

Genetic insights into human isolated gonadotropin deficiency

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Abstract The identification of naturally occurring genetic mutations has provided unique insight into the current knowledge of the human hypothalamic-pituitary-gonadal axis. In the past decade, several monogenic causes have been reported in patients with isolated gonadotropin deficiency. Kallmann Syndrome is a clinically and genetically heterogeneous disorder, characterized by isolated hypogonadotropic hypogonadism and anosmia or hyposmia. To date, loss-of-function mutations in the genes encoding anosmin-1 (*KALI*) and fibroblast growth factor receptor 1 (*FGFR1*) have been described in the X-linked and autosomal dominant forms of this syndrome, respectively. More recently, several heterozygous, homozygous or compound heterozygous mutations in the G protein-coupled prokineticin receptor-2 (*PROKR2*) and one of its ligands, prokineticin-2 (*PROK2*) were described in Kallmann syndrome. In addition, complex genetic transmission (digenic inheritance) was recently demonstrated in this condition. Regarding isolated hypogonadotropic hypogonadism without olfactory abnormalities, loss-of-function mutations in the Gonadotropin-releasing hormone (GnRH) receptor (*GnRH-R*) or the G-protein coupled receptor 54 (*GPR54*) genes, both encoding transmembrane receptors, have been described, as well as *FGFR1* mutations. Finally,

mutations of the beta sub-units of LH and FSH have been described in patients with selective gonadotropin deficiency. We review the role of these distinct genetic factors in human isolated hypogonadotropic hypogonadism.

Keywords Hypogonadotropic hypogonadism · Kallmann syndrome · Gonadotropin deficiency · Gonadotropin-releasing hormone

Introduction

The episodic secretion of gonadotropin-releasing hormone (GnRH) from the hypothalamus is a key requirement for the initiation and maintenance of normal reproductive function. In humans, the hypothalamic-pituitary-gonadal axis is fully active in the neonatal life, followed by a period of quiescence during childhood and reactivation in the beginning of puberty. Several factors that trigger the resurgence of pulsatile GnRH secretion at puberty have been described [1].

Congenital isolated hypogonadotropic hypogonadism (IHH) is defined by low gonadal sex steroid plasma levels in the setting of low or normal pituitary secretion of follicle-stimulating hormone (FSH) and luteinizing hormone (LH). It is characterized by complete or partial absence of endogenous GnRH-induced gonadotropin secretion, absence of anatomical abnormalities in the hypothalamic and pituitary region, and normal baseline and reserve testing of the remaining hypothalamic-pituitary axis [2]. IHH may occur in association with olfactory abnormalities (Kallmann syndrome), whereas a normal sense of smell defines normosmic IHH.

Kallmann syndrome is a clinically and genetically heterogeneous disorder, more prevalent in males (1:10,000)

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than in females (1:50,000) [3]. Although sporadic cases are more frequent, families with Kallmann syndrome have been reported with X-linked, autosomal dominant or recessive modes of inheritance [4–6]. In the past decade, several monogenic causes of IHH have been identified. *KALI* (Kallmann syndrome gene 1) and fibroblast growth factor receptor 1 (*FGFR1*) defects were associated with X-linked and autosomal Kallmann syndrome, respectively. More recently, several heterozygous, homozygous or compound heterozygous mutations in the G protein-coupled prokineticin receptor-2 (*PROKR2*) and one of its ligands, prokineticin-2 (*PROK2*), have been described in Kallmann syndrome. In addition, complex genetic transmission (digenic inheritance) was recently demonstrated in this condition. Mutations in the GnRH receptor (*GnRH-R*), G protein-coupled receptor-54 (*GPR54*) and its ligand kisspeptin are associated with normosmic IHH. In addition, selective hypogonadotropic hypogonadism due to mutations in the FSH beta and LH beta-subunit genes has been rarely reported.

KALI and X-linked Kallmann syndrome

Unlike most neurons in the brain, the origin of GnRH neurons lies outside the central nervous system, in the nasal placode of the embryonic nasal prominence, sharing a common origin and destiny with the olfactory neurons that migrate together across the cribiform plate toward the developing olfactory bulb [7, 8]. GnRH neurons subsequently disengage from their olfactory guidance fibers and further migrate to their ultimate destination in the medial hypothalamus [9]. Abnormalities in this migratory process explain the association of IHH and olfactory defects in patients with Kallmann syndrome [10, 11]. These abnormalities probably arise from impaired targeting and migration of the olfactory axons and of the GnRH secreting neurons [10, 11], or from alterations in the initial steps of olfactory bulb differentiation [12]. The migrational arrest of GnRH neurons within the meninges has been reported in a study of a 19-week human fetus with X-linked Kallmann syndrome [13]. Furthermore, olfactory bulb agenesis or hypoplasia has been detected by magnetic resonance imaging in some patients with this condition [14, 15].

Intragenic deletions and point mutations of *KALI* gene, located at Xp22.3, are responsible for X-linked Kallmann syndrome [10, 11, 16]. Although incomplete penetrance of hypogonadism and/or anosmia within and across families with Kallmann syndrome is frequently described, patients with *KALI* mutations exhibit an almost uniformly severe and highly penetrant reproductive phenotype [4, 17]. In addition, several non-reproductive and non-olfactory disorders are largely attributed to *KALI* defects, including midline facial defects, such as cleft lip and/or palate, short

metacarpals, renal agenesis [6, 18, 19], sensorineural hearing loss [6, 18, 20], bimanual synkinesia [20, 21], oculomotor abnormalities [6, 20] and cerebellar ataxia [20]. Renal agenesis and bimanual synkinesia show the highest incidences, occurring in approximately 30–40% and 75% of Kallmann syndrome cases, respectively [22].

KALI comprises 14 exons and encodes an extracellular protein of 680 amino acids, anosmin-1, which contains a cysteine-rich region, a whey acidic protein (WAP) domain, homologous to some serine protease inhibitors, four fibronectin-like type III (FnIII) repeats, structurally related to cell adhesion molecules, and several predicted heparin sulfate binding regions [10, 11]. Mutations in *KALI* are distributed throughout the gene, although most of the point mutations cluster in the four FnIII repeat region of anosmin-1 [16]. These mutations have been identified in approximately 8–11% of the sporadic and in 14–50% of the familial cases of X-linked Kallmann, respectively [4, 23]. No correlation has been demonstrated between phenotype and location of the described mutations.

Experiments in vitro showed that anosmin-1 has a role in the control of different cell functions, including cell adhesion and neurite/axonal elongation and fasciculation, epithelial morphogenesis as well as in the migratory activity of GnRH-producing neurons [24–27]. Molecular modeling showed that anosmin-1 domains are highly extended and have intradomain flexibility, which account for the known ability of anosmin-1 to interact with macromolecular ligands in intracellular matrix [28]. However, the molecular mechanism of anosmin-1 action is widely unknown. It has been shown that the reduction of the number of FnIII repeats determines a weaker cell surface association and a lower heparan-sulfate binding affinity [29] and can produce a protein that completely lacks in vivo activity [30, 31]. Andrenacci et al. [31] performed a structure-function analysis of the different *Drosophila melanogaster* Kal-1 domains. This study suggests that the FnIII repeats have a main and specific role for the activity of the anosmin-1, while the WAP domain might have only a modulator role, strictly connected to that of the fibronectins. In addition, the functional relevance of these different domains was shown to be dependent on the extracellular context.

FGFR1 and autosomal dominant Kallmann syndrome

The *FGFR1* gene, also called *KAL2*, is located at chromosome 8p12 and comprises 18 exons. Dode et al. [32], studying two patients with contiguous gene syndrome due to interstitial deletions at chromosome 8p11.2–12, first reported the association of loss-of-function mutations in *FGFR1* with the dominant form of Kallmann syndrome. Since then, several *FGFR1* mutations, spanning all

functional domains of the receptor, have been identified in approximately 10–17% of Kallmann syndrome affected individuals [32–39]. Similar to *KALI* defects, other non-reproductive and non-olfactory disorders are associated with Kallmann syndrome due to *FGFR1* defects, including cleft palate or lip, dental agenesis and bimanual synkinesis [32–35] (Table 1). To date, only two patients with *FGFR1* mutations and bimanual synkinesis [32, 35] have been identified; this clinical defect usually observed in *KALI* patients.

FGFR1 abnormalities have been associated with wide variability of sexual maturation, as demonstrated by the presence of phenotypes that varied from complete absence of puberty to normal reproductive function within families harboring the same mutation [39]. Isolated anosmia has also been identified as a partial phenotypic manifestation of *FGFR1* mutations in familial cases of autosomal dominant Kallmann syndrome [35, 39].

In addition, *FGFR1* defects were recently implicated in a rare variant form of Kallmann syndrome, characterized by spontaneous reversibility of reproductive function [40] and more recently, in the etiology of IHH with normal olfaction [35, 41, 42]. These reports demonstrated that *FGFR1* mutations can cause distinct subtypes of IHH, suggesting that GnRH neuronal migratory defects in these cases are not always complete and variable degrees of endogenous GnRH secretion may occur [40].

The mature FGFR1 protein, one of the four transmembrane receptors for fibroblast growth factor (FGF) ligands, consists of three extracellular immuno-globulin-like loops, an acid box between the first two immunoglobulin loops, a transmembrane domain, and an intracellular split tyrosine kinase domain [43]. The FGFR1 signaling is achieved by receptor conformational changes upon ligand binding, leading to dimerization and subsequent activation by autophosphorylation of tyrosine kinase intracellular domains. Heparin or heparan sulfate proteoglycan (HSPG) binding is essential for the dimerization and activation of the FGF–FGFR complex [44, 45].

Several studies on the expression patterns of FGF ligands and receptors during the central nervous system development indicate the critical role of FGF in the initial generation of neural tissue [46]. This activity is also present in the rostral forebrain, directly affecting the olfactory bulb development, which could influence the GnRH neuronal migratory activity [47]. Therefore, loss-of-function mutations in *FGFR1* are thought to result in a defect in GnRH neuron migration via abnormal olfactory bulb morphogenesis [22]. Consistent with this hypothesis, olfactory bulb agenesis or hypoplasia has been detected by MRI in patients with *FGFR1* mutations [32, 34, 35, 40]. However, the mechanism and effects of loss-of-function *FGFR1* mutations are poorly understood. Structural and

biochemical studies showed that some mutations in the tyrosine kinase and immunoglobulin II domains described in Kallmann syndrome patients reduced the tyrosine kinase activity of FGFR1 [41].

The clinical findings shared by *KALI* and *FGFR1* mutated patients argue in favor of a putative anosmin-1 and FGFR1 interaction, and/or activation of common pathways. Dode and Hardelin [22] proposed that such interaction could explain the higher prevalence of Kallmann syndrome in males. Since *KALI* gene escapes X-inactivation, a higher local concentration of anosmin-1 is expected in human females, which could compensate for a pathological situation of FGFR1 haploinsufficiency [22]. In fact, recent studies showed that anosmin-1 acts as a FGFR1-specific modulator and co-ligand through a heparan sulfate-dependent mechanism and amplifies the resulting downstream signaling responses [46]. Interaction of FGF2/FGFR1/anosmin-1 was also demonstrated in an experimental model of embryonic mouse optic nerve, suggesting that this system may be relevant in the context of demyelinating diseases [48]. However, the function of anosmin-1 in vivo and its connection with FGFR1 signaling are as yet unknown and several important issues remain unresolved.

Prokineticin Receptor-2 and its ligand

The gene *PROKR2*, encoding the prokineticin receptor-2, was considered as a potential causative gene of Kallmann syndrome. This fact was strongly suggested by the abnormal development of olfactory bulbs combined with severe atrophy of the reproductive system demonstrated in mutant mice lacking this G protein-coupled transmembrane receptor [49]. Indeed, very recently, Dode et al. [50] investigated 192 (144 males and 48 females) unrelated individuals affected by Kallmann syndrome and identified 10 different mutations of *PROKR2* (one frameshift and nine missense mutations) in 14 patients with variable degrees of olfactory and reproductive dysfunction. These *PROKR2* mutations were found in heterozygous (n = 10), homozygous (n = 2) or compound heterozygous (n = 2) cases. One of the patients, who carried a *PROKR2* mutation in heterozygous state, also carried a missense mutation in *KALI*, suggesting possible digenic inheritance of the disease [50]. In addition, 4 different heterozygous mutations were also identified in the main ligand of *PROKR2* in patients affected by Kallmann syndrome. These mutations were located at highly conserved amino acids and the great majority was not found in the control group [50]. However, no functional studies of the *PROKR2* and *PROK2* mutations that could confirm the insufficient prokineticin-signaling has been performed so far.

Table 1 *FGFR1* mutations in Kallmann syndrome and normosmic IHH patients

Mutation	Nucleotide change	Localization (domain)	Inheritance	Phenotypes	References
G48S ^a	142G>A	IgI	sporadic	normal sense of smell	[35]
R78C	232C>G	IgI	familial	cryptorchidism	[39]
R78C	232C>G	IgI	sporadic	cryptorchidism, micropenis	[39]
G97D	290G>A	IgI	sporadic	–	[32]
Y99C	296A>G	IgI	sporadic	–	[32]
Frameshift	303–304insCC	IgI	sporadic	–	[32]
V102I	303G>A	IgI	familial	–	[33]
V102I	304G>A	IgI	sporadic	cryptorchidism, micropenis	[39]
S107X	320C>A	IgI	sporadic	–	[34]
S107X	320C>A	IgI	familial	–	[36]
D129A	385A>C	IgI-IgII linker	sporadic	cleft palate	[33]
A167S ^b	499G>T	IgI-IgII linker	sporadic	cleft palate, corpus callosum agenesis, unilateral hearing loss, fusion of the fourth and fifth metacarpal bones	[32]
C178S ^a	535G>C	IgII	sporadic	normal sense of smell cryptorchidism, cleft palate, dental agenesis, external ears agenesis, right mandibular hypoplasia, hypertelorism	[37]
D224H	670G>C	IgII	familial	cryptorchidism, micropenis	[39]
G237S ^a	709G>A	IgII	familial	normal sense of smell	[41]
G237D	710G>A	IgII	familial	–	[39]
L245P	734T>C	IgII-IgIII linker	sporadic	cleft lip and palate	[35]
R250W	748C>T	IgII-IgIII linker	familial	mental deficiency, epilepsy	[35]
R250W	748C>T	IgII-IgIII linker	sporadic	–	[35]
R254Q	761G>A	IgII-IgIII linker	sporadic	–	[39]
V273M	810G>A	IgII-IgIII linker	sporadic	cleft palate	[33]
V273M	817G>A	IgII-IgIII linker	familial	–	[39]
E274G	821G>A	IgIII	familial	cryptorchidism, micropenis	[39]
C277Y	830G>A	IgIII	sporadic	–	[32]
(donor splite)	936G>A	IgIII	familial	dental agenesis	[32]
Y339C	1016A>G	IgIII	sporadic	–	[39]
A343V	1028C>T	IgIII	familial	–	[35]
S346C	1037C>G	IgIII	familial	–	[39]
R365fsX41	1093-1094delAG	IgIII-TM linker	familial	dental agenesis	[33]
P366L	1097C>T	IgIII-TM linker	familial	obesity, sleep disorder	[35]
S439fsX461	1317_1318delTG	TM-TK linker	familial	dental agenesis	[38]
A520T	1561G>A	TK	Sporadic	–	[33]
I538V	1612A>G	TK	familial	cryptorchidism	[39]
T585X	1755C>A	TK	sporadic	–	[39]
V607M	1819G>A	TK	familial	bimanual synkinesis	[32]
Y613fsX42	1836_1837insT	TK	familial	–	[33]
K618fsX654	1852-1854delAA	TK	familial	cubitus valgus	[35]
R622G	1864C>G	TK	sporadic	cryptorchidism dental agenesis unilateral external ear hypoplasia member length asymmetry	[37]
R622Q	1865G>A	TK	familial	cleft palate	[37]
R622X	1864C>T	TK	familial	cleft lip and palate	[32]

Table 1 continued

Mutation	Nucleotide change	Localization (domain)	Inheritance	Phenotypes	References
R622X	1864C>T	TK	familial	–	[40]
Frameshift	1970–1971delCA	TK	familial	–	[32]
W666R	1996T>A	TK	sporadic	cleft palate	[32]
(donor splite)	IVS15+1G>A	TK	sporadic	–	
Q680X ^a	2038C>T	TK	familial	normal sense of smell	[41]
(donor splite)	IVS15+1G>A	–	sporadic	–	[32]
G687R	2059G>A	TK	familial	–	[36]
G703R	2107G>C	TK	familial	cryptorchidism	[39]
G703S	2107G>A	TK	sporadic	cryptorchidism	[39]
M719R	2156T>G	TK	sporadic	–	[32]
P722S	2164C>T	TK	familial	cleft lip, bimanual synkinesis	[35]
P722H/ N724K ^a	2165C>A/ 2172C>G ^c	TK	familial	normal sense of smell cryptorchidism, dental agenesis	[41]
Y730X	2190C>G	TK	sporadic	–	[33]
P745S	2233C>T	TK	sporadic	–	[34]
P745S	2233C>T	TK	familial	micropenis	[36]
P772S	2314C>T	TK	sporadic	cleft palate, unilateral absence of nasal cartilage, iris coloboma	[32]
V795I	2383G>A	C-terminal tail	familial	–	[35]

^a Mutations identified in normosmic patients

^b All FGFR1 mutations were detected in heterozygous state, except the A167S mutation

^c Mutation identified in the same allele

Ig—immunoglobulin; TM—transmembrane; TK—tyrosine kinase, C—carboxil

GnRH and GnRH receptor gene

The gene that encodes GnRH represents a natural candidate for mutations in patients with normosmic IHH. This idea was also supported by a naturally-occurring animal model of isolated HH, mice with autosomal recessive hypogonadotropic hypogonadism caused by a *GnRH* gene deletion [51]. However, no human *GnRH* deletions or mutations have thus far been identified in patients with IHH [52–55].

The human GnRH receptor gene (*GnRH-R*) has been mapped to chromosome 4q13.2–3 and spans over 18.9 Kb. It comprises three exons that encode a 328-amino acid protein [56]. The GnRH receptor belongs to the superfamily of the G protein-coupled receptor family with seven transmembrane domains and an extracellular amino terminus, but no intracellular carboxy terminus. Activation of this receptor results in increased activity of phospholipase C and mobilization of intracellular calcium [57].

Mutations in the *GnRH-R* gene were first described by de Roux et al. [58] in 1997. To date, approximately twenty different homozygous or compound heterozygous mutations

have been reported in patients with sporadic or familial forms of IHH [58–64]. The two most frequent GnRH receptor mutations are Q106R and R262Q, accounting for approximately half of all reported GnRH-R mutations [65]. Both these mutations usually occur in a compound heterozygous state, and have been shown to cause partial loss of function in in vitro studies [66]. Approximately, 40% of autosomal recessive and 16% of sporadic IHH cases are due to mutations in the *GnRH-R* gene [64].

The phenotypic spectrum of normosmic IHH patients with *GnRH-R* mutations varies from partial to complete hypogonadism. Female patients with complete hypogonadism due to *GnRH-R* mutations do not respond to pulsatile GnRH treatment for infertility [67], whereas patients with partial IHH demonstrate dose-dependent responses to pulsatile GnRH in terms of gonadotropin secretion and ovulation [68]. Recently, subtle phenotypes such as apparent constitutional delay of growth and puberty and borderline oligospermia were reported in males with partial loss-of-function mutations of the GnRH receptor [69]. The mechanisms responsible for the loss of function of mutant GnRH receptors can comprise defects in the synthesis, in trafficking to the cell

membrane and/or in internalization, recycling, or degradation of receptors, in ligand binding, and/or in G-protein coupling and signal transduction.

GPR54 and *KISS1* genes

Recently, kisspeptin and its receptor *GPR54* have been strongly implicated in the regulation of puberty onset. In 2003, two independent groups described inactivating mutations in the *GPR54* gene in normosmic IHH patients belonging to two consanguineous families with several affected members [70, 71]. These genetic studies established *GPR54* inactivation as a new and unsuspected cause of IHH. Since then, six additional loss-of-function mutations have been described in the *GPR54* gene, comprising approximately 5% of all normosmic IHH patients investigated to date [70–73]. The majority of IHH patients identified with *GPR54* mutations are either familial or sporadic cases with consanguineous parents. In fact, considering only the familial cases of normosmic IHH, the prevalence of *GPR54* mutations increases to around 20% [70–73].

The human *GPR54* gene is located at chromosome 19p13.3 and encodes a 398-amino acid heptahelical G-protein-coupled receptor with homology to the galanin receptor family [74]. Ligand binding activates phospholipase C, increasing inositol triphosphate and resulting in the mobilization of intracellular calcium.

The endogenous ligands of the *GPR54* are derived from a 145-amino acid precursor peptide, kisspeptin-1, encoded by the *KISS1* gene. The longest of these peptides, with 54 amino acids, is kisspeptin 54 (composed by amino acids 68–121), also known as metastin. Smaller cleavage products of 14, 13 and 10 residues also occur naturally and all of them have high receptor binding affinity, which lies within the C-terminal RF-amide region [75–77]. Studies using in situ hybridization and real time PCR demonstrate that GnRH neurons co-express *GPR54* transcripts. On the other hand, *KISS1* expression was demonstrated in hypothalamic areas, such as the arcuate and anteroventral periventricular nuclei, known to send projections to the medial preoptic area, where there is an abundance of GnRH cell bodies [78]. These data suggest that kisspeptin acts directly on GnRH neurons to stimulate the secretion of GnRH.

Physiological and pharmacological studies conducted in different animal models confirmed the role of the complex *KISS1/GPR54* in the reproductive axis. Mice lacking *GPR54* were also shown to have hypogonadism [71]. Interestingly, GnRH neurons were anatomically intact in these animals, with normal GnRH content, indicating that mutations in *GPR54* affect either the processing or release of this hormone and that GnRH neurons migration occurs normally [71, 79]. Additional studies demonstrated that

low doses of kisspeptin, administered either centrally or peripherally, elicit a rapid and robust secretory burst of LH and FSH in rats, mice, sheep and primates [79–85]. Moreover, this effect is blocked by the co-administration of GnRH antagonists, suggesting that kisspeptin-stimulated gonadotropin release is GnRH-release dependent and does not reflect a direct action of kisspeptin on the pituitary [80, 81, 83, 86]. Furthermore, kisspeptin administration has no effect on *GPR54*^{−/−} mice, showing that kisspeptins act directly and uniquely through *GPR54* signaling to stimulate gonadotropin release. Recently, kisspeptin was administered to humans in a double blind study. Male volunteers received kisspeptin intravenously for 90 min, resulting in significant increases in plasma concentrations of LH, FSH and testosterone as compared to saline infusion [87].

Patients carrying *GPR54* mutations present a large phenotypic spectrum, varying from partial to severe hypogonadism. Nonetheless, the majority of patients had at least partial LH and FSH responses to GnRH stimulation. The patient described by Seminara et al. [71], who had compound heterozygosity for the R331X and X399L mutations, presented at the age of 18 years with partial hypogonadism. Although he had low basal testosterone and gonadotropin levels, response to acute GnRH stimulation (100 µg i.v.) was normal and frequent gonadotropin sampling revealed the presence of low amplitude, endogenous LH pulses. On the other end of the spectrum, Semple et al. described a compound heterozygote (C223R/R297L), who was diagnosed with hypogonadism at 2 months of age with micropenis, bilateral cryptorchidism and undetectable levels of gonadotropins, suggesting a role of kisspeptins in the activation of the hypothalamic-pituitary-gonadal axis during the neonatal or late fetal life.

Segregation analysis has shown that heterozygous carriers of *GPR54* loss-of-function mutations have undergone normal pubertal development. It is also noteworthy that male and female patients have been successfully treated, either with exogenous gonadotropin or long-term pulsatile GnRH infusion, achieving fertility and normal pregnancy outcomes [71, 72]. The fact that these patients responded to exogenous GnRH infusion corroborates the experimental observations that the kisspeptins/*GPR54* system acts above the GnRH receptor level, most likely stimulating GnRH secretion.

Given the importance of the Kisspeptin/*GPR54* complex in control of pubertal onset, the *KISS1* gene is another obvious candidate for genetic screening in cases of IHH. Nevertheless, among 277 patients with sporadic or familial normosmic IHH, only one alteration was described [73, 88]; a homozygous 20 nucleotide insertion in the 3' terminal end of the coding sequence was found in a boy with micropenis and bilateral cryptorchidism diagnosed with IHH at the age

of 3 months [88]. However, no functional studies regarding this unique finding have been published so far

LH and FSH beta-subunit genes

The gonadotropins are heterodimers consisting of specific beta-subunits that are noncovalently bound to a common alpha-subunit. Selective FSH deficiency due to FSH beta-subunit gene mutations causing hypogonadism and infertility is a very rare condition. To date, three distinct FSH beta-subunit gene mutations have been described in four unrelated females and two males with hypogonadism [89–96]. These homozygous or compound heterozygous mutations often affect the seatbelt region of the protein and interfere with the synthesis and stability of the heterodimer complex. Consequently, patients were found to have undetectable serum FSH and elevated serum LH levels. Recently, we identified an FSH beta-subunit gene mutation in a Brazilian female with delayed puberty, who presented with incomplete pubertal breast development and primary amenorrhea due to a homozygous Y76X mutation [97].

Only two LH beta-subunit gene mutations have been reported in humans [98, 99]. The first was described in a male with delayed puberty, low testosterone, arrested spermatogenesis, and elevated serum LH. A homozygous Q54R missense mutation in the long loop of LH beta, which impaired binding to its receptor, was identified in this patient [98]. The second mutation was described in a 30-year-old-male with delayed puberty and infertility due to a homozygous G36D missense mutation. This mutation disrupted a vital cytosine knot motif and abrogated the heterodimerization and secretion of LH. Circulating LH levels were not detectable. Treatment with hCG promoted virilization, increased testosterone levels, and enabled normal spermatogenesis [99].

Conclusions

Recent investigations into the pathogenesis of Kallmann syndrome have pointed out the importance of anosmin-1 and FGFR1 in the olfactory and GnRH neuronal systems. *GnRH-R* and *GPR54/Kiss1* genes have been implicated in IHH etiology of normosmic patients and few mutations of the beta sub-units of LH and FSH were described in patients with selective gonadotropin deficiency. Data on the prevalence, phenotype and mutation spectrum of each genetic subtype of isolated hypogonadotropic hypogonadism are essential to improve our understanding of this complex disorder, and can be useful for directing therapy and for genetic counseling. However, a genetic basis for IHH has been established in less than 20% of cases, indicating that additional genetic causes will probably be described in the future. In addition, clinical heterogeneity is remarkable in

some of these genetic forms of isolated hypogonadotropic hypogonadism, suggesting that environmental factors or epigenetic phenomena and/or modifier genes may influence the phenotype.

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