPANSION

KIT ligand/KIT interaction is essential during post-natal stages of spermatogenesis for the expansion of the differentiating spermatogonia pool. KL, expressed by Sertoli cells, stimulates proliferation of differentiating type A1–A4 spermatogonia both by inducing their progression into the mitotic cell cycle and by reducing their apoptotic rate. This effect is exerted by the activated KIT tyrosine-kinase using as signal transducers both PI3K-AKT and MEK-ERK1/2 (39, 40, 68). The role of KIT/KL in the maintenance and proliferation of differentiating spermatogonia has been highlighted by a mouse genetic model with a point mutation of KIT that eliminates the PI3K docking site (Y719F) through a single bp change (69, 70). While PGC specification and proliferation in both sexes is not compromised during embryonic development, KIT(Y719F)/KIT(Y719F) males are sterile due to the lack of spermatogonia proliferation during the prepuberal period and an arrest of spermatogenesis at the pre-meiotic stages. The KIT/KL system is also an important mediator of the influence of hypothalamic-pituitary axis on the spermatogenic process. Indeed, the expression of the mRNA for KL is induced by FSH in prepuberal mouse Sertoli cells cultured *in vitro*, through an increase in cAMP levels (39, 42). The cAMP-dependent increase in KL expression in Sertoli cells is mainly due to direct activation of transcription from proximal promoter elements within the KL gene (71). Stage-dependent induction of KL mRNA expression by FSH has also been observed in the adult rat testis (72), and the maximal levels of KL mRNA induction are observed in stages of the seminiferous epithelium which show the maximal sensitivity to FSH stimulation, and in which type A spermatogonia are actively dividing. Interestingly, the soluble and membrane forms of KL, produced by alternative splicing, are differentially expressed during testis development. Sertoli cells from prepuberal mice mainly express the mRNA encoding for the transmembrane form, while the mRNA encoding for the soluble form is expressed at higher levels later, in coincidence with the beginning of the spermatogenic process, and the two transcripts are expressed at equivalent levels in the adult testis (39). Moreover, FSH and/or cAMP analogs, beside increasing KL mRNA levels, also modify the splicing pattern of the two isoforms in cultured mouse Sertoli cells in favor of the mRNA encoding for the soluble form (39). In agreement with these observations is the finding that the highest levels of the transmembrane form of KL are detected immunohistochemically in stages VII–VIII of the mouse seminiferous epithelium (73), which are the less sensitive to FSH stimulation in the adult testis (74). It has been hypothesized that the transmembrane form of KL could be physiologically relevant for the progression through the blood-testis barrier of mitotic germ cells entering the first meiotic prophase at stages VII–VIII (5). Moreover, even though at the onset of meiosis KIT expression in male germ cells ceases at both the RNA and protein levels (5), KL/KIT interaction, besides its well-established role in the expansion of differentiating type A spermatogonia, is

also important for entry into the meiotic program, i.e., the transition from type B spermatogonia to pre-leptotene spermatocytes, as discussed in the next paragraph.

CONTROL OF ENTRY INTO MEIOSIS

Retinoic acid acts in a bimodal mode to promote the spermatogenic process. Indeed, besides its important role in promoting progression of SSCs to differentiating spermatogonia through activation of KIT expression, RA also promotes expression of the meiotic inducer STRA8 in spermatogonia (33, 51). Besides RA of Sertoli-cell origin, it has been reported that also RA synthesized by pre-meiotic spermatocytes cell autonomously induces meiotic initiation through controlling the RAR-dependent expression of STRA8 in the same cells (50). Targeted ablation of STRA8 revealed a crucial role for this gene in the initial stages of the meiotic process in post-natal male germ cells, either in the transition from type B spermatogonia/pre-leptotene to leptotene spermatocytes (75), or in slightly later stages of the meiotic prophase, with mutant leptotene spermatocytes undergoing a premature mitotic-like chromosome condensation (76). The mechanisms through which STRA8 regulates the initial stages of meiosis in both sexes are currently unknown. However, the role played by STRA8 in male meiosis appears to be different from that played in the induction of the meiotic process in the fetal ovary, in which STRA8 ablation leads to an arrest of pre-meiotic DNA synthesis in pre-leptotene oocytes (18), whereas the last round of germ cell DNA synthesis appears not to be affected in STRA8-deficient pre-leptotene spermatocytes (75, 76). RA was found to increase meiotic entry of mouse KIT-positive differentiating spermatogonia *in vitro*, as evaluated by both morphological and biochemical criteria (33). Increased expression of STRA8 and of early meiotic markers, such as DMC1, accompanied the morphological switch from spermatogonia to pre-leptotene and leptotene spermatocytes. RA treatment also increased STRA8 expression in *in vitro* cultured KIT-negative undifferentiated spermatogonia, which included SSCs, but this was not followed by induction of meiotic entry, suggesting that spermatogonial competence to enter meiosis is acquired only during the differentiative stages in which they undergo KIT-dependent mitotic divisions (33). Transcriptome analysis of *in vitro* cultured differentiating spermatogonia stimulated with recombinant KL revealed a pattern of RNA expression compatible with the qualitative changes of the cell cycle that occur during the subsequent cell divisions in type A and B spermatogonia, i.e., the progressive lengthening of the S phase and the shortening of the G2/M transition (41). Moreover, KL treatment was found to up-regulate in differentiating spermatogonia the expression of early meiotic genes, and to down-regulate at the same time typical spermatogonial markers, suggesting an important role for KL/KIT interaction in the transition from the mitotic to the meiotic cell cycle, and also an active role in the induction of meiotic differentiation (41). Indeed, morphological and biochemical analysis of *in vitro* cultured spermatogonia treated with KL revealed an induction of STRA8 and DMC1 expression and of meiotic entry, evaluated as a dramatic increase in the number of pre-leptotene and leptotene spermatocytes similar to the one induced by RA treatment (33). The effect of RA and KL on meiotic entry did not appear to be additive, implying that these factors converge on common signal

transduction pathways to exert this effect. Indeed, similarly to KL, RA treatment induced KIT autophosphorylation, MEK-ERK1/2 and PI3K-AKT activation, and selective inhibitors of any of these pathways inhibited the biochemical and morphological signs of meiotic entry. Thus, together with genomic effects leading to increased expression of KIT in spermatogonia and of KL in Sertoli cells, RA also exerts rapid non-genomic effects in differentiating spermatogonia and converge with KL on common KIT-dependent signaling pathways for the induction of meiotic entry (33).

In order to ensure the homeostasis of the spermatogenic process, paracrine mechanisms, and endogenous effectors which negatively regulate spermatogonial differentiation and the onset of the meiotic process in post-natal spermatogenesis must coexist with positive inducers such as RA and KL. One of these paracrine mechanisms is analogous to the one operating to prevent meiosis onset in the fetal testis, and involves FGF9 expression in the somatic environment of the seminiferous epithelium and expression of the RNA-binding protein NANOS2 in pre-meiotic germ cells. In the post-natal testis, NANOS2 was found to be specifically expressed at both the RNA and protein level in KIT-negative undifferentiated spermatogonia, but not in KIT-positive differentiating spermatogonia, nor in meiotic or postmeiotic germ cells (10). FGF9 stimulation of *in vitro* cultured differentiating spermatogonia resulted in a dramatic induction of NANOS2 expression and inhibition of the morphological and biochemical signs of entry into meiosis, without apparent effects on the expression of STRA8, whereas RA treatment resulted in a deep inhibition in the levels of NANOS2 expression in undifferentiated spermatogonia, together with the previously described stimulation of STRA8 expression (10). Thus, together with playing an essential role in preventing meiosis of gonocytes in the male fetal testis, FGF9 acts as an inhibitor of meiotic differentiation through the upregulation of NANOS2 also in post-natal male mitotic germ cells.

FUTURE PERSPECTIVES

Obviously there must be also a paracrine influence of germ cells on Sertoli-cell production of factors involved in the local control of spermatogenesis, but, up to now, little information is available in the literature about these germ cell-generated signals. On the other hand, Sertoli cells are clearly the only mediators of the influence of the hypothalamic-pituitary axis on the spermatogenic process. FSH drives both Sertoli-cell secretion of GDNF, on one side, and of BMP4 and KL, on the other side. This actually fits with the double role exerted by the pituitary hormones, as inducers of spermatogenesis at puberty (through the local mediation of BMP4 and KL), but at the same time as essential for its maintenance and quantitative output (through GDNF stimulation of SSCs self-renewal). The factors which locally control the balance between GDNF vs. BMP4 and KL secretion by Sertoli cells in response to FSH might be germ cell-generated signals, and they must be the object of further studies.

Another puzzling observation is that FGF9 exerts opposite effects in KIT-positive differentiating spermatogonia with respect to those elicited by RA and KL signaling. Indeed, it is intriguing to notice that KL and FGF9 act on the same germ cell type stimulating receptor tyrosine-kinase activities (and thus presumably partially shared signal transduction pathways), yet they exert

opposite effects (differentiation and promotion of meiosis vs. prevention of meiotic entry). It will be very important to dissect the differences in intracellular signaling elicited in differentiating spermatogonia by these two antagonistic growth factors and the downstream cascade of events that lead to RA/KL-mediated induction of meiotic entry and FGF9-mediated inhibition of the same process. For instance, it will be interesting to characterize the subtypes of FGF receptors expressed in spermatogonia, and to investigate whether activation of NODAL signaling is involved in FGF9 action in post-natal male germ cells as it has been reported for male fetal gonocytes (14–16). Preliminary results from our laboratory indicate that both FGF9 and KL stimulate transient ERK1/2 activation in spermatogonia, but PI3K-dependent AKT activation is elicited by KL, but not by FGF9 (V. Tassinari, P. Rossi, and S. Dolci, unpublished results). This might be of particular importance, in light of the notion that in the mouse testis, as mentioned previously, a point mutation of KIT that eliminates the PI3K docking site cause a total block of the spermatogenic process between 8 and 10 dpp (69, 70), coinciding with of the onset of meiosis in the male germ cell line, and that PI3K inhibitors completely block induction of meiotic entry elicited *in vitro* by RA and/or KL treatment of differentiating spermatogonia (33).

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The endocannabinoid system and spermatogenesis

Paola Grimaldi*, Daniele Di Giacomo and Raffaele Geremia

Section of Anatomy, Department of Biomedicine and Prevention, University of Rome "Tor Vergata," Rome, Italy

Edited by:

Riccardo Pierantoni, Seconda Università di Napoli, Italy

Reviewed by:

Gilda Cobellis, Second University of Naples, Italy

Silvia Fasano, Second University of Naples, Italy

***Correspondence:**

Paola Grimaldi, Section of Anatomy, Department of Biomedicine and Prevention, University of Rome "Tor Vergata," Via Montpellier 1, Rome 00133, Italy
e-mail: p.grimaldi@med.uniroma2.it

Spermatogenesis is a complex process in which male germ cells undergo a mitotic phase followed by meiosis and by a morphogenetic process to form mature spermatozoa. Spermatogenesis is under the control of gonadotropins, steroid hormones and it is modulated by a complex network of autocrine and paracrine factors. These modulators ensure the correct progression of germ cell differentiation to form mature spermatozoa. Recently, it has been pointed out the relevance of endocannabinoids as critical modulators of male reproduction. Endocannabinoids are natural lipids able to bind to cannabinoid receptors and whose levels are regulated by specific biosynthetic and degradative enzymes. Together with their receptors and metabolic enzymes, they form the "endocannabinoid system" (ECS). In male reproductive tracts, they affect Sertoli cell activities, Leydig cell proliferation, germ cell differentiation, sperm motility, capacitation, and acrosome reaction. The ECS interferes with the pituitary-gonadal axis, and an intricate crosstalk between ECS and steroid hormones has been highlighted. This mini-review will focus on the involvement of the ECS in the control of spermatogenesis and on the interaction between ECS and steroid hormones.

Keywords: male germ cells, spermatogenesis, endocannabinoid system, sex hormones, cannabinoid

INTRODUCTION

Infertility affects 10–15% of couples, and it has been estimated that a male factor is responsible in approximately half of these cases. Male infertility is diagnosed with the analysis of several semen parameters, such as the number of total sperm, sperm motility, and percentage of sperm cells with a normal morphology. It is known that marijuana, the commonest recreational drug of abuse, has adverse effects on male reproductive physiology. Its use is associated with impotence, decreased testosterone plasma level, impairment of spermatogenesis, production of spermatozoa with abnormal morphology, reduction of sperm motility and viability and, more recently, with the occurrence of non-seminoma germ cell tumors (1). The identification of endogenous cannabinoids (ECBs) that mimic some effects of delta-9-THC, the active principle of *Cannabis sativa*, has opened new studies on the biological role of ECBs in male reproduction. In this mini-review we focused on the relevance of endocannabinoids and "endocannabinoid system" (ECS) in spermatogenesis and sperm functions, and on the interplay between ECS and sex hormone.

SPERMATOGENESIS

Spermatogenesis is a complex differentiative process starting from spermatogonial stem cells (SSCs), known as A-single (A_s). The A_s cells, similarly to other stem cells, have the capability to self-renew, producing daughter A_s cells, and to progress into "undifferentiated spermatogonia" known as A-paired (A_{pr}), and A-aligned (A_{al}) that represent committed cells. The A_{al} spermatogonia then differentiate into A1-4, intermediate (In) and B spermatogonia which undergo meiosis as pre-leptotene spermatocytes (2). Spermatocytes pass sequentially through leptotene, zygotene, pachytene, and diplotene phases of prophase I, and then quickly undergo two M-phase divisions, yielding haploid spermatids, that became

spermatozoa through the morphogenetic process called spermiogenesis. Sperm released from the seminiferous epithelium into the tubule lumen are still immature and are not able to fertilize an egg. Sperm maturation occur in the epididymis. During spermatogenesis, germ cells, at each stage of differentiation, are in close contact with Sertoli cells which provide physical and metabolic support for their proliferation, meiosis, and successful progression into spermatozoa. Sertoli cells proliferate quickly during perinatal period and they switch to a mature, non-proliferative state, around the onset of puberty. Since only a limited number of germ cells can be supported by each Sertoli cell (3), in adult testis, the number of Sertoli cells will be a critical factor with obvious consequences on fertility.

Spermatogenesis continues throughout life and it is regulated by a complex assortment of hormones as well as numerous locally produced factors that include growth factors, cytokines, and chemokines, that act through autocrine and paracrine pathways. Sertoli cell-secreted growth factors are known to have direct effects mainly on spermatogonia: Gdnf acts on self-renewal of SSCs and inhibits their differentiation (4), Bmp4 has both a proliferative and differentiative effect on these cells (5), and Kit Ligand (KL), acts on the kit tyrosine-kinase receptor expressed by differentiating type A spermatogonia (6) stimulating their progression into the mitotic cell cycle and reducing apoptosis (7). The major hormonal control system of spermatogenesis is the hypothalamic-pituitary-gonadal axis, based essentially on the release of two gonadotropins, luteinizing hormone (LH) and follicle stimulating hormone (FSH), under the stimulation of hypothalamic GnRHs. Leydig and Sertoli cells, the somatic cells of the testis, are primary responders to circulating gonadotropin hormones and their failure to respond appropriately, results in male infertility (8). LH stimulates Leydig cells to synthesize testosterone (T) and FSH acts

on Sertoli cells stimulating their proliferation and expression of several trophic factors essential for spermatogenesis.

THE ENDOCANNABINOID SYSTEM

Endocannabinoids are lipid-signal molecules that are endogenous ligands for cannabinoid receptors, and together with enzymes responsible for their synthesis and degradation, they form the “ECS” (9). ECS is conserved from invertebrate to mammals and it assumes important role in physiological and pathological processes. The two best characterized endocannabinoids are *N*-arachidonoyl ethanolamine (AEA, anandamide) and 2 arachidonoyl glycerol (2-AG).

Endogenous cannabinoids bind to and activate their target receptors, causing several biological effects on different tissues. The main cannabinoid receptor targets type-1 (CB₁) and type-2 (CB₂) are seven trans-membrane G protein-coupled receptors (10). CB₁ is widely expressed in the nervous system mainly at the terminal ends of central and peripheral neurons, but it is also expressed in ovary, uterus, testis, vas deferens, and urinary bladder. CB₂ is mainly expressed in the cells of the immune system but it is also found in brainstem (11). ECBs are released from membrane phospholipid precursors by specific phospholipases, that are activated “on demand.” AEA synthesis is catalyzed by an *N*-acylphosphatidylethanolamine-specific phospholipase D (NAPE-PLD) (12). Similarly, the formation of 2-AG involves a rapid hydrolysis of inositol phospholipids by a specific phospholipase C (PLC) to generate diacylglycerol (DAG), which is then converted into 2-AG by an sn-1-DAG lipase (DAGL) (13). As lipid molecules, ECBs diffuse passively through the membrane, but the presence of a membrane transporter, EMT, that acts by a facilitated diffusion mechanism, has been hypothesized (14, 15). More recently an anandamide transporter named FLAT, which facilitates its translocation into cells has been identified in neural cells (16). The biological effects of ECBs depend on their lifespan in the extracellular space, which is limited by a re-uptake by cells. Once inside the cells ECBs are hydrolyzed by two specific enzymes: the fatty acid amide hydrolase (FAAH) cleaves AEA into arachidonic acid and ethanolamine, and the monoacylglycerol lipase (MAGL) (17) transforms the 2-AG into arachidonic acid and glycerol (18).

AEA, but not 2-AG, behaves also as an endovanilloid binding to the type-1 vanilloid receptor (transient receptor potential vanilloid 1, TRPV1) at an intracellular site (19). TRPV1 is a six trans-membrane spanning non-selective cation channel, whose expression is found mainly in specialized sensory neurons that detect painful stimuli (20). However it is now established that TRPV1 is expressed also in non-neuronal cells, such as keratinocytes and epithelial and endothelial cells, where it could play a wide variety of physiological functions.

THE ENDOCANNABINOID SYSTEM AND SPERMATOGENESIS ECS AND GERM CELLS

Following the discovery of ECS, many studies about its expression and function in male reproductive system have been carried out (21). The presence of components of ECS has been demonstrated in the testis, in the reproductive fluids and tracts, in different organisms from invertebrates to mammals. All the components

of the ECS have been identified in mammalian germ cells, from spermatogonia to spermatozoa.

First evidence of an effect of cannabinoid in male reproduction comes from a study in sea urchin in which it was demonstrated that exogenous cannabinoid THC directly reduced the fertilizing capacity of sperm (22) through the inhibition of the acrosome reaction (23). Next, endogenous cannabinoid AEA was shown to induce the same effects of THC on sea urchin sperm (24).

Endocannabinoids have been identified in human seminal plasma (25), in the amphibian cloacal fluid (26) and in mouse epididymis (27) indicating a role in the control of sperm functions. Most of the *in vitro* studies reported an adverse effect of AEA on sperm function with inhibition of motility, capacitation and acrosome reaction, and indicated a pivotal role of CB₁ receptor in mediating AEA effects. In humans, AEA inhibits sperm motility by decreasing mitochondrial activity and this effect was blocked by the CB₁ receptor antagonist SR141716 (28). In boar (*Sus scropha*), a stable AEA analog, methanandamide, reduces sperm capacitation and inhibits acrosome reaction (29). Also in frog *Rana esculenta* AEA has been shown to inhibit sperm motility through CB₁ receptor (26).

It has been described a role of CB₁ in spermiogenesis, when elongated spermatids are remodeled to form mature spermatozoa with a change in the chromatin structure. Indeed, genetic inactivation of CB₁ causes an inefficient histone displacement, poor chromatin condensation, and DNA damage in sperm (30), indicating a role of ECS in spermatid differentiation.

Further interesting findings supporting a role of AEA and CB₁ receptor on sperm function arise from the gene knockout animal models. In the absence of CB₁ signaling, sperm acquire motility precociously and the percentage of motile spermatozoa recovered from the caput of epididymis was higher with respect to wild-type mice, suggesting a physiological inhibitory regulation of endocannabinoids on sperm motility in the epididymis (31). Genetic loss of FAAH results in increased levels of AEA in the reproductive system and impairment of sperm fertilizing ability (32). These results lead to hypothesize that an “adequate tone” of AEA and the expression of CB₁ receptor are critical in the formation of morphologically and functionally normal sperm. In support of this observation, it has been recently reported that, in rats, *in vivo* administration of HU210, a synthetic analog of THC and a potent agonist of CB receptors, causes a marked impairment of spermatogenesis with reduction in total sperm count and motility, and a deregulation of the ECS, confirming the *in vitro* observations and indicating that the use of exo-cannabinoids may influence adversely male fertility (33).

Another molecular target of AEA is the vanilloid receptor TRPV1 (34), expressed in sperm cells of mouse (35), boar (29), bull (36), and humans (37). Activation of TRPV1 receptor by AEA, seems to play a role in the stabilization of the plasma membranes in capacitated boar sperm, preventing spontaneous acrosome reaction (29). Therefore, AEA can bring different signals in sperm cells, depending on the target receptor (CB₁ or TRPV1) that is activated.

Besides AEA, also the endocannabinoid 2-AG has been reported to affect male reproduction. Using mouse male germ cell populations at different stage of differentiation we highlighted a pivotal role of 2-AG and CB₂ receptor in mouse spermatogenesis (35).

We demonstrated that mammalian male germ cells, from mitotic to haploid stage, have a complete ECS which is modulated during spermatogenesis. Spermatogonia possess higher level of 2-AG that decreases in spermatocytes and drastically drops in spermatids. This correlates to higher level of biosynthetic (DAGL) and lower level of degrading enzymes (MAGL) in spermatogonia with respect to spermatocytes and spermatids. On the contrary, AEA levels remain unchanged during spermatogenesis and probably are crucial to maintain, locally, an appropriate “anandamide tone” for a correct progression of spermatogenesis as seen for normal development of mouse embryos (38). Interestingly, activation of CB₂ receptor in spermatogonia promotes their progression into meiosis as revealed by an increased number of cells positive for the meiotic marker SCP3 and by the expression of premeiotic and early meiotic genes. Thus, during spermatogenesis an autocrine endocannabinoid regulation of mitotic germ cell differentiation might occur as proposed in **Figure 1**.

Endocannabinoid 2-AG has been also found to play a role in regulating the ability of spermatozoa to become motile during their transit in the epididymis. 2-AG levels are high in mouse spermatozoa isolated from the caput of the epididymis, where they do not move regularly, and decrease dramatically in spermatozoa isolated from the cauda, where they acquire vigorous motility, suggesting that, along the epididymis, the decrease of 2-AG levels from caput to cauda promotes start-up of spermatozoa (27). Finally mouse sperm capacitation has been found to be linked to an enhancement of the endogenous tone of both AEA and 2-AG (39), underlying the important role of ECS in regulating important step of spermatogenesis and sperm functions.

With the aim to investigate, in humans, a possible relationship between male reproductive dysfunction and deregulation of the ECS, recent studies have shown a marked reduction of AEA and 2-AG content in the seminal plasma of infertile patients. This reduction in sperm from infertile versus fertile men can be determined by either an increased ratio of degradation/biosynthesis, or by lower levels of CB₁ mRNA expression (40, 41), indicating that the ECBs signaling is involved in the preservation of normal human sperm function.

ECS AND TESTICULAR SOMATIC CELLS

Endocannabinoid system components are expressed also in somatic cells of mammalian testis. Sertoli cells possess the

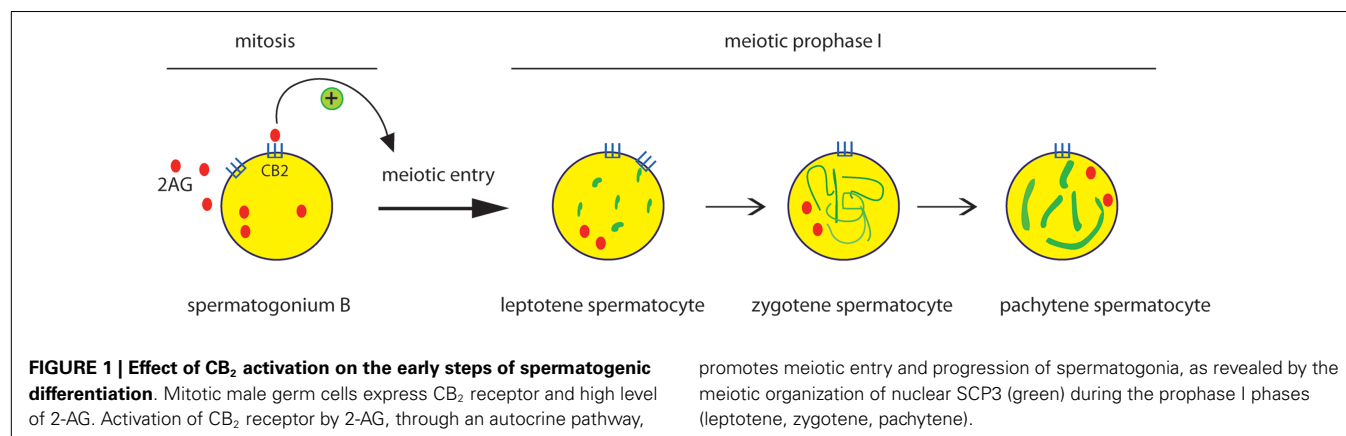
biochemical machinery to synthesize, transport, degrade, and bind both AEA (42) and 2-AG (43). Mouse Sertoli cells express a functional CB₂ receptor, an AEA membrane transporter and the AEA-degrading enzyme FAAH (42). AEA has been shown to have a pro-apoptotic effect on Sertoli cells, inducing DNA fragmentation. Lower level of AEA correlates with higher level of FAAH protein and with a decrease in Sertoli cell apoptosis, suggesting a protective and pro-survival role of FAAH in Sertoli cells. More interestingly, FAAH activity and expression is hormonally up-regulated in Sertoli cells by FSH and estrogen (43, 44).

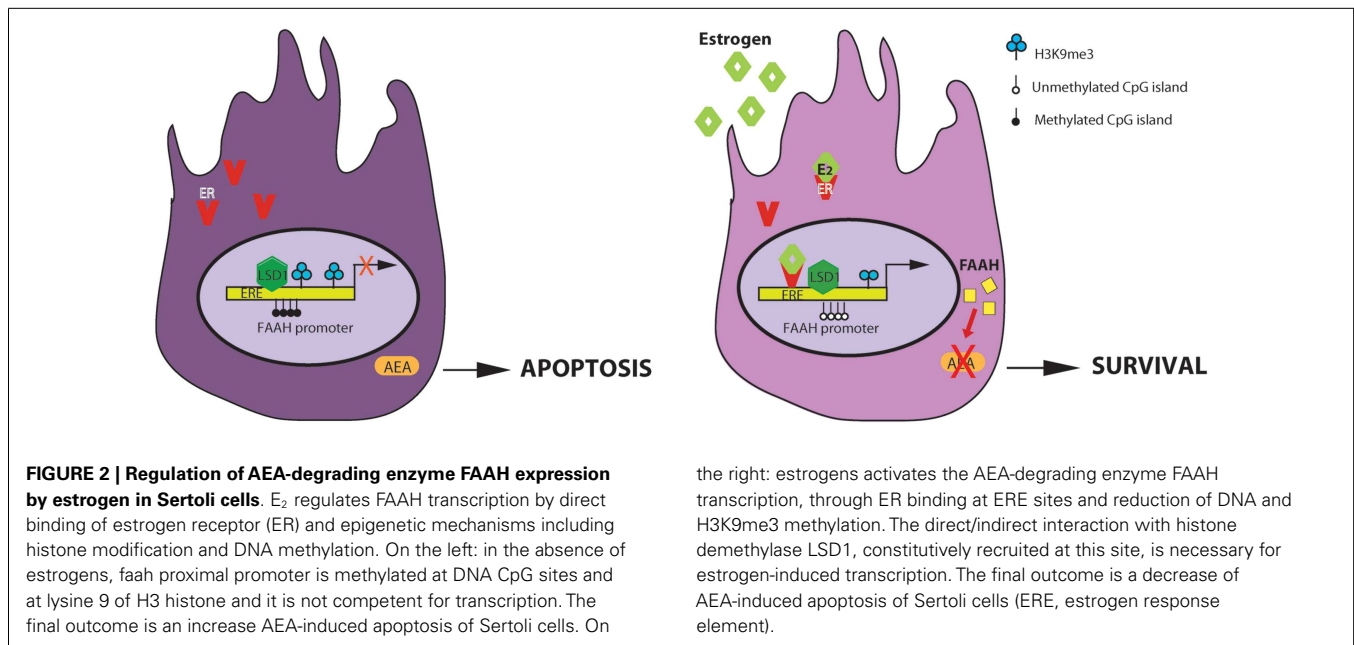
Rat Leydig cells express CB₁ which is modulated during development and it negatively correlates to cell division. Immature Leydig cells in mitosis were negative for CB₁, while immature non-mitotic Leydig cells were positive, indicating a negative effect of CB₁ on Leydig cell proliferation and suggesting that their differentiation may depend on the ECS (45).

THE ENDOCANNABINOID SYSTEM AND SEX HORMONE

As described above, the ECS is widely distributed in testicular cells and it is an important regulator of spermatogenesis and sperm functions. Recently, many evidence indicate the existence of interplay between ECS and sex hormones, testosterone and estrogen, thus stressing the relevant role of ECS in regulating male reproduction. Testosterone is produced by Leydig cells under the stimulation of LH and it is essential for the occurrence of events like blood-testis-barrier formation, germ cells progression beyond meiosis, mature sperm release. Sertoli cells are the major cellular target for the testosterone signaling and the absence of testosterone or of the androgen receptor, results in the failure of spermatogenesis and infertility. Several studies on human males smoking cannabis, reported a decrease in plasma levels of testosterone, FSH, and LH and this effect was also evident in animal studies after acute and chronic administration of THC (46, 47). Decreased levels of testosterone correlate to an inhibitory effect of cannabinoids on male sexual behavior (48). Moreover *in vitro* studies on Leydig cells showed a decrease in testosterone secretion induced by THC (49). Similarly endogenous cannabinoid AEA suppresses LH and testosterone levels in wild-type, but not in CB₁ knockout mice (50), providing evidence that the ECS acts to suppress testosterone levels.

It is now well documented that, beside testosterone, also estrogens are important modulator of male reproduction (51). The





presence of estrogens in male reproductive tracts of numerous mammals has been reported (52). Aromatase is the enzyme that converts irreversibly androgen into estrogens and is expressed, in mammals, in all testicular cells except peritubular cells. The biological effects of estrogens are mediated by the estrogen receptors α (ER α) and β (ER β), both expressed in mammalian testis. A role of estrogens in spermatogenesis is strongly supported by the observation that mice lacking estrogen receptors or aromatase are infertile and show impaired spermatogenesis in adulthood (53, 54).

Between all the components of ECS, the AEA-degrading enzyme *faah* gene has been demonstrated to be the only gene to be hormonally regulated in the testis. In Sertoli cells, FSH regulates FAAH expression and activity by triggering protein kinase A or aromatase-dependent pathway (42).

The PKA-dependent pathway enhances FAAH activity by inducing phosphorylation of other proteins that could activate the enzyme. On the other hand, the aromatase-dependent pathway, that leads to the conversion of testosterone into estrogens, induces FAAH expression at transcriptional level. Indeed we recently clarify the molecular mechanisms by which estrogens directly up-regulate *faah* gene transcription (55). This involves direct binding of ER to the ERE sites in the *faah* promoter and the induction of epigenetic modifications in order to confer transcriptional competence.

As presented in **Figure 2**, in Sertoli cells, E₂ engages ER, which binds to ERE sites in the *faah* proximal promoter determining demethylation of both DNA, at CpG site, and histone H3, at lysine 9 (H3K9). The presence of histone demethylase LSD1, which is recruited at this site, ensures estrogens stimulation of *faah* transcription. LSD1 could interact with ligand-bound ER or with other different partners and activate gene transcription. The biological relevance of E₂-stimulation of FAAH expression consists in decreasing AEA levels in Sertoli cells and protect them against apoptosis induced by AEA. The pro-survival role of E₂ in Sertoli

cells has a clear impact on spermatogenesis. In fact regulation of Sertoli cell apoptosis could be important to maintain their population size, and consequently, to sustain a normal spermatogenic output.

This is not the only example about the cross-talks between estrogens and ECS in the testis. Recent evidences reveal that estrogens affect spermiogenesis and regulate chromatin remodeling of germ cells (56). Indeed, in mice, genetic loss of CB₁ receptor causes a reduction in FSH and estrogen plasma levels and alteration in spermatid differentiation due to an inefficient histone displacement in the sperm. Estrogens treatment is able to rescue histone displacement suggesting a role in preserving chromatin condensation in spermatozoa.

CONCLUDING REMARKS

In this mini-review we highlighted the physiological role of ECS and its interplay with sex hormones, in male reproduction. A full comprehension of the molecular events regulated by ECS in the testis will allow to better define the “protective” role of this system in maintaining and ensuring the correct progression of spermatogenesis and the formation of mature and fertilizing sperm. Interfering with this system by exposure to exogenous cannabinoids, may alter the physiological function of ECS in male reproduction thus affecting male fertility.

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Does kisspeptin signaling have a role in the testes?

Hua Mei¹, Joanne Doran², Victoria Kyle³, Shel-Hwa Yeo³ and William H. Colledge^{3*}

¹ Jules Stein Eye Institute, University of California, Los Angeles, CA, USA

² Takeda Cambridge Ltd., Cambridge, UK

³ Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK

Edited by:

Riccardo Pierantoni, Second University of Naples, Italy

Reviewed by:

Rosanna Chianese, Second University of Naples, Italy

Rosaria Meccariello, University of Naples Parthenope, Italy

*Correspondence:

William H. Colledge, Department of Physiology, Development and Neuroscience, University of Cambridge, Downing Street, Cambridge, CB2 3EG, UK
e-mail: whc23@cam.ac.uk

Kisspeptins are a family of overlapping neuropeptides encoded by the *Kiss1* gene that regulate the mammalian reproductive axis by a central action in the hypothalamus to stimulate GnRH release. Kisspeptins and their receptor (GPR54 also called KISS1R) are also expressed in the testes but a functional role in this tissue has not been confirmed. We examined which cell types in the testes expressed kisspeptin and its receptor by staining for β -galactosidase activity using tissue from transgenic mice with *LacZ* targeted to either the *Kiss1* or the *Gpr54* genes. Expression of both genes appeared to be restricted to haploid spermatids and this was confirmed by a temporal expression analysis, which showed expression appearing with the first wave of haploid spermatid cells at puberty. We could not detect any kisspeptin protein in spermatids however, suggesting that the *Kiss1* mRNA may be translationally repressed. We tested whether kisspeptin could act on Leydig cells by examining the effects of kisspeptin on the immortalized Leydig cell line MA-10. Although MA-10 cells were shown to express *Gpr54* by RT-PCR, they did not respond to kisspeptin stimulation. We also tested whether kisspeptin could stimulate testosterone release by a direct action on the testes using explants of seminiferous tubules. The explants did not show any response to kisspeptin. The functional integrity of the MA-10 cells and the seminiferous tubule explants was confirmed by showing appropriate responses to the LH analog, human chorionic gonadotropin. These data suggest that kisspeptin signaling does not have a significant role in testes function in the mouse.

Keywords: kisspeptins, *Gpr54/Kiss1r*, testes, Leydig cells, testosterone secretion, spermatids

INTRODUCTION

Kisspeptins, encoded by the *Kiss1* gene, are an overlapping family of neuropeptides required for activation and maintenance of the mammalian reproductive axis [for review, see Ref. (1)]. Kisspeptins are encoded as a 145-amino-acid precursor protein in humans that is cleaved into shorter peptides (Kp54, Kp14, Kp13, and Kp10) that share a common RF-amide C-terminal decapeptide sequence. They all act as potent stimulators of GnRH release by signaling through the G-protein coupled receptor, GPR54 (also called KISS1R) expressed by GnRH neurons. Disruption of kisspeptin signaling causes hypogonadotropic hypogonadism in mice and humans (2–7). Mutant mice do not undergo sexual maturation at puberty and have low gonadotropic and sex steroid hormones levels caused by defective GnRH secretion from the hypothalamus. Conversely, activating mutations of *GPR54* cause precocious puberty in humans (8).

In addition to the role of kisspeptins in the central regulation of the reproductive axis, *Gpr54* expression has been detected in the testes of humans (9, 10), mice (3), rats (11), and frogs (12) raising the possibility that kisspeptins may also act at this location. Kisspeptins have been immunolocalized to Leydig cells in mice (13) and kisspeptin and GPR54 have been detected in human sperm, mainly localized to the head, neck, and the flagellum midpiece (14).

Although the expression profile of *Kiss1* and *Gpr54* suggests that kisspeptin signaling might have a role in the testes, very little

has been done to test this hypothesis. The data to support a role for kisspeptin in the testes is largely circumstantial and based on discrepancies between the normally direct relationship of LH and testosterone levels. For example, in rats, chronic (13 days) subcutaneous administration of kisspeptin reduced testosterone secretion without a significant decrease in plasma LH (15). In Rhesus monkeys, continuous intravenous infusion of human kisspeptin over 4 days maintained plasma testosterone levels even after the LH stimulation levels had fallen (16). When circulating testosterone levels were expressed relative to LH levels, the [T]:[LH] ratios were significantly higher in the morning in the high dose kisspeptin treatment group compared to the vehicle group. This led to the suggestion that kisspeptins might augment the LH-induced secretion of testosterone. Support for this has come from kisspeptin administration in Rhesus monkeys pre-treated with acyline, a GnRH receptor antagonist, to allow the intratesticular actions of kisspeptin to be evaluated without the confounding effects of LH release from the pituitary (17). Kisspeptin administration significantly increased human chorionic gonadotropin (hCG)-stimulated testosterone levels in acyline treated monkeys compared to hCG treatment alone (17) suggesting that kisspeptin might enhance LH responses in Leydig cells.

To further investigate the possible function(s) of kisspeptin in the mouse testes, we used transgenic mice with *Kiss1* and *Gpr54* alleles targeted with a *LacZ* reporter gene to define the testicular cell expression profile of these genes. We also tested whether

kisspeptins can stimulate testosterone release from an immortalized mouse Leydig cell line and from primary testes explants in culture.

MATERIALS AND METHODS

MOUSE LINES AND MAINTENANCE

The 129S6/SvEv mutant mice with a targeted disruption of the *Gpr54* or *Kiss1* genes were generated as described previously (2, 5). All mice were maintained on a 12:12-h light-dark cycle (light on between 6:30 a.m. and 6:30 p.m.) with *ad libitum* access to food and water. Experimental procedures were performed under authority of a Home Office Project License and approved by a Local Ethics Committee.

MA-10 CELL CULTURE

The mouse Leydig tumor cell line MA-10 (18) was a generous gift from Dr. Mario Ascoli (University of Iowa, Iowa City, IA, USA). The MA-10 cells were maintained in RPMI-1640 medium (Sigma-Aldrich, Dorset, UK) containing 10% horse serum (Sigma-Aldrich, Dorset, UK) and 10% newborn calf serum (Sigma-Aldrich, Dorset, UK), and the cells were grown at 37°C in an humidified atmosphere of 5% CO₂. The growth medium was refreshed every 2 days to provide sufficient nutrition for cell growth.

RT-PCR GENE EXPRESSION ANALYSIS OF MA-10 CELLS

Total RNA was isolated from MA-10 cells using a NucleoSpin® RNA II kit (Cat No: 740955, MACHEREY-NAGEL GmbH & Co. KG) following the manufacturer's protocol. The time of the on-column DNA digestion was extended from 15 to 45 min to ensure complete removal of genomic DNA. The RNA was reverse transcribed into cDNA using SuperScript III Reverse Transcriptase (Cat No: 18080-044, Invitrogen, UK) following the protocol provided by the manufacturer. Standard PCR was performed as follows: the samples were denatured for 5 min at 95°C and amplified for 44 cycles (30 s at 93°C, 1 min at 60°C, and 2 min at 70°C). The primer sequences were: *Kiss1* (Forward: tgctgcttctcctgtgtc; Reverse: gccgaaggagttccagtgta, 310 bp product), *Gpr54* (Forward: gccttcgctctacaacctgctg; Reverse: aagccatagagcagcg-gattgagc, 367 bp product), *GnRH* (Forward: cggcattctactgctgactg; Reverse: catcttctctgctggcttc, 229 bp product), β -actin (Forward: ctgtattccccctcatcgtg; Reverse: gggtcaggatacctctcttg, 113 bp product). RNA without a reverse transcription step was used as a negative control for identification of genomic DNA contamination and cDNA from wild-type hypothalamus was used as a positive control for *Kiss1* amplification.

X-GAL STAINING OF TESTES SECTIONS

Testes were fixed in 1% paraformaldehyde/PBS overnight at 4°C, cryoprotected with 30% sucrose/PBS overnight at 4°C, and cryosectioned at 20 μ m onto poly-lysine coated slides. Sections were air dried at room temperature, rehydrated in PBS and β -galactosidase activity detected using a *LacZ* staining solution [1 mM MgCl₂, 1 mg/ml X-gal (5-bromo-4-chloro-3-indolyl β -D-galactopyranoside), 5 mM potassium ferricyanide, 5 mM potassium ferrocyanide in PBS] at 37°C overnight, and counterstained with 1% Saffronin.

IMMUNOHISTOCHEMISTRY TO DETECT KISSPEPTIN EXPRESSION

Testes were fixed in 4% paraformaldehyde/Tris-buffered saline (TBS) for 5 h at room temperature and transferred to 30% sucrose/TBS overnight at 4°C. The testes were then cryosectioned at 15 μ m, air dried at room temperature, rehydrated in TBS, and slide-mounted immunohistochemistry was performed to detect kisspeptin expression. Polyclonal antibody AC566 raised in rabbits against mouse Kp10 was a generous gift from Alain Caraty, Tours, France. Characterization and specificity of AC566 has been described previously (5, 19–21).

Sections were treated with 3% hydrogen peroxide for 15 min to quench endogenous peroxidase and then washed in TBS. To visualize kisspeptin expression, sections were incubated with the antibody at 1:2000 dilution for 8 h at room temperature. For secondary antibody labeling, sections were incubated with biotinylated goat anti-rabbit (1:100; Cat No: BA-1000, Vector Laboratories, Peterborough, UK) immunoglobulins at room temperature followed by incubation with Vector avidin-peroxidase (1:50; Cat No: PK-4000, Vector Laboratories, Peterborough, UK). Finally, the sections were rinsed and immunoreactivity was revealed with glucose-oxidase and nickel-enhanced diaminobenzidine hydrochloride (12.5 mg/ml). Sections were counterstain with hematoxylin, dehydrated in ethanol followed by HistoClear, and then coverslipped with DPX.

PROGESTERONE RELEASE EXPERIMENTS FROM MA-10 CELLS

The MA-10 cells were seeded at 2.5×10^5 cells/well (24-well plates) 24 h before the hormone treatment. The cells were treated with increasing concentrations of Kp10 (human Metastin 45–54) (1, 10, or 20 μ M) (Cat No: M2816, Sigma-Aldrich, Dorset, UK) or Kp10 followed by hCG (0.012 IU/ml as the final concentration) (Cat No: CG5, Sigma, Saint Louis, MO, USA). PBS was added as a negative control. Each condition was tested in triplicate. After 4 h, the media was collected for progesterone measurement. After collection of media, the MA-10 cells were rinsed twice with PBS and lysed in 1 \times lysis buffer (reporter lysis buffer, Cat No: E397A, Promega, UK) by a freeze-thaw cycle. The lysate was briefly centrifuged and the protein content of the supernatant determined with a Bio-Rad Bradford Assay following the standard protocol.

PRIMARY CULTURE OF TESTES EXPLANTS

The testes from adult wild-type mice were cut into two pieces (approximately 40 mg/piece) without removing the tunica and each piece was cut and flattened to a 1-mm thickness on a Nylon membrane (Cat No: 1417240, Boehringer-Mannheim, Indianapolis, IN, USA) floating in phenol red-free DMEM medium (Cat No: 21063, GIBCO) (300 μ l/well for 12-well plate) supplemented with 1 \times penicillin/streptomycin. The tissues were immediately treated with vehicle, Kp10 (1 μ M), hCG (0.6 IU/ml), or a mixture of Kp10 (1 μ M) and hCG (0.6 IU/ml), respectively. Each condition was tested in at least four repeat wells. The tissues were cultured at 37°C in an atmosphere of 5% CO₂ and the media collected at different time points. Fresh media was added at each time point after media collection.

HORMONE ASSAYS

Testosterone and progesterone were measured using ELISA kits (Cat No: EIA1559 and EIA1561 from DRG International, USA)

according to the manufacturer's instructions. The testosterone ELISA kit had a sensitivity of 0.083 ng/ml, an inter-assay variation of 6.7%, and an intra-assay variation of 3.3%. The progesterone ELISA kit had a sensitivity of 0.045 ng/ml, intra-assay variation of 7%, and inter-assay variation of 5%.

RESULTS

Gpr54 AND *KISS1* ARE EXPRESSED IN THE MOUSE TESTES

The *Gpr54* and *Kiss1* alleles in the transgenic mice have been tagged with a *LacZ* gene that allows their gene expression patterns to be visualized by staining for β -galactosidase activity. Staining was observed within seminiferous tubules from both *Kiss1*^{+/-} (Figure 1A) and *Gpr54*^{+/-} mice (data not shown) but not in wild-type mice (Figure 1A). Background staining was observed in the epididymis and the vas deferens of wild-type mice as the epithelial cells in these tissues express an endogenous galactosidase-like enzymatic activity. To define the cells in which *Kiss1* and *Gpr54* are expressed, cryosection of testes were stained for β -galactosidase activity. The staining in cryosections was localized to the region of the seminiferous tubules that contained round spermatids (arrowed in Figures 1B,C). The spermatids are easily recognized as they have smaller nuclei than spermatocytes and are four-times more abundant as they have just completed meiosis. Very faint β -galactosidase staining was also found in the Leydig cells in the *Gpr54*^{+/-} mice (Figure 1D) but not in the *Kiss1*^{+/-} mice (data not shown).

To confirm that the β -galactosidase expression was localized to spermatid cells, the time point at which expression was first observed during the first spermatogenic cycle was determined. Expression of *Kiss1* and *Gpr54* could not be observed prior to 3 weeks of age but staining was seen from 1 month of age which corresponds to the time at which the spermatids first appear in mice (Figure 2).

Kisspeptin protein expression in the mouse testes was visualized using a well characterized rabbit antiserum highly specific for mouse Kp10 (20). Strong immunoreactivity was found in Leydig cells with no staining in spermatids (Figure 1E). As a control for antibody specificity, testes sections from *Kiss1* mutant mice lacking kisspeptin protein were used and no immunoreactivity was observed (Figure 1E). This Leydig staining may be non-specific however, as no kisspeptin protein was detected in *Gpr54* mutant mice (data not shown).

Kp10 DOES NOT STIMULATE STEROIDOGENESIS IN THE LEYDIG CELL LINE, MA-10

To test whether Kp10 could stimulate testosterone release, the mouse Leydig cell line, MA-10, was used (18, 22). MA-10 cells, like normal Leydig cells, express LH receptors and respond to hCG stimulation. MA-10 cells have low expression and activity of P450c17 that is the enzyme that converts progesterone into 17-OH progesterone and finally into testosterone, thus MA-10 cells produce progesterone as the principle steroid hormone instead of testosterone (18, 22).

The MA-10 cells were examined for expression of *Kiss1* and *Gpr54* to determine whether they might be capable of responding to kisspeptins. There was a PCR product for *Gpr54* (Figure 3A), indicating that MA-10 cells endogenously express this gene but

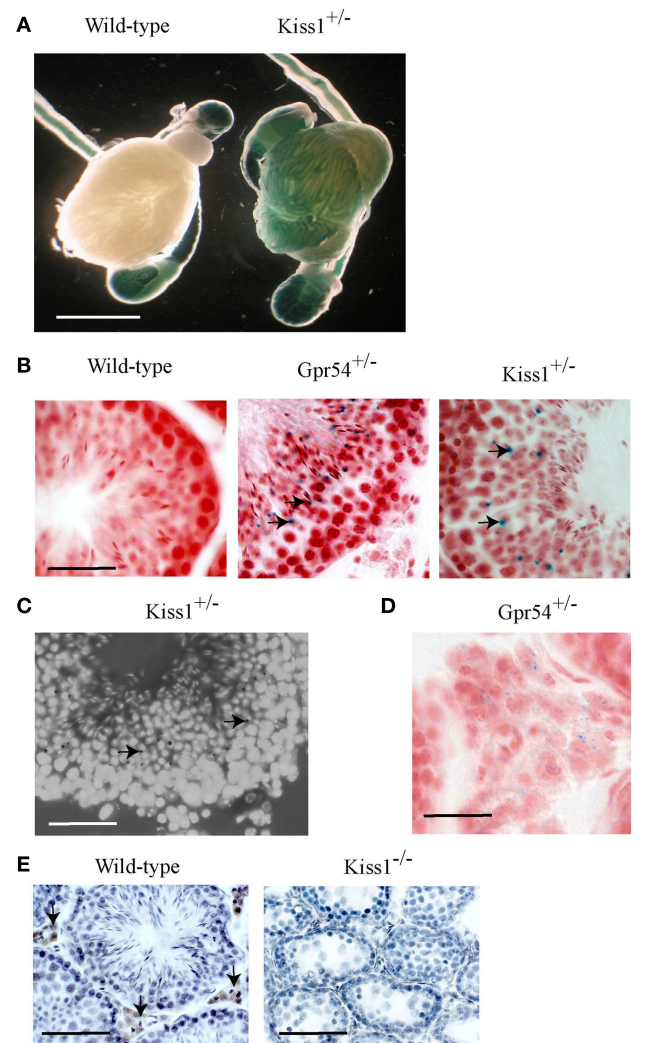
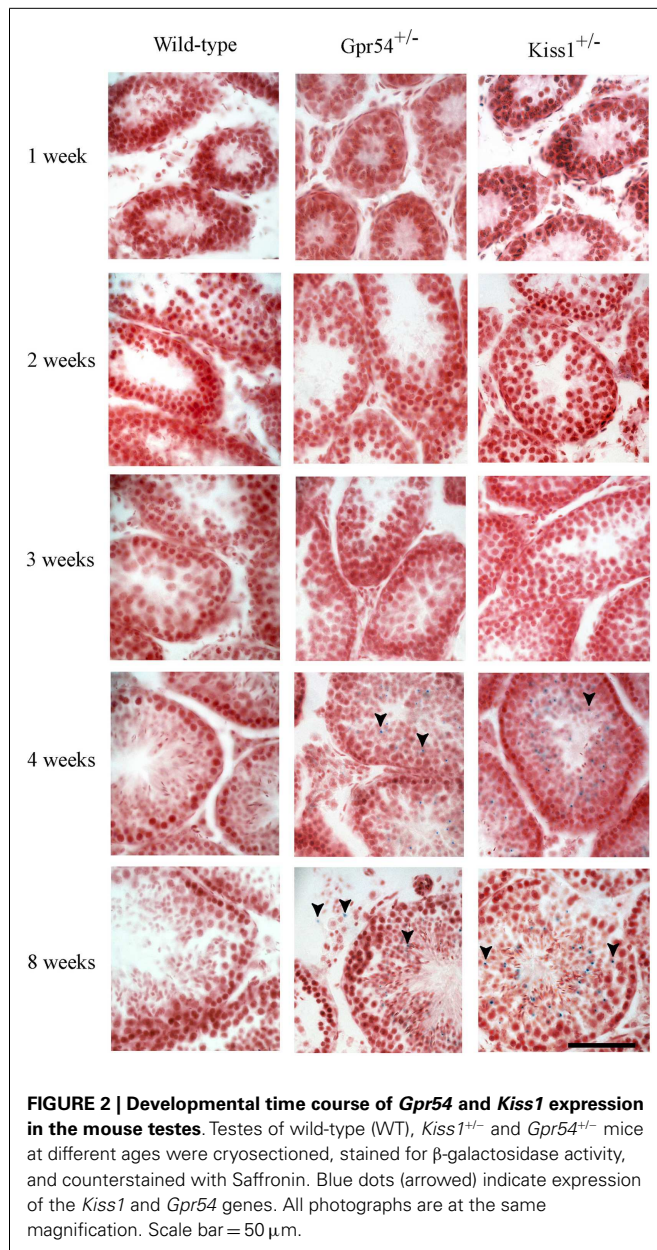


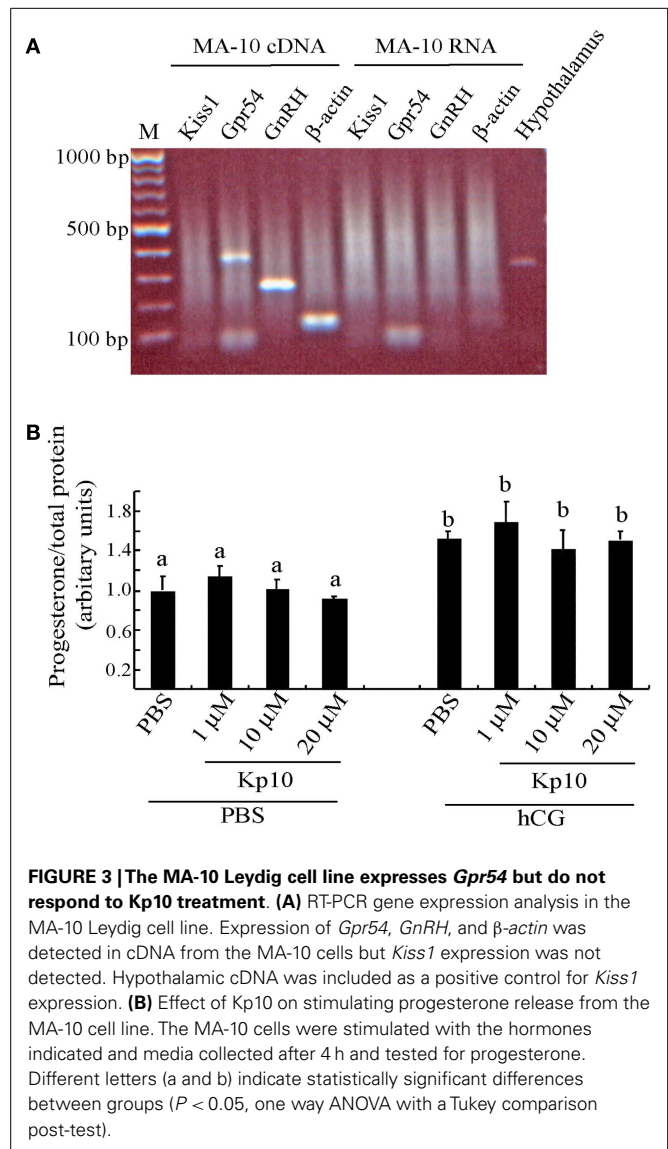
FIGURE 1 | *Kiss1* and *Gpr54* expression in the mouse testes.

(A) Expression of *Kiss1* in seminiferous tubules of the testes visualized by X-gal staining (blue) for β -galactosidase activity. Note the non-specific staining in the epididymis and vas deferens of the wild-type testes. Scale bar = 5 mm. (B) Cryosections of testes from adult wild-type, *Gpr54*^{+/-}, and *Kiss1*^{+/-} mice showing expression (arrowed) localized to spermatid cells of seminiferous tubules. Sections were stained for β -galactosidase activity (blue) and counterstained with Saffronin (red). Scale bar = 100 μ m. (C) Testes cryosection from *Kiss1*^{+/-} mice stained for β -galactosidase activity (black dots, arrowed) and counterstained with DAPI to visualize cell nuclei illustrating clearer expression in spermatid cells. Scale bar = 100 μ m. (D) Low expression of *Gpr54* in Leydig cells visualized by X-gal staining. Scale bar = 50 μ m. (E) Kisspeptin immunoreactivity localized to Leydig cell in wild-type mice (arrowed) but not *Kiss1* mutant mice. Scale bar = 200 μ m.

there was no detectable *Kiss1* expression in the MA-10 cells. The MA-10 cell also expressed GnRH and β -actin transcripts (Figure 3A). No products were observed when non-transcribed RNA was used as the template, indicating that the RNA was free of genomic DNA contamination. A *Kiss1* product was observed when hypothalamic cDNA was used from wild-type mice as a positive control.



As the MA-10 cells expressed the kisspeptin receptor, they were tested to see whether Kp10 could stimulate progesterone release. The cells were divided into two experimental groups. The first group was treated with increasing concentrations of human Kp10 followed by PBS, and the second group was treated with Kp10 followed by hCG to examine possible synergistic effects. After 4 h, the media was assayed for progesterone, which was normalized to the protein content of the cell lysate to correct for variations in cell number. No significant difference in progesterone release was found between the vehicle (PBS) treatment and any of the three concentrations of Kp10 (**Figure 3B**), indicating that Kp10 cannot enhance progesterone release from the Leydig cell line even at a high concentration (20 μ M). There was also no significant difference in progesterone release between the cells treated with hCG



alone or those treated with hCG and Kp10 (**Figure 3B**), which suggests that Kp10 has no synergistic effect on progesterone release from MA-10 cells activated by hCG. However, there was a significant difference ($P < 0.05$) in progesterone release between the cells treated with PBS and those treated with hCG (**Figure 3B**), which indicates the functional responsiveness of the cells to hormonal stimulation.

Kp10 DOES NOT STIMULATE TESTOSTERONE RELEASE FROM TESTES TISSUE CULTURE EXPLANTS

To examine the possible action of Kp10 in a more physiological system, we tested whether Kp10 could stimulate testosterone release from primary explants of mouse testes. Pieces of adult wild-type mouse testes of similar weight (approximately 40 mg/piece) were treated with vehicle (PBS), Kp10 (1 μ M), hCG (0.6 IU/ml), or a mixture of Kp10/hCG. Each condition was repeated with at least four samples. The media was collected at different time intervals for testosterone measurements. During the 0- to 4-h

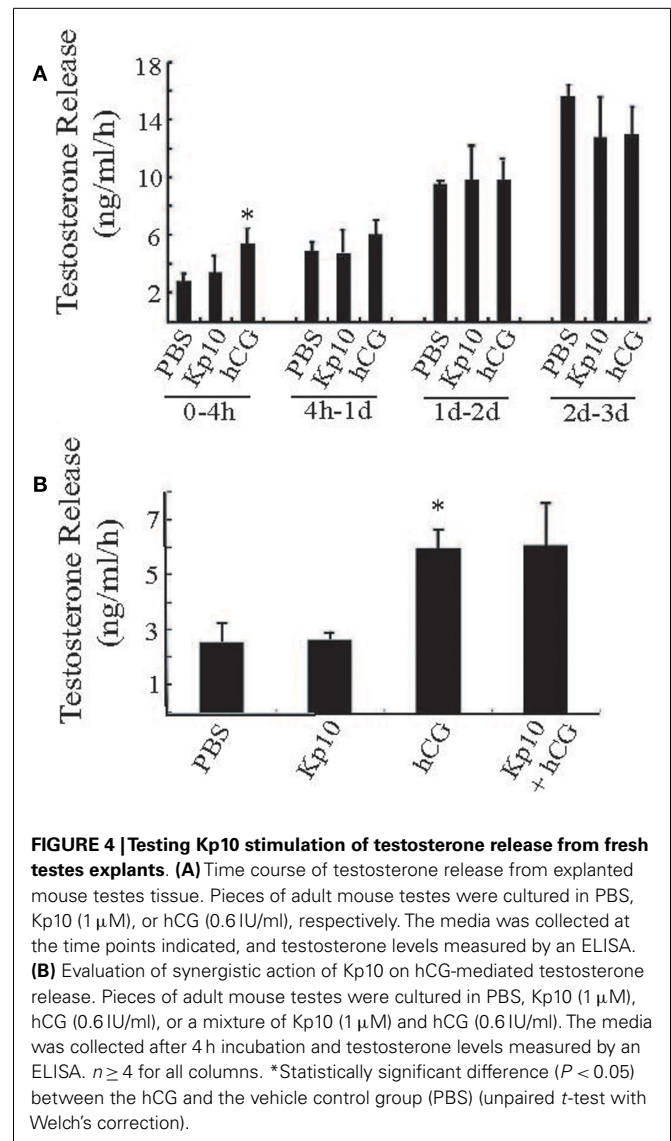
time period, the testosterone released after hCG treatment was significantly higher than that with the vehicle (PBS) treatment (Figure 4A), indicating that the cultured testes maintained the ability to respond to hormone stimulation. However, there was no obvious stimulation of testosterone release after Kp10 treatment. Also, the testosterone released in the PBS and hCG groups was not significantly different at incubation times >4 h due to increased unstimulated testosterone release (Figure 4A). Therefore, a 4-h incubation time was used to test whether there was any synergy between Kp10 and hCG in stimulating testosterone release (Figure 4B). Once again, testosterone release after hCG treatment was significantly higher than after PBS treatment (Figure 4B). No difference in testosterone release was detected between the testes fragments cultured in PBS or Kp10. There was also no difference in testosterone release between testes treated with hCG only and testes treated with hCG and Kp10 together. These data indicate that Kp10 has no effect on testosterone release from adult mouse testes and it has no synergistic action on testosterone release stimulated by hCG.

DISCUSSION

Kisspeptin neuropeptides are important central regulators of the mammalian reproductive axis with kisspeptin neurons acting upstream of GnRH neurons to stimulate GnRH release. In addition to this central role however, the expression profiles of *Kiss1* and *Gpr54* suggest that they may also have a function in peripheral tissues including the testes. We have shown using expression of a gene targeted *LacZ* reporter gene, that *Kiss1* and *Gpr54* are expressed by round spermatid cells in the mouse testes. Expression profiling during postnatal gonadal maturation confirmed this as the expression only started to emerge after 1 month of age, which is the time when the spermatids first appear. As both *Kiss1* and *Gpr54* were found to be expressed in spermatids, this raises the possibility that autocrine or paracrine kisspeptin signaling might be involved in spermiogenesis.

Round spermatid cells have just completed meiosis and will subsequently undergo the structural changes required to produce spermatozoa. During this structural remodeling, most of the cytoplasm is removed from the spermatids by the Sertoli cells, which will result in loss of β -galactosidase activity, which might explain why we do not observe staining in elongating spermatids and spermatozoa. Similarly, this cytoplasmic removal would remove any kisspeptin protein but GPR54 should be retained by virtue of its location in the plasma membrane. Indeed, GPR54 has been detected in the head region of human sperm and addition of kisspeptin can produce a modest rise in $[Ca^{2+}]_i$ and sperm motility (14).

The functional significance of *Kiss1* and *Gpr54* expression in spermatids and sperm is still not clear however. The infertility of the *Kiss1* and *Gpr54* mutant mice prevents performing functional tests with mutant sperm. It might be possible to initiate spermatogenesis in the mutant mice with pulsatile FSH and subcutaneous testosterone delivery. Although we have shown that *Kiss1* and *Gpr54* mutant mice can initiate a low level of spermatogenesis when given a chow diet containing phytoestrogens (23), the number of sperm that can be isolated from the vas deferens and epididymis is too small for functional studies. It is noteworthy,



however, that several male patients with mutations in *GPR54* and hypogonadotropic hypogonadism have responded to exogenous hormone treatment and achieved fertility [for review, see Ref. (24)] suggesting that in humans, GPR54 function is not essential for sperm function.

There is an important caveat to this expression data however. Although the *LacZ* expression indicates that the *Kiss1* promoter is transcriptionally active in round spermatid cells, we could not detect kisspeptin immunoreactivity using a validated antibody capable of visualizing kisspeptin in the hypothalamus of mice (25). It is possible that the expression level of the kisspeptin protein is below the limits of detection and that X-gal staining for β -galactosidase activity is more sensitive. Alternatively, it is possible that *Kiss1* transcripts are not translated into protein in spermatid cells. Several gene transcripts encoding proteins required for late spermiogenesis are expressed in round spermatids and translationally repressed until the elongating spermatid stage (26). Translationally repressed mRNAs have unusually long poly(A) tails

of approximately 180 nt and translation is associated with shortening of these tails (27). The presence of long poly(A) tails on *Kiss1* transcripts, which are not subsequently shortened, might provide a mechanism for the proposed translational repression in spermatids.

We detected kisspeptin immunoreactivity in Leydig cells of wild-type mice similar to that reported by Anjum and colleagues (13). The specificity of this immunoreactivity was suggested by absence of staining in *Kiss1* mutant mice, which do not produce any kisspeptin protein (5). This notwithstanding, we believe that the kisspeptin immunoreactivity found in the Leydig cells may not be authentic for the following reasons. Firstly, we did not detect *Kiss1* promoter activity in Leydig cell by β -galactosidase staining in *Kiss1*^{+/-} mice. Secondly, we did not detect *Kiss1* transcripts by RT-PCR in the immortalized Leydig cell line MA-10 although this may be a consequence of the cell immortalization process and the tendency for *Kiss1* expression to be suppressed during cell transformation and tumorigenesis. Finally, we failed to detect kisspeptin immunoreactivity in the Leydig cells of *Gpr54* mutant mice, which can produce kisspeptin protein. We believe that the staining pattern observed in the Leydig cells of the wild-type mice is an artifact perhaps associated the high levels of steroidogenesis in these cells, which does not occur in *Kiss1* or *Gpr54* mutant mice.

We also observed a very low level of β -galactosidase staining in Leydig cells from *Gpr54*^{+/-} mice suggesting that these cells might express GPR54 protein. This was consistent with our detection of *Gpr54* transcripts in the immortalized mouse Leydig cell line MA-10. Unfortunately, there are no anti-GPR54 antibodies with sufficient specificity to confirm expression of the endogenous GPR54 protein in the Leydig cells.

If there was co-expression of GPR54 and kisspeptin in Leydig cells, this would allow local autocrine or paracrine action within the testes. Previously published work has suggested that kisspeptins are able to enhance testosterone release after LH stimulation (17). We therefore examined whether Kp10 was able to stimulate testosterone release from the MA-10 cell line as well as testes fragments in culture. We found no evidence that Kp10 could directly stimulate testosterone release or enhance the actions of LH. This is in contrast to the recent data that kisspeptin administration significantly increased hCG-stimulated testosterone levels in acyline treated Rhesus monkeys compared to the responses with hCG treatment alone (17). As the acyline inhibits endogenous LH secretion from the pituitary, these responses suggest a direct, synergistic action of kisspeptin on the testes. The reason for the difference from our data is not known, but apart from a species difference, it might be that the enhancement by kisspeptin requires a sub-threshold level of LH stimulation and the concentration of hCG that we used was too high. It would be informative to test Kp10 responses to a lower range of hCG treatments in the testes explants. It is noteworthy, however, that Huma and colleagues have found that an intravenous injection of the kisspeptin antagonist p234 does not alter plasma testosterone levels in adult Rhesus macaques (28) suggesting that any action of kisspeptin on the testes is small. This conclusion is consistent with the observation that fertility can be restored in *Gpr54* mutant mice by expression of a *Gpr54* transgene in GnRH neurons (29) indicating that

GPR54 expression in the testes is also not essential for fertility in mice.

In summary, we have shown that the *Kiss1* and *Gpr54* are both expressed in round spermatid cells of the mouse testes and *Gpr54* is expressed by Leydig cells but we have not found any supporting data that kisspeptin signaling in the testes has a major role in spermatogenesis or testosterone secretion in the mouse.

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Hypothalamic-pituitary-gonadal endocrine system in the hagfish

Masumi Nozaki *

Sado Marine Biological Station, Faculty of Science, Niigata University, Sado, Japan

Edited by:

Silvia Fasano, Second University of Naples, Italy

Reviewed by:

Rosanna Chianese, Second University of Naples, Italy

Rosaria Meccariello, University of Naples Parthenope, Italy

***Correspondence:**

Masumi Nozaki, Sado Marine Biological Station, Faculty of Science, Niigata University, Tassha, Sado, Niigata 952-2135, Japan
e-mail: nozaki@cc.niigata-u.ac.jp

The hypothalamic-pituitary system is considered to be a seminal event that emerged prior to or during the differentiation of the ancestral agnathans (jawless vertebrates). Hagfishes as one of the only two extant members of the class of agnathans are considered the most primitive vertebrates known, living or extinct. Accordingly, studies on their reproduction are important for understanding the evolution and phylogenetic aspects of the vertebrate reproductive endocrine system. In gnathostomes (jawed vertebrates), the hormones of the hypothalamus and pituitary have been extensively studied and shown to have well-defined roles in the control of reproduction. In hagfish, it was thought that they did not have the same neuroendocrine control of reproduction as gnathostomes, since it was not clear whether the hagfish pituitary gland contained tropic hormones of any kind. This review highlights the recent findings of the hypothalamic-pituitary-gonadal endocrine system in the hagfish. In contrast to gnathostomes that have two gonadotropins (GTH: luteinizing hormone and follicle-stimulating hormone), only one pituitary GTH has been identified in the hagfish. Immunohistochemical and functional studies confirmed that this hagfish GTH was significantly correlated with the developmental stages of the gonads and showed the presence of a steroid (estradiol) feedback system at the hypothalamic-pituitary levels. Moreover, while the identity of hypothalamic gonadotropin-releasing hormone (GnRH) has not been determined, immunoreactive (ir) GnRH has been shown in the hagfish brain including seasonal changes of ir-GnRH corresponding to gonadal reproductive stages. In addition, a hagfish PQRamide peptide was identified and shown to stimulate the expression of hagfish GTH β mRNA in the hagfish pituitary. These findings provide evidence that there are neuroendocrine-pituitary hormones that share common structure and functional features compared to later evolved vertebrates.

Keywords: hagfish, agnathan, cyclostomes, HPG axis, pituitary gland, gonadotropin, GnRH, estradiol

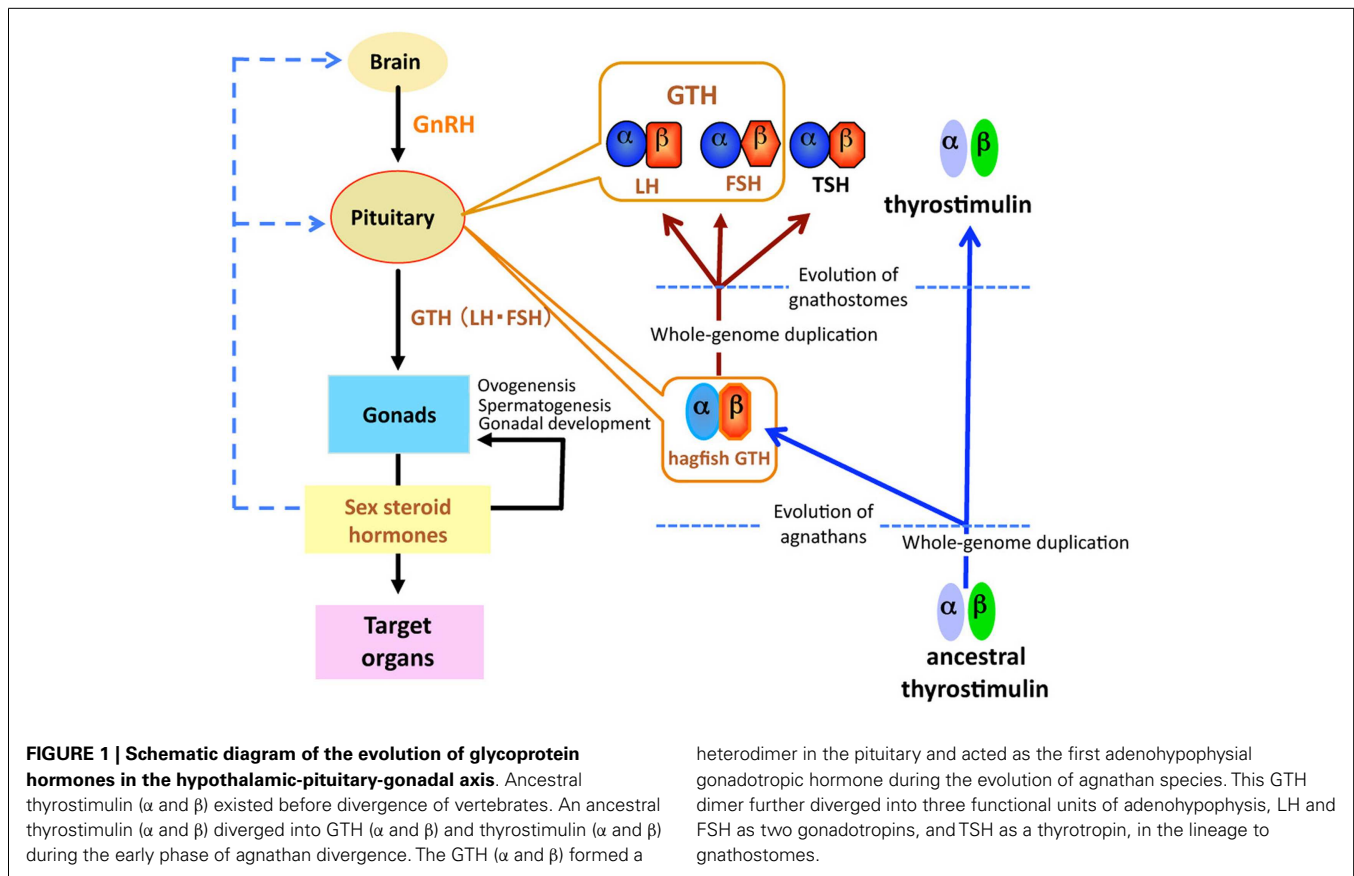
INTRODUCTION

Reproduction in gnathostomes (jawed vertebrates) is controlled by a hierarchically organized endocrine system called the hypothalamic-pituitary-gonadal (HPG) axis (1). In spite of the diverged patterns of reproductive strategies and behaviors within this taxon, this endocrine network is remarkably conserved throughout gnathostomes. In response to hypothalamic gonadotropin-releasing hormone (GnRH), gonadotropins (GTHs) are secreted from the pituitary and stimulate the gonads, where they induce the synthesis and release of sex steroid hormones, which in turn elicit growth and maturation of the gonads (Figure 1).

The pituitary gland is present in all vertebrates from agnathans (jawless fishes) to mammals and consists of the same two principal elements, the neurohypophysis and adenohypophysis. The neurohypophysis develops from the floor of the diencephalon as an infundibular extension, whereas the adenohypophysis develops from the epithelium that comes in contact with this infundibulum. The enigma of the pituitary gland is that evolution of a composite organ with such a complex double developmental origin must have been associated with some functionally adaptive value.

Yet demonstration of this adaptive value in the agnathans themselves remains elusive. Most surprising facts are that not only the pituitary gland but also all major adenohypophysial hormones such as GTHs, growth hormone (GH), prolactin, and adrenocorticotropin (ACTH) and their receptors are also considered to be vertebrate novelties (2). Thus, the hypothalamic-pituitary system, which is specific to vertebrates, is considered to be a seminal event that emerged prior to or during the differentiation of the ancestral agnathans. Such an evolutionary innovation is one of the key elements leading to physiological divergence, including reproduction, growth, metabolism, stress, and osmoregulation in subsequent evolution of gnathostomes.

Lampreys and hagfish are the only two extant representatives of agnathans. Paleontological analysis of extinct agnathans had suggested that lampreys were more closely related to gnathostomes than either group is to the hagfishes (3, 4). However, both recent molecular phylogenetic analyses (5–7) and developmental study on the craniofacial pattern of the hagfish (8) strongly support the monophyly of the cyclostomes (lampreys and hagfishes as closest relatives). Therefore, studies on reproduction of the cyclostomes are important for understanding the evolution of the HPG axis



related to vertebrate reproduction. Findings from many molecular, biochemical, physiological, and morphological studies indicate that the HPG axis is present in the lamprey [for review, see Ref. (1)]. In contrast, endocrine regulation of reproduction in the hagfish is poorly understood [for reviews, see Ref. (9, 10)]. For example, until the recent identification of functional GTH in the brown hagfish, *Paramyxine atami* (11), it was not established whether the hagfish pituitary gland contains tropic hormones of any kind. Herein, this report summarizes the recent findings of the HPG endocrine system involved in reproduction in hagfish.

HAGFISH PITUITARY GLAND

The hagfish is considered the most primitive vertebrate known, living or extinct (3) (Figure 2). In addition to their primitive external body features, hagfish possess the most primitive hypothalamic-pituitary system among the vertebrates (12). The neurohypophysis is a flattened sac-like structure, whereas the adenohipophysial consists of a mass of clusters of cells embedded in connective tissue below the neurohypophysis (12, 13) (Figures 3A,B). The adenohipophysial and the neurohypophysis are completely separated by a layer of connective tissue, and there is no or little anatomical relationship between them (14, 15) (Figure 3B). In addition, there is no clear cytological differentiation between the pars distalis and the pars intermedia (12, 13) (Figure 3B). The question arises whether the simplicity of the hagfish pituitary gland is a primitive or a degenerate feature. For example, some authors have claimed that the pars intermedia seems to have been lost via a

secondary degenerative process (13, 16). Moreover, until recent identification of a functional GTH in the hagfish pituitary (11), it had not been established whether the hagfish pituitary gland contained adenohipophysial hormones of any kind (9). Because of the simplicity and primitiveness of the pituitary morphology and equivocal data on the adenohipophysial hormones in the hagfish, many researchers had questioned whether there were any functional adenohipophysial hormones (9, 17). On the other hand, arginine vasotocin (AVT), as a single neurohypophysial hormone, was identified in the hagfish (18). In addition, the presence of GnRH has been suggested in the hagfish hypothalamus by both radioimmunoassay (RIA) and immunohistochemistry (19–22) (Figure 4). Thus, the hagfish appears to have neurohypophysial and hypothalamic hormones similar to those of other vertebrates.

At present, the adenohipophysial of the hagfish is the least understood of all the vertebrates. However, our immunohistochemical studies provided the first clear-cut evidence for the presence of GTH and ACTH in the hagfish (23–25). Although not conclusive, our data also suggested the presence of GH in the hagfish (23). In addition, these three adenohipophysial hormones were suggested to be the ancestral adenohipophysial hormones that have maintained their original functions throughout vertebrate evolution. On the other hand, the later derived hormones, such as prolactin and thyroid-stimulating hormone (TSH), may have contributed to the expansion of vertebrates into new environments, as suggested by Kawauchi et al. (26) and Kawauchi and Sower (27). Moreover, our study further revealed that GTH

cells, ACTH cells, and unidentified cells which were assumed to include both undifferentiated cells and GH cells, were packed together in the same cell cluster of the hagfish adenohypophysis, and thus each cluster appeared to serve as a separate functional unit (10, 24) (Figures 3C–E). If the absence of the pars intermedia is the most ancestral vertebrate pituitary gland, melanophore-stimulating hormone (MSH) activity seems to be gained secondarily together with the differentiation of the pars intermedia. Further studies are needed to clarify this possibility.

GLYCOPROTEIN HORMONE FAMILY

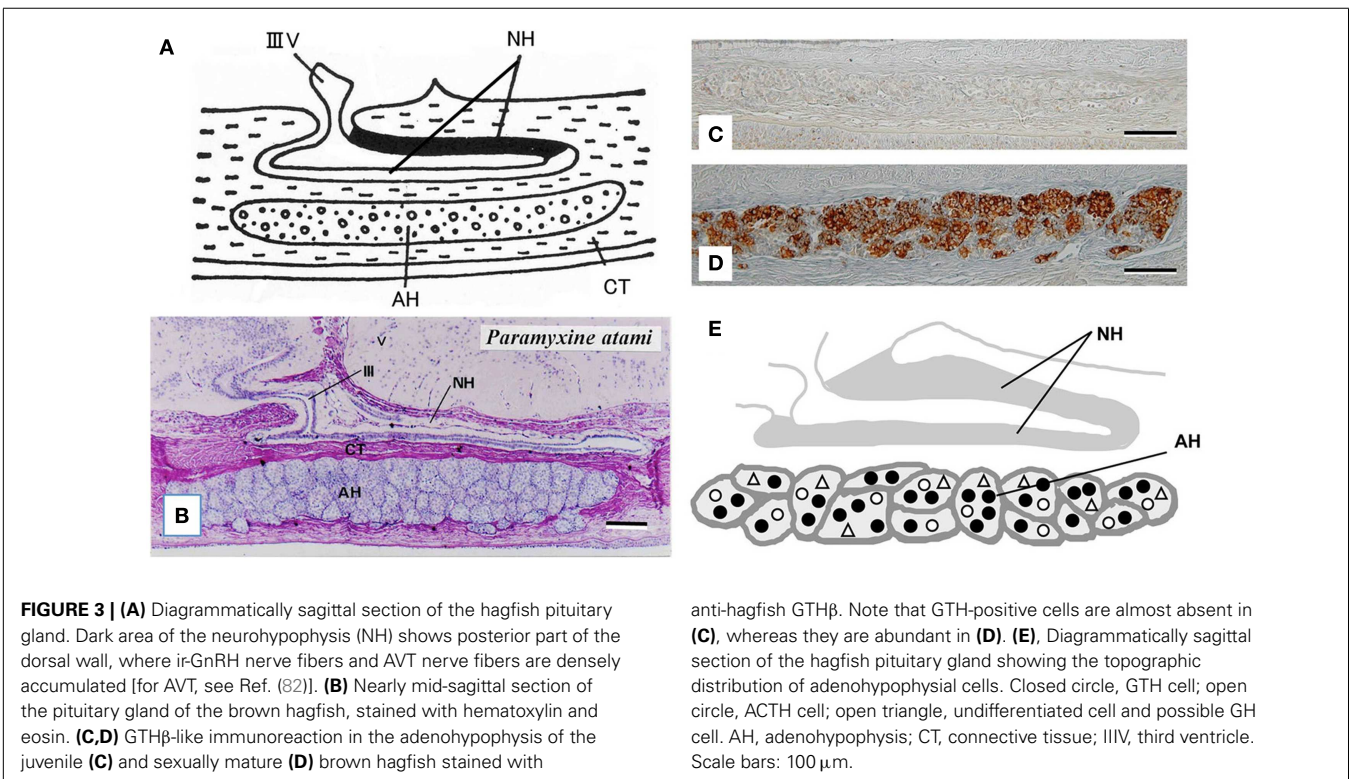
Gonadotropins, in response to hypothalamic GnRH, are released from the pituitary and act on the gonads to regulate steroidogenesis and gametogenesis. Two GTHs, follicle-stimulating hormone (FSH) and luteinizing hormone (LH), together with TSH form a family of pituitary hormones (Figure 1). They are heterodimeric glycoproteins consisting of two subunits, an α -subunit and a unique β -subunit. These glycoprotein hormones (GPH) are believed to have evolved from a common ancestral molecule through duplication of β -subunit genes and subsequent divergence (27, 28). Two GTHs have been identified in all taxonomic groups of gnathostomes, including actinopterygians (29, 30), sarcopterygians (31), and chondrichthyans (32), but not in agnathans.

A single β -subunit of GTH was identified from the sea lamprey pituitary gland after extensive and exhaustive research for over 20 years (27, 33). However, the α -subunit of lamprey GTH is not found even in the lamprey genome (34). This is very strange fact, since a huge amount of physiological and morphological evidence has suggested the presence of GTH in the lamprey (33, 35–38). The lack of α -subunit of lamprey GTH makes difficulty to study the HPG axis in relation to GTH functions in the lamprey. The second form of β -subunit of pituitary GPHs as a candidate for TSH β is not found in the lamprey genome (34), and thus the lamprey does not have TSH.

Recently, a fourth heterodimeric GPH has been discovered in the human genome and termed “thyrostimulin” due to its thyroid-stimulating activity (39). The thyrostimulin α -subunit, called glycoprotein α -subunit 2 (GPA2), is homologous but not identical to the common α -subunit (GPH α or GPA1). With the



FIGURE 2 | Brown hagfish, *Paramyxine atami*.



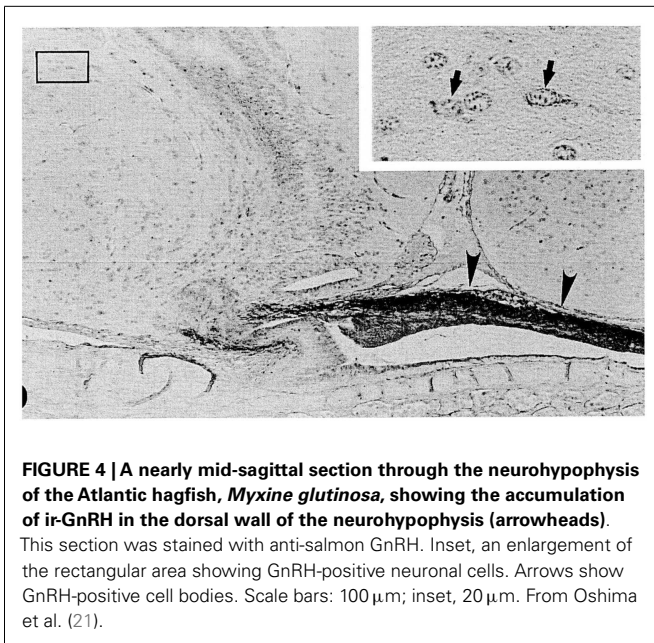


FIGURE 4 | A nearly mid-sagittal section through the neurohypophysis of the Atlantic hagfish, *Myxine glutinosa*, showing the accumulation of ir-GnRH in the dorsal wall of the neurohypophysis (arrowheads).

This section was stained with anti-salmon GnRH. Inset, an enlargement of the rectangular area showing GnRH-positive neuronal cells. Arrows show GnRH-positive cell bodies. Scale bars: 100 μm ; inset, 20 μm . From Oshima et al. (21).

discovery of GPA2 and glycoprotein β -subunit 5 (GPB5, thyrostimulin beta) homologs not only in other vertebrates but invertebrates including fly, nematode, and sea urchin (40, 41), it is proposed that ancestral glycoprotein existed before the divergence of vertebrates/invertebrates, and that later gene duplication events in vertebrates produced the thyrostimulin (GPA2 and GPB5) and GTH/TSH [GPH α and GPH β (LH β /FSH β /TSH β)] (40) (Figure 1). The basal lineage of chordates such as tunicates and amphioxus contains GPA2 and GPA5 in their genome but not GPH α or GPH β (2, 42–45). Lamprey also has GPA2 and GPB5 genes in addition to the canonical GTH β (1, 33, 34, 42). At present, no information is available as to the presence of GPA2/GPB5 in the hagfish.

IDENTIFICATION OF HAGFISH GTH

A single GPH, which comprises α - and β -subunits, was recently identified in the pituitary of the brown hagfish, *P. atami*, one of the Pacific hagfish (11) (Figure 2). Both subunits of GPH are produced in the same cells of the adenohypophysis, providing definitive evidence for the presence of a heterodimeric GPH in the hagfish. GPH increases at both the gene and protein levels corresponding to the reproductive stages of the hagfish (Figures 3C,D). Moreover, purified native GPH induces sex steroid release (estradiol-17 β and testosterone) from cultured testis in a dose-dependent manner. From the phylogenetic analysis, the hagfish GPH α forms a clade with the gnathostome GPH α s. The hagfish GPH β forms a clade with the TSH β s, however the bootstrap values are low and hagfishes evolved prior to the gnathostomes. The sea lamprey GTH β also groups with the GPH β s but appears to be one of the outgroups of the LH β s. These results clearly show that the GPH identified in the hagfish acts as a functional gonadotropin, and hereafter it is referred as to GTH. Hagfish GTH is the earliest evolved pituitary GPH that has been identified in a basal vertebrate leading to the gnathostome GTH and TSH lineages.

FEEDBACK REGULATION OF HAGFISH GTH SYNTHESIS AND SECRETION

Gonadal steroid hormones and hypothalamic hormones play major roles in controlling the synthesis and release of LH and FSH in gnathostomes. Both positive and negative feedback effects of gonadal steroids have been demonstrated in teleosts, depending on modes of administration and reproductive stages of animals. In general, in sexually mature fish, sex steroids are considered to regulate gonadal maturation and recrudescence, whereas in juvenile fish, sex steroids are considered to regulate puberty. Thus, negative feedback effects of estradiol and testosterone are evident during the latter stages of gonadal development; specifically, it has been shown that gonadal removal increases LH secretion in salmon (46), goldfish (47), and African catfish (48). The observed increases in LH levels can be suppressed by treatment with estradiol, testosterone, or both. FSH is also controlled by steroid-dependent negative feedback loops in rainbow trout (49), salmon (50), and goldfish (51). The negative feedback effects of steroids may be mediated primarily at the levels of the hypothalamic GnRH neurons (52–54), because both *in vivo* and *in vitro* studies have shown that the expression of LH β mRNA or FSH β mRNA is often unchanged or increases following exposure to estradiol, testosterone, or both (49, 53, 55). However, in sexually immature teleosts, sex steroids appear to exert primarily a positive feedback effect that acts directly at the level of the pituitary and via effects on the GnRH system (55, 56). LH content and LH mRNA levels of the pituitary in juvenile fish increase in response to estrogens and aromatizable androgens (49, 57).

Estradiol treatment in the juvenile brown hagfish resulted in the marked accumulation of both immunoreactive (ir)-GTH α and ir-GTH β in the pituitary (58). However, mRNA levels of GTH α and GTH β in the pituitary were not, or only transiently, increased by the estradiol treatment (58). The latter results suggest that syntheses of both α - and β -subunits of GTH were not, or only transiently, affected by the estradiol treatment. Accordingly, the marked accumulation of both ir-GTH subunits could be attributed to the suppression of GTH secretion from the pituitary. From that study, the feedback effects of estradiol appeared to be inhibitory rather than stimulatory, and mediated by the possible suppression of the secretion of GTH from the pituitary in these juvenile hagfish. These conditions in juvenile hagfish resembled those in adults, but not in juveniles, of teleosts (49, 53, 55). Such suppression of GTH secretion in the hagfish is probably regulated by the hypothalamic factors including GnRH, as mentioned below.

On the other hand, testosterone treatment in the juvenile brown hagfish had no effect on the staining intensities of the ir-GTH α and ir-GTH β in the pituitary (58). Nevertheless, testosterone treatment resulted in the suppression of mRNA expressions of both GTH α and GTH β in the pituitary (58). Therefore, testosterone probably acts to suppress both the synthesis and the secretion of GTH. This conclusion follows from the reasoning that if the secretion of GTH was not suppressed, the intensities of immunoreactions of both GTH α and GTH β would have decreased due to decreased levels of mRNA expressions of both GTH subunits. Thus, it seems likely that estradiol and testosterone differ with regard to their roles in the regulation of synthesis and secretion of GTH in the pituitary of the hagfish.

PLASMA LEVELS OF SEX STEROID HORMONES IN THE HAGFISH

Only a few studies exist regarding sex steroid hormonal profiles in relation to gonadal function in hagfish. Matty et al. (17) reported that estradiol and testosterone were measurable in the plasma of *Eptatretus stouti* using RIA; however, the observed levels of these steroids were near the lower limit of RIA sensitivity. Schützinger et al. (59) found using a more sensitive RIA that plasma estradiol content increased in relation to the stages of ovarian development in female Atlantic hagfish, *Myxine glutinosa*. Powell et al. (60, 61) also reported using *in vitro* organ cultured ovaries that the number of females with large eggs increased following estradiol peaks in January in *M. glutinosa*. Thus, estrogen seems to be involved in the ovarian development.

Plasma concentrations of estradiol, testosterone, and progesterone were examined with respect to gonadal development, sexual differences, and possible function of atretic follicles in the brown hagfish, *P. atami*, using a time-resolved fluoroimmunoassay (62). In females, plasma estradiol levels showed a significant positive correlation with ovarian development, while plasma testosterone and progesterone levels were highest in non-vitellogenic adults (62). Thus, our data on plasma estradiol levels in female *P. atami* were consistent with the results of Schützinger et al. (59) and Powell et al. (60). In another study, Yu et al. (63) demonstrated that the synthesis of hepatic vitellogenin was inducible by estrogens, estradiol, and estrone, in *E. stouti*. Based on these results, estrogenic control of ovarian development and hepatic vitellogenesis seemed to have arisen early in vertebrate evolution.

In males, no clear relationships were observed between plasma estradiol or testosterone concentrations and testicular development, while plasma progesterone concentrations showed a significant inverse relationship with testicular development (62). However, in that study data on sexually mature males with high incidences of spermatids or spermatozoa were lacking, since they were very few in our populations (62). Therefore, it is still possible to consider that estradiol and testosterone are involved in the regulation of male reproduction in hagfish. In support of this possibility, it is reported that purified native hagfish GTH induced secretion of estradiol and testosterone from cultured hagfish testes (11). Moreover, intraperitoneal administration of these steroids in juvenile hagfish affected on the GTH functions as mentioned above.

On the other hand, in relation to our failure to correlate plasma concentrations of estradiol or testosterone to testicular development, recent studies in the lamprey have emphasized the importance of non-classical steroids, such as androstenedione and 15 α -hydroxylated sex steroids (15 α -hydroxytestosterone and 15 α -hydroxyprogesterone) in serving as functional androgens (64–67). Indeed, evidence demonstrating testosterone functionality in lampreys was scarce [see Ref. (68)], while androstenedione was found in substantial amounts within the testicular tissue of lampreys, and plasma and tissue levels of the hormone increased significantly in prespermiating male sea lampreys after injection of GnRH (66). In addition, prespermiating males implanted with androstenedione reached maturation significantly faster and exhibited larger secondary sex characteristics than placebo or non-implanted males (66). A receptor for androstenedione was recently

described by Bryan et al. (66). 15 α -Hydroxylated steroids are also suggested to be involved in the regulation of lamprey reproduction (67). Since hagfish gonads also produce substantial amounts of unusual androgens, such as 6 β -hydroxy testosterone and 5 α -androstane-3 β , 7 α , 17 β -triol, as well as androstenedione (69–71), some of these steroids may act as functional androgens in the hagfish.

HYPOTHALAMIC FACTORS REGULATING THE GONADOTROPIC FUNCTION OF HAGFISH

The synthesis and secretion of GnRH is the key neuroendocrine function in the hypothalamic regulation of the HPG axis. To date, two to three isoforms have been identified in representative species of all classes of gnathostomes and lampreys (1). GnRHs are also identified in tunicates (72), and several invertebrates belonging to lophotrochozoans [mollusk and annelid; (73, 74)], but not in the ecdysozoan lineages. On the other hand, adipokinetic hormone (AKH) has been identified as the ligand of the GnRH receptor of the insects, *Drosophila* and *Bombyx* (75). An AKH-GnRH-like neuropeptide has been identified in the nematode *C. elegans* (76). A comparative and phylogenetic approach shows that the ecdysozoan AKHs, lophotrochozoan GnRHs, and chordate GnRHs are structurally related and suggested that they all originate from a common ancestor (77).

In the hagfish, GnRH has not yet been identified, but previous chromatographic and immunohistochemical studies have suggested the presence of a GnRH-like molecule in the hypothalamic-neurohypophysial area (19, 20). Kavanaugh et al. (22) reported the seasonal changes in hypothalamic ir-GnRH contents in relation gonadal reproductive stages in the Atlantic hagfish (*M. glutinosa*). In *M. glutinosa*, a dense accumulation of GnRH-like immunoreaction was observed in the dorsal wall of the neurohypophysis with the use of antisera against chicken GnRH-II, salmon GnRH, lamprey GnRH-I, and lamprey GnRH-III (19, 21) (Figure 4). Neuronal cells containing ir-GnRH were found in the preoptic nucleus and the dorsal hypothalamic nucleus (20, 21). In another study, Osugi et al. (78) identified several PQRamide peptides in the brain of the brown hagfish (*P. atami*). Based on *in situ* hybridization and immunohistochemistry, hagfish PQRamide peptide precursor mRNA and its translated peptides were localized in the infundibular nucleus of the hypothalamus. Dense ir fibers were found in the infundibular nucleus and some of them were terminated on blood vessels within the infundibular nucleus. They further showed that one of the hagfish PQRamide peptides significantly stimulated the expression of GTH β mRNA in the cultured hagfish pituitary. The latter result clearly indicates that GTH functions of the hagfish pituitary are controlled by the hypothalamic factors.

Puzzling aspect of the hagfish hypothalamic-pituitary system is that there is no or little anatomical relationship between them. It is generally considered that the hypothalamic factors, such as GnRH, reach the adenohypophysis simply by diffusion (79, 80). However, the dorsal wall of the hagfish neurohypophysis, where ir-GnRH nerve fibers are terminated (Figure 4), is far from the adenohypophysis by the presence of the neurohypophysis itself. On the other hand, the blood vessels are richly distributed on the surface of the dorsal wall, and make the posterior hypophysial vascular

plexus (14, 15). Although most blood in the posterior hypophysial vascular plexus enter the posterior hypophysial vein of the anterior cardinal system, several small vessels proceed from the dorsal wall to the adenohypophysis in *Eptatretus burgeri* (15). These small vessels may contribute the regulation of the adenohypophysial functions. A pair of small blood vessels from the hypothalamus also enters the posterior hypophysial vascular plexus (14). Together with the fact that some PQRamide neuronal fibers terminated on the blood vessels within the hypothalamus (78), further studies are needed to understand the hypothalamic-pituitary system of the hagfish.

CONCLUSION

Not only the pituitary gland but also all major adenohypophysial hormones and their receptors are considered to be vertebrate novelties. Since hagfish represent the most basal and primitive vertebrate that diverged over 550 millions years ago (81), they are of particular importance in understanding the evolution of the HPG axis related to vertebrate reproduction. Our data clearly show that the hagfish has a functional HPG axis similar to that of more advanced gnathostomes. It is strongly expected that the functional GTH found in hagfish pituitary helps to delineate the evolution of the complex HPG axis of reproduction in vertebrates. Furthermore, this HPG system likely evolved from an ancestral, pre-vertebrate exclusively neuroendocrine mechanism by gradual emergence of components of a new control level, the pituitary gland.

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