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The Kisspeptin Signaling Pathway and its Role in Human Isolated GnRH Deficiency

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Abstract

Amplification of the neurosecretory activity of the GnRH system is the defining neuroendocrine even for sexual maturation. The physiological mechanisms that drive GnRH secretion at puberty have been difficult to identify but the discovery in 2003 that the G protein coupled receptor KISS1R is a key regulator of pubertal development in mice and men has ushered in a new chapter in reproductive neuroendocrinology. KISS1R is activated by endogenous peptides derived from a precursor protein, kisspeptin. Despite kisspeptin's importance in driving the reproductive cascade, relatively few patients with GnRH deficient states and mutations in the kisspeptin pathway have been described. Yet, these cases, coupled with loss-of-function mouse models, provide unique and complementary information into the biological role of this signaling system in the control of GnRH secretion. This article will examine some of the subtleties in genotype-phenotype correlations in both mice and men carrying disabling mutations in the kisspeptin pathway.

Introduction to Genetics of GnRH Deficiency

As outlined in Chapter 1 by Balasubramanian and Crowley, in the last two decades, several genes and pathways which govern GnRH ontogeny have been discovered by studying humans with GnRH deficiency, a condition characterized by abnormal pubertal development and low gonadotropins and sex steroids. These pathways include genes whose protein products influence GnRH neuronal migration to the hypothalamus such as *KALI* (1-2), *FGFR1* (3-4), *FGF8* (5), *NELF* (6-7), *PROK2* (8-9); GnRH synthesis (*GNRHI*) (10-12); GnRH responsiveness at the pituitary (*GNRHR*) (13-15); and biologic functions yet to be understood (*CHD7*) (16) and possibly *WDR11* (17). In 2003, homozygosity mapping and candidate gene analysis of two large consanguineous pedigrees led to the identification of loss of function mutations in *KISS1R* (a G protein coupled receptor with homology to the galanin receptor family) by two investigative groups (18-19). In parallel, the *Kiss1r*^{-/-} mouse demonstrated a phenotype that reinforced the human GnRH deficient state, demonstrating that the function of KISS1R/Kiss1r is conserved across mammalian species (19-20). Just prior to these human genetic discoveries, the ligand for KISS1R (also known as GPR54), was discovered to be kisspeptin, an RF amide using both biological and bioinformatic approaches (21-23). Soon thereafter, laboratories around the world began assembling expression, physiologic, transgenic, knock out/down, and electrophysiologic data to tell the biologic story of kisspeptin and its important role in regulating GnRH

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secretion. This article will examine genotype phenotype correlations within the kisspeptin pathway in both mice and men.

The Role of the Kisspeptin Signaling Pathway in Reproduction

Whereas loss of function mutations in *Kiss1r* and *KISS1R* causes hypogonadotropic hypogonadism in mice and men (18-19), *Kiss1r*^{-/-} mice permitted an examination of the hypothalamic content of GnRH which proved to be normal, leading to the hypothesis that kisspeptin does not affect GnRH neuronal fate specification, migration, or migration nor its biosynthesis but rather, its release (19). Soon thereafter, kisspeptin administration, either centrally or peripherally, was shown to selectively stimulate the secretion of GnRH and, in turn, LH and FSH. Moreover, this peptide proved to be the most potent GnRH releasing hormone that had ever been studied (24). Vaginal opening in juvenile mice treated with kisspeptin (25) is advanced and kisspeptin administration can rescue the delayed puberty caused by leptin deficiency (26). Kisspeptin expression in the hypothalamus of rodents and non-human primates increases at the time of sexual maturation (27-28), an important finding since kisspeptin is thought to mediate sex steroid feedback (27, 29-33), estrous cycle regulation (33-34), seasonal breeding (35-41), and to convey information about the energy status of the organism (42-43). Thus, it was evident early in the kisspeptin story that the kisspeptin signaling system plays a central role in integrating numerous signals previously demonstrated to modulate GnRH neuronal secretion. Kisspeptin is thus a key gatekeeper for the activation of the GnRH axis.

Summary of KISS1R Mutations

Curiously, relatively few loss-of-function mutations in *KISS1R* have been reported. Biallelic mutations include a homozygous 155 base pair deletion (18), a homozygous frameshift (1001_1002insC) (44), a homozygous splice acceptor site mutation (45), homozygous L102P (46), L148S (19, 47-48) and F272S missense mutations (49), and compound heterozygous mutations R331X/X399R (19, 48) and R297L/C223R (50) (cf Figure 1). As can easily be appreciated from this listing, mutations in this G protein coupled receptor are variable in type (large deletion, frameshift, splice site, nonsense, nonstop, and missense). Thus single nucleotide changes leading to putative missense changes occur throughout the receptor and are not clustered into a single hot spot.

While biallelic mutations in *KISS1R* are clearly associated with hypogonadotropism, it is important to recall that GnRH deficiency can be partial or complete (by history, physical examination, and baseline neuroendocrine and gonadal testing) (51), permanent or reversible (52), and congenital or adult in onset (53). In addition, GnRH deficient patients can be responsive or unresponsive to exogenous GnRH during single bolus stimulation testing but typically respond to prolonged pulsatile GnRH therapy in most cases (54). Therefore, the more complete the baseline neuroendocrine profile and the subsequent charting of responsiveness to long term GnRH administration in patients carrying variants in *KISS1R*, the greater the pathophysiologic insights that can be obtained by study of their genotype/phenotype correlations.

Neuroendocrine Phenotypes in Patients Carrying Biallelic Complete Loss of Function Mutations in KISS1R: Evidence for Persistent GnRH Secretion

Typically, patients carrying biallelic complete loss-of-function mutations serve as markers of the most extreme phenotype that can be associated with loss of a particular gene. However, complete loss of kisspeptin signaling is not always associated with complete

GnRH deficiency. The following three cases illustrate this concept (cf. Table 1 for phenotypic details).

Five affected siblings from a large consanguineous family with GnRH deficiency were found to carry a homozygous 155 base pair deletion in *KISS1R* (18). The only affected female presented with some partial breast development and one episode of uterine bleeding. Although her sexual maturation was clearly abnormal, her breast development and uterine bleeding suggest her endogenous estradiol levels were above pre-pubertal values. As part of her baseline diagnostic evaluation, she received 100 µg of GnRH IV which caused her LH to rise from 2.0 to a peak of 11.8 mIU/mL and her FSH from 3.4 to 6.4 mIU/mL, suggesting some gonadotrope responsiveness most likely due to some prior pituitary exposure to GnRH.

An African American patient male carrying the compound heterozygous mutations R331X/X399R presented at age 17 10/12 y for pubertal delay and decreased libido (19, 48). However, despite physical examination correlates of severe androgen deficiency from the ‘minipuberty’ of infancy (microphallus and pre-pubertal sized testes), his gonadotropin levels rose robustly after a GnRH challenge. During frequent blood sampling (q 10 minutes), the patient demonstrated 9 low amplitude LH pulses (19). Eight months after long-term therapy with exogenous pulsatile GnRH (q 2h SC), the R331X/X399R patient demonstrated a left shifted dose-response curve to exogenous GnRH compared to 6 normosmic GnRH deficient men undergoing an identical protocol. Collectively, his responses to the single bolus GnRH test, his baseline LH pulses, and his dose-response study all suggest the presence of some degree of low-level, endogenous pulsatile GnRH secretion.

These observations were echoed in a female proband of Syrian descent who carries homozygous L102P mutations in the first extracellular loop of *KISS1R* (46). This patient also showed a robust LH response (peak value approximately 32 IU/L) in response to a 100µg GnRH stimulation test at baseline assessment. Although only 6 hours of frequent blood sampling was performed, she manifested low amplitude LH pulses occurring approximately once per hour. Another Middle Eastern proband from a separate family, a male carrying homozygous L102P (46), received 6 GnRH stimulation tests from age 12.5 to 21.6 years. Over time, in response to the exogenous GnRH, this patient's LH/FSH ratio changed from less than one (ages 12.5 to 18 y) to greater than one (ages 19.8 to 21.6 years). This maturational switch in gonadotropin ratio values, directly the same as occurs in boys undergoing a normal puberty, could also be explained by the presence of faint but present endogenous GnRH secretion and resultant pituitary priming.

Therefore, the phenotypes of patients carrying the homozygous 155 base pair deletion, compound heterozygous R331X/X399R, and homozygous L102P collectively suggest that evidence for some endogenous GnRH secretion can exist in the face of loss of function kisspeptin receptor mutations. This residual GnRH secretion might be caused by persistent kisspeptin signaling if the *KISS1R* mutations were not completely disabling. However, all 3 sets of mutations listed above have dramatic effects on kisspeptin signaling when tested *in vitro*. The 155 base pair deletion removes the splicing acceptor site of the intron 4-5 junction and part of exon 5 (18). Even if the mutant alleles containing this deletion were transcribed, they would create a receptor protein lacking transmembrane domains 6 and 7 that would presumably be unable to stimulate second messenger signaling. The R331X and X399R mutations create transcripts that are hypothesized to undergo degradation by nonsense- and nonstop-mediated decay mechanisms (19). Even if these transcripts escaped their respective decay processes, *in vitro* studies demonstrated that the mutant receptors created by each of these transcripts functioned poorly. Finally, the L102P mutation is a missense mutation as opposed to a frameshift, nonsense or nonstop. However, L102P was found to completely

abolish inositol phosphate accumulation *in vitro* (46). Therefore, despite apparently completely disabling mutations at least by this bioassay, three individuals with severe biallelic *KISS1R* mutations demonstrated evidence for persistent, albeit abnormal, GnRH secretion as attested to by their partial phenotypes. So either these mutations retain some degree of signaling that was not evident in the *in vitro* assay systems used or there is some 'kisspeptin-independent' GnRH. This theme of kisspeptin-independent GnRH signaling is echoed in *Kiss1^{-/-}* and *Kiss1r^{-/-}* mice, described later in this article.

A Case of Genotype/Phenotype Discordance?

A challenging case is that of a boy of who presented with micropenis and cryptorchidism who was found to harbor C223R/R297L variants in *KISS1R* (50). Neuroendocrine data obtained from the first ten years of life suggested that this patient has severe GnRH deficiency with defects at multiple levels of the hypothalamic-pituitary-gonadal axis. However, this patient did not have two severe mutations. Although the C223R mutation was found to impair signaling profoundly, the R297L variant resulted in a much milder impairment of receptor activity, evidenced by effect on real-time measurements of calcium flux.

So how does one resolve this patient's severe neuroendocrine phenotype with the relatively "mild" genotype evidenced by functional studies of his mutations? That this evaluation was performed before the expected time of puberty may be relevant. The principal modulators of GnRH secretion during the neonatal window may not be identical to those that predominate during adolescent puberty, raising the possibility that with increasing age, this patient might indeed come to display some of the neuroendocrine patterns of the previously-described patients. For example, although his response to the GnRH stimulation test at 10 y was poor, it remains possible that his response to GnRH might improve if he were tested through his teens or early twenties. This patient's poor response to exogenous hCG is notable since other patients bearing *KISS1R* mutations have been responsive to exogenous GnRH/gonadotropins (see below), but may just reflect a negative impact of delayed orchidopexy on testicular function. Although the patient's R297L mutation was not completely disabling in the calcium assays employed, it cannot be excluded that other functional assays looking at, for instance, synthesis, expression at the plasma membrane, and ligand binding, might reveal more deleterious effects. Finally, it is possible that this patient might carry mutations in other genes for GnRH deficiency so that his phenotype is a composite of multiple genetic defects (55).

Some phenotypic aspects of the C223R/R297L case are echoed in a family carrying a homozygous F272S mutation which almost completely inhibited kisspeptin-induced receptor signaling *in vitro* (49). F272S males had cryptorchidism and microphallus; all demonstrated blunted responses to GnRH stimulation during early infancy, again suggesting that *KISS1R* is required for normal functioning of the hypothalamic-pituitary-gonadal axis in infancy. (Notably, individual B3 also had a bifid scrotum and mild chordee.) Interestingly, short and prolonged hCG stimulation tests performed in infancy, childhood, adolescence and early adulthood failed to show a normal testosterone response except in one individual.

Neuroendocrine Phenotypes and Variable Expressivity

KISS1R mutations can also demonstrate variable expressivity within a family. Although four brothers with GnRH deficiency and a homozygous 155 base pair deletion in *KISS1R* demonstrated a severe phenotype, a sister bearing the same homozygous mutations had a less severe phenotype with partial breast development and one episode of uterine bleeding (17). Although all the brothers exhibited a blunted response to GnRH, the affected sister had

a peak LH of 11.8 and FSH of 6.4 units/mL. In another family with a homozygous L102P mutation, a GnRH challenge resulted in a robust LH increase in one affected female (peak approximately 8.5 IU/L) but an affected sister had practically no response. Causes of this variable expressivity are not well understood. Additional genetic inputs (oligogenicity) could account for this phenotypic heterogeneity (53). In contrast to the 155 base pair deletion pedigree, all males in the F272S family exhibited the same clinical features from infancy to adulthood, including undescended testes, microphallus, and absence of pubertal development (49). Therefore, variable expressivity is not uniformly observed within families

Fertility Phenotypes

Although fertility data is available on only a subset of patients, mutations in *KISS1R* do not appear to impact fertility potential. Despite bilateral cryptorchidism and mild hypospadias, a male patient carrying a homozygous *KISS1R* 1001_1002insC mutation responded to exogenous pulsatile GnRH, normalizing testosterone levels and inducing spermatogenesis (44). Even though his semen analysis showed oligoasthenozoospermia, pregnancy, albeit achieved with assisted reproduction, was possible. The male proband harboring R331X/X399R also received pulsatile GnRH and experienced steady increases in testicular volume and the appearance of normal spermatogenesis (48). After approximately 1 ½ years of pulsatile GnRH therapy, with a testicular volume of 12 cc bilaterally and sperm count of 7 M/mL, his partner conceived. A homozygous L148S female had 1) intact responses to exogenous GnRH and gonadotropins, 2) multiple conceptions using the aforementioned therapies as well as IVF, 3) two uncomplicated pregnancies of healthy children, 4) spontaneous initiation of uterine contractions, and 5) lactation for several months post-partum (48). While this data are consistent with an intact ovarian response, no details are available regarding the quality of her follicular response, her ability to ovulate spontaneously, and need for luteal phase support. However, in general, mutations in *KISS1R* do not appear to preclude steroidogenesis and gametogenesis.

Neuroendocrine Phenotypes in Patients Carrying Monoallelic Loss of Function Mutations in *KISS1R*

The contribution of heterozygous mutations in one or more genes (i.e. oligogenicity) is being increasingly recognized in genes for GnRH deficiency (53). For example, the gene encoding the prokineticin receptor, *PROKR2*, is a rich source of mutations in GnRH deficiency, the overwhelming majority of which are heterozygous (monoallelic), as opposed to biallelic variants (56-57). For *KISS1R*, not only are homozygous and compound heterozygous mutations rare, but the number of individuals carrying monoallelic variants is also small.

Previously reported heterozygous, non-synonymous variants in patients' coding sequence of *KISS1R* include L364H (50)(42), A189T (45, 58) and H360L (58). Screening a cohort of 746 probands with GnRH deficient individuals (Kallmann syndrome and normosmic hypogonadotropic hypogonadism) has revealed additional non-synonymous variants including L164F, A194D, C389X, and c.739-7delC (located just before the start of exon 5). These changes were not identified in 324 healthy controls, dbSNP (<http://www.ncbi.nlm.nih.gov/projects/SNP/>), and the 1000 Genome Project (<http://www.1000genomes.org/>). Software programs used to assess the functional significance of variants included PolyPhen (59), Mutation Taster (60), PMUT (61). All three programs suggested that L164F is benign but A194D was predicted by both PMUT and Mutation Taster to be damaging. C398X could only be evaluated by Polyphen which predicted that it was "possibly damaging," although conventionally, premature termination codons are pathologic. For c.739-7delC, Human Splice Finder (62), suggested that the splice acceptor site may

remain the same, or it could be shifted 6 bp in the 3' direction, deleting the first 6 bp's of exon 5. Mutation Taster predicted that even if these two amino acids were to be deleted, the change was still benign. Therefore, while not all of the newly identified heterozygote variants appear to be pathologic, others have a high likelihood of being damaging (C389X and A194D). Although detailed phenotyping information is not yet available on the patients carrying the C389X and A194D heterozygous variants, the information that is available suggests that both individuals have severe GnRH deficiency. The C389X mutation was identified in a Pakistani female who presented with primary amenorrhea, and the A195D variant was identified in a male patient with Kallmann syndrome. While the precise contribution of these heterozygous variants to the GnRH deficient phenotype is unclear, the occurrence of heterozygous mutations in genes for GnRH deficiency is being increasingly recognized—for example, the overwhelming majority of mutations in the gene encoding the prokineticin receptor, *PROKR2*, are heterozygous (56-57). Although these patients carrying C389X and A194D may also have as-yet undiscovered genetic mutations in non-coding regions of *KISS1R*, it is also possible that the previous traditional monogenic status of *KISS1R* genetics may need to be supplanted by an oligogenic framework, as has been demonstrated for many other genes for GnRH deficiency (9, 63).

Insights Gained from *Kiss1^{-/-}* and *Kiss1r^{-/-}* Mice

In general, *Kiss1^{-/-}* and *Kiss1r^{-/-}* mice phenocopy humans bearing *KISS1R* mutations. Both *Kiss1^{-/-}* and *Kiss1r^{-/-}* mice have abnormal sexual maturation, with small gonads, low gonadotropins, and abnormal gametogenesis (19-20, 64-65). Migration of GnRH neurons into the hypothalamus is normal in *Kiss1^{-/-}* animals along with appropriate axonal connections to the median eminence and total GnRH content (64). Both *Kiss1^{-/-}* and *Kiss1r^{-/-}* mice are infertile as pregnancies do not occur when either mouse is housed with WT mice of proven fertility (65).

However, *Kiss1^{-/-}* animals exhibit considerable phenotypic variability that is reminiscent of their human counterparts. *Kiss1^{-/-}* female mice with small vaginal openings, decreased ovarian size, and scant folliculogenesis respond with the largest increments in LH and FSH to exogenous kisspeptin whereas *Kiss1^{-/-}* mice with larger gonadal weights, larger vaginal openings, and persistent vaginal cornification on their smears have a less robust gonadotropin response (65). *Kiss1^{-/-}* males also have a more modest phenotype than their *Kiss1r^{-/-}* counterparts, although although some animals of both lines have sperm counts approaching those of WT animals (64-65).

Despite their infertility, *Kiss1^{-/-}* female mice can develop follicles up to the pre-ovulatory level, although no spontaneous ovulations are observed (66). Both *Kiss1^{-/-}* and *Kiss1r^{-/-}* females alternate between periods of prolonged diestrus and prolonged estrus. These transitions increase in frequency with increasing age and are not associated with changes in hypothalamic *GnRH1* mRNA expression. Administration of the competitive GnRH antagonist acyline completely disrupts the estrus exhibited by *Kiss1^{-/-}* and *Kiss1r^{-/-}* female mice, thus demonstrating that this estrus is due to GnRH activity. Although frequent blood sampling studies have not been performed in either wild type, *Kiss1^{-/-}*, or *Kiss1r^{-/-}* mice, the low amplitude LH pulsations observed in multiple patients with *KISS1R* mutations appears to be echoed in the persistent GnRH activity documented in *Kiss1^{-/-}* and *Kiss1r^{-/-}* mice. Kisspeptin-independent GnRH activity, whether in mice or men, could be due to low level constitutive activity of GnRH neurons or could be induced by other neuroendocrine pathways that modulate GnRH neuronal secretion.

Understanding the contribution of other pathways to the regulation of GnRH neurons will undoubtedly be enhanced by future genetic discoveries.

From Loss of Function to Gain of Function in the Kisspeptin Signaling Pathway

The kisspeptin pathway stands in unique contrast to all the other pathways involved in GnRH deficiency as it harbors gain of function mutations in patients with central precocious puberty (CPP), a contrarian phenotype to GnRH deficiency. The first patient reported to carry a gain of function mutation was an 8 year old adopted Brazilian female who experienced slowly progressive premature breast development since birth (67). A rare sequence variant was detected in the C terminal tail of KISS1R (R386P). When tested, R386 mutant receptors did not increase constitutive activity of KISS1R, its binding capacity, or responsiveness to kisspeptin. However, the decline in inositol phosphate accumulation was slower in cells transfected with the R386P mutant receptor compared with WT, and the phosphorylation of extracellular signal-regulated kinase was prolonged, indicating a significant reduction in the rate of desensitization of the mutant KISS1R. Recent studies have demonstrated that R386P prolongs kisspeptin responsiveness by decreasing the degradation of its receptor (68). Thus, this case stands as a model of nonconstitutive KISS1R activation associated with precocious pubertal development.

Recently two *KISS1* mutations (P74S and H90D) were identified in three unrelated children with idiopathic CPP. The P74S mutation was identified in a boy with pubertal development beginning at 12 months (69). At 17 months, his penis was 8×2 cm, with testes of 2.3×1.5 cm (right) and 2.6×1.2 cm (left). His bone age was advanced to 3 years. His basal FSH was 8.3 U/L, and his basal LH was 11.5 U/L which rose after GnRH stimulation to 47.2 U/L. His testosterone was 600 ng/dL and a brain MRI was normal. He was successfully treated with a GnRH analog for 9 years. The H90D variants were identified in two girls who underwent puberty at 6 and 5.5 years of age. Both had advanced bone age and pubertal levels of estradiol and basal LH. *In vitro*, the P74S and H90D mutants stimulated IP production to a similar degree. After incubation in 50% human serum for 2 h, the dose-response curves of both the WT and P74S mutant shifted to the right; the P74S had less of a rightward shift than the WT suggesting that this variant may be more resistant to degradation. Because the P74S is located in a PEST sequence, a region associated with rapid degradation of proteins, a potential gain of function mutation might result in increased protein availability due to decreased degradation. Although the H90D variant did not show resistance to degradation, the *in vitro* studies of the P74S mutant kisspeptin suggest that it might play a role in the patient's precocious puberty phenotype.

Phenotypes Outside the Reproductive Cascade

Metabolic stress is well known to affect reproductive function and the physiologic basis for the connection between energy balance and reproduction is an area of intense investigation. It has been hypothesized that kisspeptin neurons may be sensitive to the energy reserve of the organism and may transmit information regarding metabolic status to the rest of the gonadotropic axis. This hypothesis originally emerged when it was demonstrated that rats subjected to a 3 day fast demonstrate a significant drop of *Kiss1* mRNA in the hypothalamus (26). Similarly, rats in whom uncontrolled diabetes has been induced by streptozotocin develop hypogonadotropism and suppression of hypothalamic *Kiss1* mRNA (43). Links between leptin, a major indicator of energy status, and kisspeptin were first demonstrated when mice with congenital lack of leptin were shown to have significant reduction of *Kiss1* mRNA in the arcuate nucleus (42). Despite the evidence suggesting that kisspeptin neurons might mediate leptin's effects on the reproductive cascade, there are additional, kisspeptin-independent pathways that may convey leptin's effects on the reproductive axis, such as those localized to the ventral pre-mammillary nucleus (70). While the molecular mechanism underlying leptin's regulation of kisspeptin are largely unknown, recent data suggest that the

mammalian target of rapamycin (mTOR) and its downstream effectors may be a conduit from leptin to *Kiss1* gene expression (71). As increasing number of patients with *KISS1R* mutations are identified, more provocative phenotyping studies will be required to determine if there are abnormalities in the integration of metabolic status and reproductive function.

Summary

Although mutations in *KISS1R* are not a common cause of hypogonadotropism, they reveal the critical role played by the kisspeptin signaling pathway in pubertal initiation and reproductive function.

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Abbreviations

GnRH	gonadotropin-releasing hormone
LH	luteinizing hormone
FSH	follicle stimulating hormone

Table 1
Clinical characteristics and hormone profile of patients bearing biallelic mutations in *KISS1R*

Patient	Mutation (Biallelic) & Ref ID	History	Baseline	GnRH Challenge (Basal--Peak)			Treatment			Outcome
				LH	FSH	LH & FSH	T & E2	LH & FSH	G-nRH	
IV:6	L148S #19, 47, 48	Delayed puberty	LH< 1IU/L	↑ 40-50%	↑ 40-50%	Y	Y	Y	Y	Fertility
		TV 3 cc	FSH 0.8 IU/L							
IV:2		Delayed puberty	T 3 ng/dL	3--8.4 IU/L	2--4.6 IU/L	Y	Y	Y	Y	Fertility
		TV 2 cc	LH 4.1 IU/L							
IV: 4		1° amenorrhea	T 29 ng/dL							
IV: 5		"Short" penis	LH 0.5 IU/L	0.5--3 IU/L	0.7--5 IU/L	Y	Y	Y	Y	Fertility
		TV 1 cc	FSH 0.7 IU/L							
IV:15		TV 5 cc	T 14 ng/dL							
		P2-3	LH 2.8 IU/L							
IV:11		B3	FSH 3.7 IU/L							
		P4	T 37 ng/dL							
III:2	Del 155 bp # 18	P3	LH 0.53 IU/L	1.5--3.6 mIU/mL	0.5--1.7 mIU/mL	Y	Y	Y	Y	Fertility
		Penis 7 cm	FSH 2.55 IU/L							
III:3			E2 28 ng/dL							
III:4			T 26 ng/dL	1.5--1.4 mIU/mL	0.5--1.5 mIU/mL	Y	Y	Y	Y	Fertility
			T 19 ng/dL							
III:6			T 5 ng/dL	1.1--1.9 mIU/mL	4.1--4.1 mIU/mL	Y	Y	Y	Y	Fertility
			T 5 ng/dL							
III:7	R331X/X399R # 19, 48	Partial breast	E2 17 ng/dL	2.0--11.8 mIU/mL	3.4--6.4 mIU/mL	Y	Y	Y	Y	Fertility
			T 5 ng/dL							
C223R/R297L		↓ hair	LH 2.2 IU/L	2.4--12.7 mIU/mL	8.1--23.4 mIU/mL	Y	Y	Y	Y	Fertility
		Penis 5 cm	FSH 3.2 IU/L							
		TV 1.2 mL	T 10 ng/dL							
		Microphallus	2 mo:	10 years:						

Patient	Mutation (Biallelic) & Ref ID	History	Baseline	GnRH Challenge (Basal--Peak)			Treatment		Outcome
				LH	FSH	LH & FSH	T & E2	GnRH	
	# 50	Cryptorchidism	LH<0.5mIU/mL FSH<0.5mIU/mL	<0.7--1.0 IU/L	<0.2--1.1 mIU/mL				
	1001-1002	Mild hypospadias	LH 1.1 IU/L	peak 10.5 IU/L	peak 5.7 IU/L	Y	Y	Y	Fertility
	insC	Cryptorchidism	FSH 2.2 IU/L						
	# 44		T 3.4 nmol/L						
Family I, I.1	L102P	1° amenorrhea	LH 2.8 IU/L			Y		Y	Fertility
	# 46	B4	FSH 5.9 IU/L						
Sister		1° amenorrhea	E2 24 pmol/L						
Brother		Delayed puberty							
Family II, II.1		Cryptorchidism	LH 0.5 IU/L	0.5--2.5 IU/L	2.0--4.0 IU/L	Y		Y	
			FSH 1.62 IU/L	Over 10 y; ↑LH/FSH					
			T 0.1 ng/mL						
II.2		1° amenorrhea	LH <0.5 IU/L	0.5--0.5 IU/L	2.0--1.2 IU/L	Y		Y	Bleeding
		P5	FSH 1.1 IU/L						
		B3	E2 <50 ng/mL						
II.3		1° amenorrhea	LH 1.3 IU/L	1.5--8.5 IU/L	4.0--9.0 IU/L	Y		Y	Bleeding
		P3	FSH 4.0 IU/L						
		B3	E2 <50 ng/mL						
II.4		Cryptorchid	LH <0.5 IU/L					Y	
		TV 3 mL	FSH <0.4 IU/L						
		Penis 5 cm	T 0.34 ng/mL						
Older	IVS2-4_-2	Microphallus	T 24 ng/dL	0.37--4.34 IU/L	2.3--6.39 IU/L				
	delGCA	Cryptorchidism							
	insACCGGCT								
Younger	# 45	Microphallus	LH <0.1 IU/L						
		Cryptorchidism	FSH 1.2 IU/L						
A1	F272S	TV 1.5 mL	T <0.7 nmol/L	<0.1--0.3 IU/L	0.45--2 IU/L				

Patient	Mutation (Biallelic) & Ref ID	History	Baseline	GnRH Challenge (Basal--Peak)			Treatment		Outcome
				LH	FSH	T & E2	LH & FSH	GnRH	
A2	# 49	Penis 5.5 cm TV 0.5 mL							
B1		Penis 3.2 cm TV 1 mL	T < 0.7 nmol/L	< 0.1--0.6 IU/L	0.4--3.6 IU/L				
B2		Penis 5 cm TV 2 mL	T < 0.4 nmol/L	< 0.1--1.7 IU/L	0.6--2.7 IU/L				
B3		Penis 5.5 cm TV 1 mL	T < 0.4 nmol/L	< 0.1--1.5 IU/L	0.8--4.0 IU/L				
B4			LH < 0.07 IU/L FSH 1.54 IU/L E2 undetectable						