Focus on Gonadotrophin Signalling

An update of the pathophysiology of human gonadotrophin subunit and receptor gene mutations and polymorphisms

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Abstract

New information about mutations and polymorphisms in the genes for the gonadotrophins and their receptors has become available in the last few years. In this short review mutations and polymorphisms in gonadotrophins, their receptors and their pathophysiological effects and implications are discussed. An increasingly clear picture about the structure–function relationships of gonadotrophin action is emerging from the combining the types and the locations of the mutations with their phenotypic effects and the information about the crystal structure of these molecules.

Introduction

The most recent comprehensive overview of mutations in gonadotrophin subunit and receptor genes and their pathophysiological consequences was published some 5 years ago (Themmen & Huhtaniemi 2000). Since the knowledge in this field has expanded considerably during the past years I will present here an update on the information in the field that has accumulated in the last 5 years since the publication of the review.

The general principles of pathophysiological consequences of mutations and polymorphisms affecting gonadotrophin action will be introduced, followed by the recent advances in the field. New polymorphisms and mutations that have been detected in the genes for luteinising hormone (LH) and follicle-stimulating hormone (FSH) and their receptors (LH receptor and FSH receptor) will be discussed in detail. In Themmen and Huhtaniemi (2000) a comprehensive overview of the topic up to the year 2000 can be found. That paper contains extensive tables and figures specifying most of the mutations and variants of the common-α, LHβ, FSHβ, LH receptor and FSH receptor genes.

Functional consequences of mutations and polymorphisms affecting gonadotrophin action

Gonadotrophin receptors

The LH and FSH receptors together with their homologue the receptors for thyrotrphin-stimulating hormone (TSH), constitute the family of glycoprotein hormone receptors, a subfamily of the large group of G protein-coupled receptors (GPCRs). The TSH and FSH receptors (gene names: TSHR and FSH receptor) both have a single ligand, TSH and FSH respectively, whereas the LH receptor binds both LH and chorionic gonadotrophin (hCG in humans), an LH analogue produced by the placenta during pregnancy in primates and equine species. The LH receptor is therefore also known as the LH/CG receptor (gene name: LHCGR). These receptors have a rhodopsin-like transmembrane (TM) domain (Palczewski et al. 2000, Themmen & Huhtaniemi 2000, Dias & Van Roey 2001, Ascoli et al. 2002, Szkudlinski et al. 2002) in common with the superfamily of GPCRs. In addition, they have a large N-terminal extracellular domain (ECD; 359–414 amino acid residues; homology ~40%), which conveys specific hormone binding to the receptors (Braun et al. 1991, Cornelis et al. 2001, Remy et al. 2001). The TMs of individual glycoprotein hormone receptors appear to be functionally interchangeable and display high sequence homology (~70%) between the different glycoprotein hormone receptors.

Based on sequence analysis and comparison with other proteins (Kobe & Deisenhofer 1993), the ECDs of the glycoprotein hormone receptors were suggested to contain nine leucine-rich repeats (LRR) flanked by N- and C-terminal cysteine-rich regions. LRR motifs have been recognized in a large number of distinct proteins (Kobe & Kajava 2001) and are thought to form a horseshoe-like structure.
Together, these repeats form a flat concave surface consisting of short β turns to which the large ligand can bind. This structure is stabilized by short, parallel α-helical stretches that connect the beta-strands. The hormone binds to the β surface using multiple contact points and the helical segments are aligned to form the outer convex side of the ECD (Jiang et al. 1995, Kajava et al. 1995, Bhownick et al. 1996).

Very recently, the report of the crystal structure of a complex of FSH with the ECD of the FSH receptor has corrected and further refined the existing models (Fan & Hendrickson 2005). This report shows that the β-sheet contains 9 parallel strands and a 10th that is contributed by the N-terminal cystine repeat. Furthermore, the curvature of the hormone-binding concave β-sheet is less strong (Fan & Hendrickson 2005). In the FSH–FSH receptor crystal, FSH is positioned in the FSH receptor tube formed by the concave β-sheet with its long axis perpendicular. The structure also suggests that the FSH receptor may either dimerize upon FSH binding, or may exist as a pre-formed dimer complex without ligand. In addition, the crystal reveals detailed information on the identity of the amino acids that are involved in the interaction between FSH and its receptor. The seat belt structure of FSH (see below) is directly involved in hormone–receptor interaction (Fan & Hendrickson 2005).

Gonadotrophin subunits

The glycoprotein hormones are heterodimers, each consisting of an α and a β subunit. The α subunit is identical in all hormones, whereas the β subunit confers the specificity to the hormone (Themmen & Huhtaniemi 2000). The crystal structures of deglycosylated hCG and FSH are known (Lathorn et al. 1994, Fox et al. 2001) and, as expected, they are very similar. Although the α and β subunits show no amino acid sequence similarity, their three-dimensional structures are remarkably similar, having an elongated shape defining the long axis with two β-hairpin loops on one side and a single hairpin loop on the other side. The β-hairpins are stabilized by disulphide bridges. The α and β subunits form an elongated slightly curved structure and are non-covalently associated in a head-to-tail orientation by means of a cystine knot motif. Thus, the gonadotrophins are members of the superfamily of cystine knot growth factors. Other members include nerve growth factor and platelet-derived growth factor–β. The cystine knot motif is characterized by a cluster of cystine disulphide bonds in each subunit. The cystine knot consists of an eight amino acid ring through which an intra-subunit disulphide bond is formed. The α–β dimer is held together by a ‘seatbelt’ structure formed by the C-terminal amino acids of the β subunit wrapped around the α subunit and stabilized by one of the disulphide bonds. Both the association of the subunits and the binding of the heterodimer to the receptor are dependent on this seatbelt.

Extensive studies on site-directed mutagenesis have unravelled the role of a number of amino acids in the tertiary structure of this subunit, including the structures necessary for glycosylation, proper folding, heterodimerization with the β subunit and receptor binding and signal transduction of the dimeric hormone.

Mutations and polymorphisms in human luteinizing hormone and its receptor

LH receptor

As reviewed previously (Themmen & Huhtaniemi 2000), LH receptor mutations (Fig. 1) can be activating, causing precocious puberty in boys, and inactivating, disrupting sex differentiation in men and causing anovulation in women. In the following sections, we will review the recent new mutations that have been described in the LH receptor gene.

Activating LH receptor mutations

A missense Leu368Pro mutation located in the first transmembrane helix of the transmembrane domain was found in two Brazilian brothers showing typical precocious puberty at an early age (2 and 3 years of age) (Latronico et al. 2000). In vitro expression of this mutant showed a similar pattern to many of the mutant LH receptors that are constitutively active (Themmen & Huhtaniemi 2000). Thus, cAMP production was increased in the absence of added hCG, and at higher hCG concentrations the receptor responded with further increases in cAMP, never reaching the levels attained at maximal response in the non-mutant LH receptor. As noticed in other families (Rosenthal et al. 1996), the mother of these two sons was also a carrier of the mutation, indicating that carriership of an activating mutation in the LH receptor gene has no adverse effects on female infertility (Latronico et al. 2000).

Amino acid Asp578 in the LH receptor deserves special discussion with respect to activating LH receptor mutations. Asp578Gly is one of the most common activating mutations found in the LH receptor gene (Shenker et al. 1993, Laue et al. 1995), while tyrosine (Tyr) or glutamate (Glu) at this position also cause precocious puberty (Laue et al. 1995, 1996). However, Asp578His causes Leydig cells to undergo transformation and their increased growth results in adenoma formation (Liu et al. 1999). Interestingly, this mutation appears only to occur somatically, i.e. it is found only in the Leydig tumours themselves, but not in the germ line. Other case reports describe the same mutation (Canto et al. 2002, Richter-Unruh et al. 2002b), while another two studies on sex cord tumours failed to reveal any LH receptor mutations (Giacaglia et al. 2000, Vieira et al. 2002), indicating that not all Leydig cell adenomas are caused by the Asp578His somatic mutation in the LH receptor gene.

Another LH receptor mutation in the 2nd transmembrane α-helix, Met398Thr, has been reported in case reports (Ignacak et al. 2000, 2002). This mutation is of
special interest, since it shows incomplete penetrance, i.e. not all male family members that are carriers of the mutation show the precocious puberty phenotype (Evans et al. 1996). It will be of interest to study these families in more detail, since the incomplete penetrance may indicate interaction with a modifier gene that silences the activating effects of the amino acid change in the LH receptor.

Inactivating LH receptor mutations

Inactivating mutations can take many forms (Themmen & Huhtaniemi 2000) – large partial gene deletions to smaller deletions of just two amino acids and nonsense mutations resulting in truncated LH receptor protein have been described. As an example, the homozygous insertion of one base pair (T) at codon 589 can be mentioned (Richter-Unruh et al. 2005). This insertion causes a frameshift in the LH receptor gene resulting in a truncated LH receptor protein. The functional consequences of this truncation were not tested in vitro. The patient, a 46XY patient with complete pseudohermaphroditism, showed lack of responsiveness to LH/hCG with concomitant undetectable serum testosterone (Richter-Unruh et al. 2005).

Inactivating LH receptor mutations have also been identified in the extracellular hormone-binding domain. In a complete 46XY pseudohermaphrodite patient a very low number of testicular Leydig cells was found accompanied by a low LH receptor expression (Gromoll et al. 2002). The patient was found to be homozygous

Figure 1 The currently known mutations and amino acid altering polymorphisms in the human LH receptor gene. The green circles depict the activating mutations, the red squares inactivation mutations, and the asterisks the polymorphisms. Stp = nonsense (stop) codon.
for a missense Phe194Val mutation located in exon 7 in a motif that is conserved in the glycoprotein hormone receptor family. The Phe194Val LH receptor did not respond at all to hCG in vitro. Phe194 is located in an interesting motif, AFNGT, conserved in the gonadotrophin receptors. N195GT is a glycosylation motif and the change of the homologous Ala189 in the FSH receptor to Val, identified in some patients with hypergonadotrophic ovarian dysgenesis (Aittomäki et al. 1995), causes complete inactivity of the FSH receptor due to intracellular sequestration of the mutant receptor protein (Rannikko et al. 2002). An Asn191Ile change in the FSH receptor, which was found in a heterozygous patient without phenotype, leads to decreased coupling to the cAMP pathway (Gromoll et al. 1996b).

From the same group an interesting follow-up to the del(exon 10) LH receptor mutant has been published. This deletion was originally described in a patient who had normal male sex differentiation, but did not show signs of puberty, apparently because the del(exon10) LH receptor did not respond to LH, while it was sensitive to hCG, hence the intact male sex differentiation (Gromoll et al. 2000). Indeed, in vitro expression of the del(exon10) LH receptor shows a nearly normal response to hCG whereas the dose–response relationship for LH is severely shifted to the right (Muller et al. 2003). The human del(exon10) LH receptor mutation has an interesting parallel in the marmoset monkey. The marmoset uses CGβ rather than LHβ for LH receptor stimulation. The marmoset pituitary does not express LHβ (Muller et al. 2004). Concomitantly, the marmoset monkey LH receptor always misses the amino acids equivalent to the exon 10 encoded amino acid residues (Zhang et al. 1997). The authors propose that owing to an unknown mutational event in evolution, expression of marmoset LH was completely abolished, and marmoset CG – which, unlike LH, acts normally even when exon 10 is missing from the LH receptor – took over its function.

A homozygous Val144Phe mutation in the LH receptor gene was found in a 46XY patient with an almost complete female phenotype. In vitro, the mutant LH receptor protein was not transported to the plasma membrane. Inability of the protein to be transported to the cell surface has also been shown with some other missense or truncation mutations such as Cys343Ser, Cys543Arg (Martens et al. 2002), Leu502Pro (Leung et al. 2004) and Tyr612Stop (Salameh et al. 2005).

Both Val144 and Phe194 are thought to be located (based on a previously published model of the extracellular domain of the LH receptor; Jiang et al. 1995) on the convex side of the leucine-rich repeat domain of the LH receptor protein (Val144 in the 4th helical segment; Phe194 in the 6th), so apparently are not directly involved in ligand binding.

**LH receptor polymorphisms**

The LH receptor gene carries a large number of single nucleotide polymorphisms (SNPs). According to the SNPper website (http://SNPper.chip.org) 282 SNPs are found in the LH receptor gene, resulting in an average distance between SNPs of 306 base pairs. Exact allele frequencies are not available for most of these polymorphisms. The most frequent LH receptor polymorphisms that involve an amino acid change are the absence or presence of a two amino acid insertion at position 18 in exon1 (insLQ; allele frequency 29%), and two variable amino acids at position 291 and 312 respectively: N291S (S allele: 10%) and N312S (N allele: 45%) (Richter-Unruh et al. 2002a). In addition, an R124Q has been described as an SNP but with low frequency. Powell and coworkers (2003) recently reported that breast cancer patients have a significantly worse overall survival when they are either homozygous or heterozygous carriers of the insLQ allele (Hazard Ratio 2.4; P = 0.006) (Powell et al. 2003). In addition, trends were observed for associations between the insLQ carriers and nodal involvement or larger tumour size. These results indicate that the insLQ polymorphic insertion probably has an effect on LH receptor protein function, although one report showed that in vitro hCG signal transduction of the two LH receptor variants was not different (Rodien et al. 1998b). The finding of an association of breast cancer disease with insLQ needs independent confirmation. A plausible explanation for the observed association of insLQ with breast cancer could be through an effect of LH through the LH receptor, with or without insLQ, causing an increase in the levels of oestrogens in the serum, which, in turn, may stimulate breast cancer cells and therefore cause recurrence of the disease. Alternatively, direct effects of LH on breast cancer cells themselves have been suggested (Guo et al. 2004). Since LH is a major regulator of ovarian steroid hormone production, further investigations are needed into the possible role of the polymorphism in other steroid hormone-related diseases. These include prostate cancer in the male and oestrogen-related disease endpoints such as bone density or fractures in elderly women.

**LHβ subunit**

As yet, only a few mutations are known in the gonadotrophin subunit genes (Fig. 1). None of these mutations are activating the genes, all appear to be loss-of-function mutations. Two subjects with LHβ and 7 with FSHβ inactivation have been described in the literature (Themmen & Huhtaniemi 2000, Layman et al. 2002, Valdes-Socin et al. 2004). Conspicuously, no germ line mutations in the common-α subunit or hCGβ subunits are known. The reason may be that such mutations would inactivate chorionic gonadotrophin (hCG), which may be embryo lethal, or even incompatible with implantation.
LHβ mutations

Compared with the rare loss-of-function LH receptor mutations (n = 17), mutations in the LHβ gene (Fig. 2) have proven to be very rare. Only the second report of a homozygous carrier of a missense inactivating mutation in the LHβ gene was published recently (Valdes-Socin et al. 2004). In the hypogonadal 30-year-old 46XY patient, low circulating LH was found with concomitant reduced spermatogenesis and hypoplastic Leydig cells, hallmarks of absent LH signalling as found in patients with inactivating LH receptor gene mutations (Valdes-Socin et al. 2004). The patient's mutant Gly36Asp LHβ was expressed in vitro together with the common α-subunit, and showed absence of α/β heterodimerization and therefore no LH bioactivity (Valdes-Socin et al. 2004). The Gly36Asp in the LHβ subunit disrupts a 5-amino acid motif that allows the formation of a cystine knot (see above). In the absence of the cystine knot structure no dimerization can occur, and no bioactive LH can be produced.

This effect of the mutation is different from the other published inactivating LHβ mutation (Weiss et al. 1992). In this case the Gln54Arg abolished interaction of the LHα/β dimer with the LH receptor, resulting in delayed puberty and absent testosterone production and spermatogenesis in the patient (Weiss et al. 1992). Both LHβ mutations illustrate the role of LH during sex differentiation. Apparently, LH is not necessary for male differentiation before birth, since both patients had a male phenotype and descended testes. The fetal activation of Leydig cell proliferation, differentiation and testosterone production is taken care of by placental hCG, allowing these patients to undergo fetal male sex differentiation and insulin-like factor 3-mediated testis descent.

LHβ polymorphisms

The best-studied polymorphism in the LHβ gene is a combination of two SNPs (T82C/T104C) that are in complete linkage disequilibrium and results in a combination of two amino acid changes: Thr8Arg/Ile15Thr (Furui et al. 1994, Pettersson et al. 1994). This polymorphism (V-LH) is found worldwide at highly variable frequencies in cohorts studied from different countries and different ethnic groups. Most recent association studies of the V-LH gene polymorphism were carried out using relatively small cohorts or were case reports (Okuno et al. 2001, Takahashi et al. 2000a, 2001). The V-LH polymorphism can be studied in two ways: using PCR-based techniques that analyse the polymorphisms at the DNA level, and using an ELISA based on a specific antibody that does not recognize V-LH and therefore reports lower LH levels than do other assays (Pettersson et al. 1992). Several studies were conducted to investigate possible effects of the two amino acid changes on LH function and to identify possible associations with disease endpoints (reviewed in Themmen & Huhtaniemi 2000). No association of the V-LH allele with infertility was found in cohorts of 95 male infertility patients (Lee et al. 2003), in a comparison of 145 infertile with 200 fertile men (Ramanujam et al. 2000), or in association studies of several endocrine-related cancers (Cramer et al. 2000, Powell et al. 2003). Nevertheless, V-LH appears to have functional effects, since in a study of 40 healthy Japanese women, V-LH carriers appeared to respond to...
a gonadotrophin-releasing hormone challenge with a higher maximal LH response (Takahashi et al. 2000b). Further evidence for the functional differences of V-LH from normal LH was obtained by comparing the in vitro and in vivo behaviour of recombinant forms of the two hormones. V-LH displayed higher biopotency in vitro, whereas its half-life in the circulation was shorter than that of normal LH (Manna et al. 2002). Moreover, the carbohydrate side chain composition of V-LH was clearly different, suggesting different pathways in its intracellular processing.

A second polymorphic variant of the LHβ gene is an SNP that causes a Gly102 to Ser amino acid change (Lamminen et al. 2002). The frequency of this LHβ polymorphism appears to be low, and in cohorts from Finland, India, Denmark, Rwanda and Korea the Ser allele was absent (Kim et al. 2001, Lamminen et al. 2002, Lee et al. 2003). In one study (Singaporean Chinese), the Ser allele polymorphism was detected in infertile men (5 out of 145) but not in the fertile control group (n = 200) (Ramanujam et al. 2000).

A third polymorphic variant of the LHβ gene was identified by Jiang and colleagues (2002). This SNP causes an Ala to Thr change three amino acid residues before the signal peptide cleavage site (Ala3Thr). The Thr variant was confirmed by Jiang and colleagues (2002). This SNP causes an impairment of LH β protein, although the mature proteins are essentially identical with respect to their amino acid composition. Thus, Ser<sup>-3</sup> LHβ was more potent in stimulating cAMP in treated cells, whereas the Thr<sup>-3</sup> LHβ appears to be more effective in stimulating phosphatidylinoside (PI) turnover (Jiang et al. 2002).

One possible polymorphism in the hCGβ gene has been reported, an SNP that causes a change from Val to Met at position 79 (Fig. 2) (Miller-Lindholm et al. 1999). In this report the frequency of the Met allele appeared to be quite high (4.2%). Upon in vitro expression in cultured cells Met79-LHβ was unable to fold correctly and this resulted in impaired ability to associate with the α subunit, suggesting that the Met79 allele may have deleterious effects. However, when the same polymorphism was searched for in 580 DNA samples from 4 European populations, not a single case was found (Jiang et al. 2004). The real frequency and significance of this polymorphism thus remains unknown.

Mutations and polymorphisms in human follicle-stimulating hormone and its receptor

FSH receptor

As with the LH receptor gene, FSH receptor gene mutations exist, in principle, in gain-of-function or activating and in loss-of-function or inactivating forms (Fig. 3). Until now only one case of an activating FSH receptor mutation has been described in a case of persistent spermatogenesis of a hypophysectomized man (Gromoll et al. 1996a). The number of inactivating FSH receptor mutants is slowly increasing.

Activating FSH receptor mutations

Whereas no additional activating FSH receptor mutations have been described, in vitro FSH receptor mutagenesis showed that such amino acid changes are certainly possible (Tao et al. 2000). It remains to be established whether activating FSH receptor mutations cause a phenotype other than the very special case of the hypophysectomized man in which the single FSH receptor mutation was detected (Gromoll et al. 1996a) and searches for activating FSH receptor mutations in candidate diseases, such as premature ovarian failure, ovarian tumours, megalotestes, precocious puberty and twin pregnancies have been unsuccessful (Giacaglia et al. 2000, Montgomery et al. 2000, de la Chesnaye et al. 2001, Takakura et al. 2001, Tong et al. 2001, Sundblad et al. 2004). An animal model for an activating FSH receptor mutation would be seminal in resolving this intriguing question.

The similarity of the glycoprotein hormones makes the receptors vulnerable to mutations that would relax ligand specificity, especially during early pregnancy when hCG levels in women are extremely high. Indeed, such mutations have been described in the TSH receptor gene causing hCG-induced hyperthyroidism during pregnancy (Rodien et al. 1998a). Similarly, the FSH receptor may become sensitive to hCG during pregnancy causing ovarian hyperstimulation syndrome (OHSS). Such FSH receptor mutations were recently reported in women who had recurrent OHSS during consecutive pregnancies (Kaiser 2003, Smits et al. 2003, Vasseur et al. 2003, Montanelli et al. 2004). Expression of the mutant FSH receptors showed stimulation of cAMP production by hCG through the mutant FSH receptors (Kaiser 2003, Smits et al. 2003, Vasseur et al. 2003). In two of the cases (Asp567Asn and Thr449Ala), low levels of constitutive receptor activation and response of the mutated receptor to TSH were also found (Montanelli et al. 2004). The location of the mutations in the FSH receptor protein was surprising. Neither of the changed amino acids (Thr449Ile, Ala and Asp567Asn) are located in the extracellular hormone binding domain, but rather in the transmembrane part of the FSH receptor. In addition, no high affinity hCG binding to the mutant receptors could be demonstrated. In one of the papers it is suggested that weakening of interhelical locks between the transmembrane helices by the mutations might make the receptor more vulnerable to low affinity activation by other glycoprotein hormones (Montanelli et al. 2004).

Inactivating FSH receptor mutations

Altogether 9 inactivating mutations are known in the human FSH receptor gene. The first one, Ala189Val,
was described about 10 years ago (Aittomäki et al. 1995) in subjects of multiple Finnish families with a phenotype of hypergonadotrophic hypogonadism, primary or early onset secondary amenorrhea, variable development of secondary sex characteristics and arrest of follicular maturation between the primordial and pre-antral stages. This mutation appears to be unique to the Finnish population. The mutant FSH receptor protein does not traffic to the plasma membrane, rendering the gene inactive (Rannikko et al. 2002). In addition, when homozygous Ala189Val FSH receptor patients were treated with massive doses of recombinant FSH, no functional responses of the ovaries or testes were observed (Vaskivuo et al. 2002). A similar patient was described who was homozygous for a Pro419Thr mutation (Meduri et al. 2003). The affected female presented with hypergonadotrophic premature ovarian failure, very low oestrogen and inhibin B levels, and total lack of response to high doses of recombinant FSH. Pro419 is located in the 2nd extracellular loop of the transmembrane domain in a conserved motif in the glycoprotein hormone receptors. Histological analysis of ovarian biopsies showed a similar pattern to that found in patients with the Ala189-Val FSH receptor mutations: arrest of follicular maturation beyond the primary stage. Also this receptor was completely unable to traffic to the plasma membrane, reminiscent of many of the inactivating LH receptor mutants (see above).

Figure 3 The currently known mutations and amino acid altering polymorphisms in the human FSH receptor gene. The green circles depict the activating mutations, the red squares inactivation mutations, and the asterisks the polymorphisms.
Other patients with FSH receptor gene mutations had less severe phenotypes, with secondary amenorrhoea, gonadotrophin resistance, normal ovarian size and presence of follicles up to the antral stage (Beau et al. 1998, Touraine et al. 1999). These patients were carriers of combinations of complete and partially inactivating mutations. Several additional FSH receptor mutations have recently been discovered, all in women. It appears that the male phenotype of inactivation of the FSH receptor gene is quite weak, with normal androgen production, reduced sperm quality but maintained fertility (Tapanainen et al. 1997).

A patient with a compound heterozygous mutation of Ala189Val and Ala419Thr was recently reported (Doherty et al. 2002). She appeared to be less affected than the homozygous Ala189Val patients described before (Aittomäki et al. 1995). At 17 years of age she had primary amenorrhoea, normal secondary sex characteristics, very low oestrogen levels but clear signs of endometrial oestrogen stimulation in transvaginal ultrasound investigation, and a normal progestin challenge test. The Ala419Thr FSH receptor bound FSH normally, but did not signal in vitro (Doherty et al. 2002).

The last mutation reported was a Pro348Arg substitution just outside the transmembrane domain of the receptor protein completely abolishing FSH binding, although it was not investigated whether this was due to intracellular sequestration of the receptor or to a genuine lack of ligand binding to a plasma membrane-expressed receptor (Allen et al. 2003). The female patient was hypergonadotrophic with delayed puberty and primary amenorrhoea.

Despite the rarity of the currently known FSH receptor mutations there is good correlation between the phenotype and the degree of receptor inactivation, as well as the site of mutation and its functional consequences, in the same fashion as with the larger number of LH receptor mutations (Themmen & Huhtaniemi 2000). Mutations in the extracellular domain (Ile160Thr, Ala189Val, Asn191Ile, Asp224Val and Pro346Arg) completely abolish FSH receptor function and are found in the patients with the severest phenotypes. Transmembrane domain mutations (Ala419Thr, Arg573Cys and Leu602Val) have decreased but not completely abolished signalling and these patients have a less severe phenotype. Patients with milder mutations may still respond to high doses of FSH stimulation, and the molecular diagnosis of these rare patients may help in the design of a rational treatment for their infertility. All heterozygotes for the mutations so far studied have been free from phenotype, indicating that a single functional FSH receptor gene allele is sufficient for normal reproductive function.

**FSH receptor polymorphisms**

Besides the inactivating and activating mutations, a large number of SNPs have been identified in the human FSH receptor gene (http://www.ncbi.nlm.nih.gov/SNP/). The number is large, >700, but can be explained by the large size of the FSH receptor gene (191 kb), and the average SNP distance (282 bp) is similar with that of the LH receptor (306 bp). The majority of the polymorphisms are intronic, 5 are located in the FSH receptor coding region and one in the promoter. The exonic polymorphisms are all in the transmembrane domain encoding exon 10 and all cause an amino acid change (Ala307Thr, Arg524Ser, Ala665Thr and Ser680Asn), except the SNP at codon 392 that is silent.

The best-studied polymorphisms in the FSH receptor gene are Ala307Thr and Ser680Asn, which have been found to be in linkage disequilibrium in most of the studies. The two most common allelic variants, Thr307/Asn680 and Ala307/Ser680, are almost equally distributed in Caucasian populations (Simoni et al. 2002). The other alleles represent less than 5% of the total. In several studies the association of the Ser680Asn polymorphism with endpoints that relate to FSH sensitivity have been investigated. Thus, the amount of FSH needed to reach similar oestradiol levels in *in vitro* fertilization (IVF) cycles was higher in women that carried the Ser680 FSH receptor allele, suggesting that the Ser680 FSH receptor allele encodes a less active FSH receptor protein that is less sensitive to FSH than the Asn680 allele (Perez Mayorga et al. 2000, Sudo et al. 2002, de Castro et al. 2003, 2004), although this finding could not be confirmed in all studies (Laven et al. 2003). In an association study of the Ser680 allele with OHSS (Daelemans et al. 2004), it was found that the Ser680 allele was enriched in a control IVF population compared with the general population, but that the OHSS population had even higher enrichment of this allele in comparison with controls (57 vs 39%), which is difficult to reconcile with the suggested lower sensitivity of the Ser680 FSH receptor.

Some studies have shown an association of the Ser680 polymorphism with amenorrhoea or anovulation (Sudo et al. 2002, Laven et al. 2003) but no association with premature ovarian failure (Conway et al. 1999, Sundblad et al. 2004). Association studies with polycystic ovarian syndrome have yielded conflicting results in different populations (Conway et al. 1999, Tong et al. 2001, Sudo et al. 2002). Neither is there an association with twinning and the FSH receptor allele (Hasbargen et al. 2001), and no relationship to male fertility parameters has been found (Simoni et al. 1999, Asatiani et al. 2002). Recently, in a study of menstrual cycle parameters in women homozygous for either allele, an association of the Ser680 FSH receptor allele was found with higher FSH and lower inhibin A, oestradiol and progesterone in the luteo-follicular transition phase of the cycle, and a longer menstrual cycle (Greb et al. 2005). The Ser680 and Asn680 FSH receptor proteins appear to have identical characteristics upon *in vitro* expression, which leaves a molecular explanation for the observed clinical associations open for further research (Simoni et al. 1999, Sudo et al. 2002).
FSHβ subunit

FSHβ mutations

A total of four different FSHβ gene mutations have been published (Fig. 2). One of these involves a two base-pair deletion at codon 61 of the gene, causing a frame shift, premature stop and a truncation of the FSHβ protein, rendering it completely inactive (Matthews et al. 1993). The second mutant, Tyr76X, also causes truncation of the protein (Layman et al. 2002) and in vitro expression of the mutant causes complete abrogation of both immuno- and bio-activity. The other two mutations, Cys51Gly and Cys82Arg (Themmen & Huhtaniemi 2000) both affect cysteines involved in the cystine knot structure which is essential for dimerization and bioactivity of the FSHβ/α dimer (see above). The deletion mutants, in addition, lack the ‘cystine noose’ necessary for receptor recognition, and the seat belt domain needed to stabilise the FSHβ/α dimer. Hence, from the molecular point of view, the current knowledge about the genetic and crystalline structure of FSH provides sufficient background information to explain the hormone inactivation at the molecular level.

The patients with these inactivating FSHβ mutations present with a phenotype that can be expected on the basis of the physiological function of FSH. Thus, the women all show sexual infantilism and infertility as a result of a lack of follicle growth and differentiation in the absence of bioactive FSH. However, the three men with FSHβ mutations are all normally masculinized but azoospermic (Lindstedt et al. 1998, Phillip et al. 1998, Layman et al. 2002). This phenotype is at variance with the male phenotype caused by FSH receptor mutations where, notwithstanding reduced sperm quality, fertility is maintained (Tapanainen et al. 1997).

The siblings with the Tyr76X mutation showed some evidence of puberty, whereas no residual bioactivity could be found in the studies by Layman et al. (2002) suggesting that other factors might preserve gonadal steroidogenesis in the absence of FSH or that current bioassays cannot discriminate among very low FSH levels.

All 4 women with inactivating FSHβ gene mutations have largely similar phenotypes, which in the complete form includes absent puberty and infertility due to lack of follicular maturation. Other features are absence of breast development, primary amenorrhoea, low oestrogen production, undetectable serum FSH, and increased LH. As expected, a large number of undeveloped follicles, usually in the primordial stage but sometimes more advanced, can be found in the ovaries of the affected individuals. The two previously characterized men had azoospermia - one had normal puberty and in the other puberty was delayed.

FSHβ polymorphisms

Somewhat surprisingly, and in contrast to LHβ, the FSHβ subunit appears to be highly conserved. Only a few silent polymorphisms in the exons and totally conserved promoter region were found in the FSHβ gene when studied recently in 50 Danish and 50 Finnish DNA samples (I T Huhtaniemi, personal communication).

Concluding remarks

In the coming years one of the focuses of pathophysiologic research in the gonadotrophin field will be on the association studies of gene polymorphisms with endpoints of disease in cohorts of sex differentiation and infertility patients, and other patients with aberrations of hormonal homeostasis. In this way also one of the important questions in the LH receptor field may be answered i.e. what, if any, is the role of the extra-reproductive system expression of the gonadotrophin receptors, especially the LH receptor. The author declares that there is no conflict of interest that would prejudice the impartiality of this scientific work.

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