A novel homozygous splice acceptor site mutation of KISS1R in two siblings with normosmic isolated hypogonadotropic hypogonadism

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Abstract

Context: Loss-of-function mutations of the kisspeptin-1 receptor gene, KISS1R, have been identified in patients with normosmic isolated hypogonadotropic hypogonadism (nIHH).

Objective: To investigate KISS1R defects in patients with absent or delayed puberty.

Patients: We investigated KISS1R gene defects in a cohort of 99 Brazilian patients with nIHH or constitutional delay of puberty (CDP).

Methods: The entire coding region of KISS1R was amplified by PCR followed by automatic sequencing. In addition, screening for KISS1R exonic deletions was performed by multiplex ligation-dependent probe amplification.

Results: One novel homozygous KISS1R mutation was identified in two siblings with nIHH. This variant was an insertion/deletion (indel) mutation characterized by the deletion of three nucleotides (GCA) at position +2 to +4, and by the insertion of seven nucleotides (ACCGGCT) at the same position, within the 3′ splice acceptor site of intron 2 of KISS1R. The brothers who carried this KISS1R mutation had no clinical evidence of pubertal development at the ages of 14 and 20 years. Computational analysis of this indel mutation predicted the generation of an abnormal protein. In addition, a new heterozygous KISS1R variant (p.E252Q) was identified in a male patient with sporadic nIHH. However, in vitro studies of this variant did not demonstrate functional impairment. Only known polymorphisms were identified in patients with CDP.

Conclusion: Loss-of-function mutations of KISS1R represents a rare cause of nIHH, and was absent in patients with CDP. We have described a novel KISS1R homozygous splice acceptor site mutation in the familial form of nIHH.

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important role in the physiologic regulation of puberty (3, 8). Indeed, the relevance of the kisspeptin system in human puberty onset was also highlighted by the recent identification of a unique nonconstitutively activating mutation of the KISS1R gene in a girl with central precocious puberty (9). Here, we investigated KISS1R gene defects in a cohort of Brazilian patients with normosmic IHH or constitutional delay of puberty (CDP).

Subjects and methods

Subjects

We studied 69 Brazilian patients (43 males and 26 females) with nIHH and 30 patients (25 boys and 5 girls) with CDP. Nine patients with nIHH and ten patients with CDP had a history of other affected members in their families. Written informed consent was obtained from all patients. The collection of blood samples for genetic studies and the clinical protocols were approved by the Ethical Committee of the Hospital das Clínicas da Faculdade de Medicina da Universidade de São Paulo, São Paulo, Brazil. Chronic diseases were ruled out in these subjects.

IHH was defined as inappropriately normal or low gonadotropin levels together with prepubertal concentrations of sex steroids and absence of other pituitary hormonal deficiencies. All patients were normosmic, as assessed by smell tests (Smell Identification Test or Alcohol Sniff Test) (10). Magnetic resonance imaging appearances of the pituitary, hypothalamus, and olfactory bulbs were normal in all patients.

CDP was defined by lack of breast development by the age of 13 years in girls and lack of testicular enlargement in boys by the age of 14 years (11). All the 30 patients with CDP were followed until they were over 18 years. They exhibited slow progression of secondary sexual characteristics and delayed bone age. Pubertal development was completely achieved either spontaneously or after a brief course of sex steroid therapy.

The control population was derived from a Sao Paulo Clinical Hospital cohort of Brazilian subjects. One hundred and twenty unrelated individuals (age ranging from 18 to 56 years) who experienced normal pubertal development at the appropriate chronological age were used as controls. Pubertal development was addressed by a questionnaire that included the age at first signs of puberty, age of menarche for women, and a history of fathering or giving birth to child.

DNA analysis of KISS1R

Genomic DNA was extracted from peripheral blood leukocytes, and the five coding exons of KISS1R (Genbank accession no. – AY253981), including exon–intron boundaries, were amplified using Platinum TaqPCRx DNA Polymerase (Invitrogen Life Technologies) and intronic primers, as described previously (3).

All amplified fragments were examined on 1% agarose gel electrophoresis. The PCR products were pretreated with an enzymatic combination of exonuclease I and shrimp alkaline phosphatase (United States Biochemical Corp., Cleveland, OH, USA), and directly sequenced using the BigDye terminator cycle sequencing ready reaction kit in an ABI PRISM 3100 automatic sequencer (Perkin Elmer Cetus, Waltham, MA, USA). All genetic variants were confirmed by automated sequencing using forward and reverse primers of two distinct PCR products. Computational splice site prediction was performed using NetGene2 software (http://genome.cbs.dtu.dk/services/NetGene2/).

Multiplex ligation-dependent probe amplification assay

The multiplex ligation-dependent probe amplification assay (MLPA) is a recent method for relative quantification of ~30–40 different DNA sequences in a single reaction. It has been used successfully for the detection of deletions and duplications in cell lines and tumor samples (12). MLPA was performed on genomic DNA obtained from all patients with IHH using SALSA MLP A kit P133 Kallmann-2 (MRC Holland), containing probes for FGFR1 (exons 1–3, 5, 6, 8, 10, 11, 13, and 14), KISS1R (exons 1 and 4), GNRH1 (all three exons), GNRHR (all three exons), and NELF (exons 5, 11, and 15). Briefly, genomic DNA (20–500 ng) isolated from blood leukocytes was denatured at 98 °C for 5 min and hybridized to MLPA probes according to the manufacturer’s protocol. PCR was performed on a thermal cycler, and separation and detection of amplification products were performed by capillary electrophoresis on an ABI 310 DNA Genetic Analyzer (Applied Biosystems). Analysis was carried out by simple visual examination of the capillary electrophoresis peak profiles generated by the GeneScan Software (Applied Biosystems) compared with the control sample. Genetic dosage quotients near 1.0 are described as disomic.

Generation of E252Q KISS1R by site-directed mutagenesis

The E252Q KISS1R mutant was generated by site-directed mutagenesis with the QuikChange II Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA, USA), using the mammalian expression vector pCMVsport6 containing the full-length wild-type (WT) human KISS1R as template (9). The presence of the mutation was confirmed by direct sequencing.
**Inositol phosphate assay**

COS-7 cells were transiently transfected with 100 ng WT KISS1R (WT), E252Q KISS1R, or empty vector (EV) (pCMVsport6) using GenePORTER Transfection Reagent (Gene Therapy Systems, San Diego, CA, USA). Measurement of total inositol phosphate (IP) production was performed 1 h following stimulation with increasing concentrations of kisspeptin as previously described (13). In brief, 24 h after transfection with WT or E252Q KISS1R or pCMVsport6, media on transfected COS-7 cells were replaced with inositol-free DMEM for 2 h at 37°C, after which 2 μCi/ml myo-[2-3H]-inositol (Perkin Elmer) was added, followed by the addition of 10 mM LiCl 15 min later. After overnight incubation, IP production was stimulated by the addition of 10−10 M kisspeptin-10 for 1 h. Cells were extracted with formic acid, lysates were neutralized and centrifuged, and protein content was determined. Supernatants were loaded onto previously equilibrated AG-X8 resin anion exchange columns (Fisher Scientific, Pittsburgh, PA, USA). The columns were washed, and total IP was eluted. Radioactivity was quantified by liquid scintillation and corrected for protein content. All assay points were performed in triplicate, and each experiment was repeated at least three times.

**Results**

**DNA analysis of KISS1R**

Automatic sequencing of KISS1R revealed the presence of two new variants in three patients with IHH. The first variant was an insertion/deletion (indel) mutation characterized by the deletion of three nucleotides, GCA, at position −2 to −4, and by the insertion of seven nucleotides, ACCGGCT, at the same position, within the 3′ splice acceptor site of intron 2 of KISS1R. This complex IVS2 -4_-2delGCAinsACCGGCT mutation was identified in the homozygous state in two male siblings with nIHH (Fig. 1). These two brothers had no clinical evidence of any pubertal development at the ages of 14 and 20 years. At birth, both had presented with micropenis and cryptorchidism, and exhibited prepubertal testosterone levels associated with low basal gonadotropins (patients 1 and 2, Table 1). The oldest brother underwent a GNRH stimulation test, and had prepubertal gonadotropin levels in response (patient 1, Table 1). Their mother carried the same mutation in the heterozygous state and reported normal pubertal development. Their father is believed to have had normal reproductive maturation and function, but was not available for testing.

The second KISS1R variant identified was characterized by a c.754G>C transversion in exon 5, resulting in the substitution of glutamic acid by glutamine (p.E252Q) in the third intracellular loop of the receptor. This change was identified in the heterozygous state in a male patient with sporadic nIHH, who exhibited micropenis and cryptorchidism at birth (patient 3, Table 1). DNA analysis of his mother did not reveal the p.E252Q mutation. His father was not available for molecular studies.

These two KISS1R variants identified in this study were absent in a control group composed of 120 ethnically matched individuals. Previous analyses of FGFR1, GNRHR, GNRH1, PROK2, PROKR2, TAC3, TACR3, and KISS1 genes did not reveal any additional genetic abnormalities in the patients carrying these KISS1R mutations. Six polymorphisms were also found, five of them previously described (Table 2). No KISS1R mutations were found in the group of patients with CDP.

**MLPA analysis**

KISS1R deletions involving exons 1 and 4 of the KISS1R gene were ruled out by MLPA study in the patient who carried the KISS1R p.E252Q variant. Additionally, exonic deletions of the FGFR1, GNRH1, GNRHR, and NELF genes were not detected using MLPA in this patient nor in the remaining group with nIHH.
Computational splice site prediction

The splice site KISS1R mutation (IVS2 -4_-2delGCAin-sACCGGCT) was analyzed by NetGene2 software. This mutation is predicted to have the potential to generate four different abnormal KISS1R proteins using alternative acceptor sites (Fig. 2). The use of sites 1 and 4 results in truncated proteins after the second intracellular and second extracellular loops respectively. The use of site 2 results in a longer 410-amino acid protein, while the use of site 3 results in a receptor lacking four conserved amino acids (QVSV).

Computational E252Q variant prediction

We applied two in silico algorithms, the PolyPhen algorithm (http://genetics.bwh.harvard.edu/cgi-bin/ggi/ggi.cgi) and the SIFT algorithm (http://sift.jcvi.org) to predict the putative effect of the E252Q amino acid substitution on KISS1R function. This substitution was predicted to be tolerated (benign) using both SIFT and PolyPhen algorithms.

Functional analysis of the E252Q variant

IP production was measured in COS-7 cells transiently transfected with WT or E252Q KISS1R or EV, and the response to stimulation with increasing concentrations (10^{-10} – 10^{-6} M) of human kisspeptin-10 was measured. Kisspeptin dose–response curves were similar for WT and E252Q KISS1R, with no notable loss of activity of the E252Q mutant (Fig. 3). Cells transfected with EV failed to show any IP induction in response to kisspeptin-10 treatment (not shown).

Discussion

Since the first description in 2003, eight different loss-of-function mutations have been described in the KISS1R gene in patients with nIHH. These mutations include six point mutations (p.L148S, p.R297L, p.C223R, p.R331R, and p.L102P) (3, 5, 14), one 155-bp deletion (4), and one insertion (c.1001_1002insC) (6). Taking into consideration the 312 patients with normosmic IHH reported to have been screened, including the 69 patients from this study, mutations reported in KISS1R gene are responsible for < 5% of cases of normosmic IHH. Therefore, inactivating KISS1R mutations have been shown to be responsible for only a small number of familial and, even less commonly, sporadic cases of normosomic hypogonadotrophic hypogonadism.

Patients with inactivating KISS1R mutations present with delayed puberty and no apparent associated conditions. Micropenis and cryptorchidism are described in some cases, suggesting that the kisspeptin–KISS1R system may play an important role in GNRH secretion during fetal development in utero (3–6, 14). The acute response to GNRH stimulation was variable among patients with KISS1R mutations and ranged from totally blunted to normal. The present report describes two novel variants in KISS1R gene. The first variant was identified in two siblings with isolated hypogonadotropic hypogonadism who presented with micropenis and cryptorchidism at birth. The alteration is a homozygous indel mutation characterized by a deletion of three nucleotides at position K+2 to K+4 and by an insertion of seven nucleotides (IVS2 -2_-4delGCAinsACCGGCT) in the same position in the 3′ splice acceptor site of intron 2. This mutation was absent in 240 alleles of normal individuals. Although experimental studies are necessary to fully characterize the effect of this mutation, single nucleotide changes in the canonical AG/GT nucleotides at the splice junctions have been described in several disorders (15).

Table 1 Clinical and hormonal characteristics of three patients with normosmic isolated hypogonadotropic hypogonadism associated with KISS1R mutations.

<table>
<thead>
<tr>
<th>Case</th>
<th>Age (years)</th>
<th>Sex</th>
<th>Basal LH (IU/l)</th>
<th>Peak LH (IU/l)</th>
<th>Basal FSH (IU/l)</th>
<th>Peak FSH (IU/l)</th>
<th>Testo (ng/dl)</th>
<th>KISS1R mutations</th>
<th>State</th>
</tr>
</thead>
<tbody>
<tr>
<td>1a</td>
<td>20</td>
<td>M</td>
<td>0.37</td>
<td>4.34</td>
<td>2.3</td>
<td>6.39</td>
<td>24</td>
<td>IVS2 -2_-4delGCA insACCGGCT</td>
<td>Homozygous</td>
</tr>
<tr>
<td>2a</td>
<td>14</td>
<td>M</td>
<td>&lt;0.1</td>
<td>–</td>
<td>1.2</td>
<td>–</td>
<td>24</td>
<td>IVS2 -2_-4delGCA insACCGGCT</td>
<td>Homozygous</td>
</tr>
<tr>
<td>3</td>
<td>18</td>
<td>M</td>
<td>0.7</td>
<td>–</td>
<td>2.4</td>
<td>–</td>
<td>20</td>
<td>p.E252Q</td>
<td>Heterozygous</td>
</tr>
</tbody>
</table>

M, male; Testo, testosterone. Hormonal levels measured by electrochemiluminescence. LH sensitivity, 0.1 IU/l; FSH sensitivity, 0.1 IU/l; testosterone sensitivity, 2 ng/dl.

*Patients 1 and 2 are brothers.

Table 2 Prevalence of exonic variants in KISS1R gene in the 69 isolated hypogonadotrophic hypogonadism patients.

<table>
<thead>
<tr>
<th>dbsNP ID</th>
<th>SNP</th>
<th>Amino acid</th>
<th>Prevalence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ss14700521</td>
<td>c.24A&gt;G</td>
<td>p.G08G</td>
<td>23.6</td>
</tr>
<tr>
<td>rs350132</td>
<td>c.83G&gt;C</td>
<td>p.S61S*</td>
<td>13.1</td>
</tr>
<tr>
<td>rs8111938</td>
<td>c.565G&gt;A</td>
<td>p.A189T</td>
<td>34.2</td>
</tr>
<tr>
<td>rs8111938</td>
<td>c.615A&gt;C</td>
<td>p.A205A</td>
<td>2.6</td>
</tr>
</tbody>
</table>

*A new variant.
Computational splice site prediction confirms that the substitution of the GCA nucleotides by ACCGGCT in the KISS1R mutated patients could result in aberrant intron retention or exon 3 skipping due to disruption of the constitutive sites and the use of cryptic splice acceptor sites. Both events would be predicted to result in the synthesis of severely truncated receptors, based on the introduction of premature stop codons or the insertion/deletion of different residues in the protein (Fig. 2). We hypothesize that this novel KISS1R indel mutation leads to the production of abnormal transcripts and therefore to receptor loss-of-function.

The p.E252Q variant was identified in the heterozygous state in a male with sporadic IHH. The glutamic acid at position 252 is conserved in pig, zebrafish, and urchin, but not in primate, mouse, or rat. This KISS1R missense variant was also absent in 240 alleles of ethnically matched controls. The E252Q variant was predicted to be benign using both SIFT and PolyPhen algorithms. Surprisingly, no other KISS1R exonic mutation or deletion was identified in this patient, except for known polymorphisms. In addition, FGFR1, GNRHR, GNRH, PROK2, PROKR2, TAC3, TACR3, and KISS1 mutations were not detected in this patient. All previously described KISS1R mutations associated with patients with IHH are in the homozygous or compound heterozygous state, suggesting an autosomal recessive mode of inheritance for this condition. As we examined primarily the coding sequence in this study, it is certainly possible that the patient carries a variant in the non-coding regions not analyzed, such as introns or regulatory regions. We cannot rule out the possibility that the p.E252Q variant represents a rare and novel polymorphism which does not have a functional effect on KISS1R, since the in vitro studies of this variant were not able to demonstrate functional impairment.

CDP is the most common cause of delayed puberty within the general population (16–18). It frequently aggregates in families, suggesting that it is genetically determined (19). The most frequent pattern of inheritance described in patients with CDP is autosomal dominant; however, an autosomal recessive pattern of inheritance has been described in ~2–4% of CDP cases (11). Since KISS1R mutations constitute a rare cause of autosomal recessive HH, we hypothesized that variations in this gene could be associated with the unusual autosomal recessive form of CDP and less severe KISS1R mutations. However, in this study, no KISS1R mutations were identified in this group of patients, in agreement with a previous publication (5).

In conclusion, we have described a complex KISS1R splice site mutation in two patients with IHH. This indel mutation potentially impairs KISS1R function leading to the nIHH phenotype.
Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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