R31C GNRH1 mutation and congenital hypogonadotropic hypogonadism

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R31C GNRH1 Mutation and Congenital Hypogonadotropic Hypogonadism

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Abstract

Normosmic congenital hypogonadotropic hypogonadism (nCHH) is a rare reproductive disease leading to lack of puberty and infertility. Loss-of-function mutations of GNRH1 gene are a very rare cause of autosomal recessive nCHH. R31C GNRH1 is the only missense mutation that affects the conserved GnRH decapeptide sequence. This mutation was identified in a CpG islet in nine nCHH subjects from four unrelated families, giving evidence for a putative “hot spot”. Interestingly, all the nCHH patients carry this mutation in heterozygosis that strikingly contrasts with the recessive inheritance associated with frame shift and non-sense mutations. Therefore, after exclusion of a second genetic event, a comprehensive functional characterization of the mutant R31C GnRH was undertaken. Using different cellular models, we clearly demonstrate a dramatic reduction of the mutant decapeptide capacity to bind GnRH-receptor, to activate MAPK pathway and to trigger inositol phosphate accumulation and intracellular calcium mobilization. In addition it is less able than wild type to induce lh-beta transcription and LH secretion in gonadotrope cells. Finally, the absence of a negative dominance in vitro offers a unique opportunity to discuss the complex in vivo patho-physiology of this form of nCHH.

Introduction

The gonadotropin-releasing hormone (GnRH) is essential in mammalian reproduction. This decapeptide, released from hypothalamic GnRH-neurons, triggers an intracellular cascade involving IP3 accumulation, calcium mobilization and MAPK phosphorylation through its cognate receptor GnRHR. The activation of these signaling pathways ultimately stimulates the synthesis and secretion of gonadotropins (LH and FSH) by pituitary gonadotrope cells.

The decapeptide sequence is conserved among most mammals and the amino and carboxyl termini are conserved in mammals and invertebrates [1–4].

Mutations of the human GNRH1 gene, encoding a 92 amino-acid pre-pro-GnRH, are a very rare cause of normosmic congenital hypogonadotropic hypogonadism (nCHH). A frame shift resulting in a failure to translate the GnRH peptide sequence gives rise to nCHH with autosomal recessive inheritance [5]. Subsequently a p.R31C GNRH1 mutation in which arginine is substituted by cysteine has been described [6,7]. This is the sole mutation affecting the GnRH decapeptide sequence. The arginine in position 8 of the GnRH decapeptide has been shown to be crucial for biological activity [2–4] and shown to interact with an acidic residue in the mouse [8] and in the human [9] GnRHRs. This mutation, though identified in two nCHH families in two independent series [6,7], has not been characterized. In these families, the somehow afflicted individuals were heterozygous. This observation is surprising as the frame shift GNRH1 mutation only resulted in nCHH in homozygous patients [5].

Here we report on the identification of p.R31C mutation in three individuals in two additional unrelated nCHH families. All the individuals are heterozygous for the mutation. We have undertaken a comprehensive molecular characterization of the
mutation in order to understand the mechanism of nCHH in these individuals.

### Results

**Genetic analysis**

We identified the GNRH1 c.91C>T (p.R31C) mutation in two unrelated French families with nCHH. Demographic, clinical, biological and genetic data are reported in Table 1. Interestingly, the two pedigrees are very different in terms of presentation (Fig. 1). In family 1, nCHH is sporadic. The boy (II.1) presented at 19 years old with a failure to progress through puberty. At physical examination he had a partial pubertal development with 12-mL bilateral testes volume. He had no olfactory impairment. Hormone assays revealed very low testosterone levels and low gonadotropin levels. No secondary causes were found for central hypogonadism (see Table 1).

In the second family the GNRH1 mutation was present in heterozygosis and segregated with disease. The boy (II.1) was diagnosed having hypogonadotropic hypogonadism because of small testis volume (10 mL at left, 12 mL at right testis), low serum testosterone and low gonadotropins. His pubertal stage was P3 according to Tanner. He had no anosmia. Common causes of secondary hypogonadism were excluded. His mother (I.2) was affected by primary amenorrhea, and conceived after ovarian stimulation by exogenous gonadotropins, although a formal diagnosis was not established at that time. She was re-evaluated later at the age of 65, and hormone assays revealed low sex steroids accompanied with inappropriately low gonadotropins. She had no other apparent secondary causes (see Table 1). The father (I.1) was not available for genetic analysis.

We did not identify a second genetic event after genomic regulatory region analysis of GNRH1 locus and GNRH1 cDNA sequencing in all propositi.

**Predictive analysis**

The GNRH1 c.91C>T nucleotide substitution did not create any donor or acceptor aberrant splice site according to prediction tools with Alamut® software. This nucleotidic substitution induces a missense at codon 31, replacing Arginine-31 by a Cysteine in the pre-pro-GnRH (GNRH1 p.R31C).

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**Figure 1. Pedigree of nCHH families carrying c.91C>T (p.R31C) GNRH1 mutation.** In the family 1, the propositus (II.1) has a de novo mutation and his filiation has been confirmed by DNA microsatellites. In the family 2 the mutation was transmitted from the mother (I.2) to her son (II.1). She required medical assistance for procreation. Clinical and demographic data of all patients are reported in Table 1. Electropherogram represents the heterozygous mutation in the individual II.1 from family 1. In the panel below, pre-pro-GnRH amino acid sequence conservation. Decapeptide is shown in red.

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In vitro molecular characterization

R31C and wild-type (WT) decapeptides were stable over 24-hours at room temperature in water and culture medium. No dimerization of the mutant decapeptide was found (Fig S1).

The R31C GnRH peptide bound the GnRH-R with an affinity more than 100-fold lower than that of WT GnRH (Fig 2A and 2B). Dose-response curves with SRE-luciferase assay showed an almost 100-fold reduction of R31C agonist versus WT (Fig 3A). The EC-50 was 4 nM for WT GnRH and 314 nM for R31C GnRH (p<0.0001, Fig 3B). ERK1/2 phosphorylation was maximal at 5 minutes. R31C GnRH showed similar kinetics, but the degree of phosphorylation was reduced (Fig 4A).

WT GnRH induced a rapid and transient calcium mobilisation in LbetaT2 cells. Calcium response by R31C was significantly reduced compared to WT in terms of peak and area under the curve (p<0.05, see Fig 5). Pre-treatment with 100 nM GnRH-antagonist cetrorelix abolished responses to both ligands (data not shown). The IP accumulation dose-response curve demonstrated that the R31C GnRH (EC-50, 199 nM) was more than a 100-fold less potent than WT GnRH (0.5 nM), (p<0.01, Fig 6A and B). The maximal IP generated by both ligands was the same indicating that the R31C GnRH peptide was a full agonist, as was found in the SRE-luciferase assay.

WT GnRH significantly increased lhb transcript levels in gonadotropes (p<0.01), whereas R31C GnRH did not significantly increase these levels over baseline (not significant, Fig 7A).

WT GnRH strongly stimulated LH secretion over baseline (p<0.001). R31C GnRH significantly stimulated LH secretion in LbetaT2 cells supernatants over baseline (p = 0.042, Fig 7B).

The above findings clearly show that in binding, signaling and functional assays, the R31C GnRH is less potent than WT GnRH. Since the heterozygous condition was associated with nCHH in our patients, that could suggest a dominant negative effect, we studied the effects of combining WT GnRH with R31C GnRH.

We hypothesized that the cysteine in position 8 of the R31C GnRH might form disulfide bridges with cysteine residues in the receptor that are not in disulfide bridges. There are three such cysteines: cysteine 218, cysteine 279 and cysteine 317. In order to examine this possibility the effects of R31C GnRH pre-incubation on subsequent binding of a radio-labelled GnRH analog was examined. We determined from the competition binding study that both WT GnRH and R31C GnRH can be fully removed as well as in medium-treated cells (Fig. 2B). These findings indicate that in silico prediction

Table 1. Clinical, biological and genetic characterization of patients.

<table>
<thead>
<tr>
<th></th>
<th>II.1 (Family 1)</th>
<th>II.1 (Family 2)</th>
<th>I.2 (Family 2)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Clinical data</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sex</td>
<td>M</td>
<td>M</td>
<td>F</td>
</tr>
<tr>
<td>Age at diagnosis</td>
<td>19</td>
<td>21</td>
<td>65</td>
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<tr>
<td>Total testosterone (ng/mL)</td>
<td>0.8</td>
<td>0.77</td>
<td>NA</td>
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<tr>
<td>Estradiol (pg/mL)</td>
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<td>7</td>
<td>&lt;12</td>
</tr>
<tr>
<td>LH (mU/mL)</td>
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<td>1</td>
<td>2.8</td>
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<tr>
<td>FSH (mU/mL)</td>
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<td>1.4</td>
<td>5.8</td>
</tr>
<tr>
<td>LH pulsatility</td>
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<td>Absent</td>
<td>NA</td>
</tr>
<tr>
<td>AMH (mol/l)</td>
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<tr>
<td>Inhibin B (ng/mL)</td>
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<td>101</td>
<td>&lt;15</td>
</tr>
<tr>
<td>Ferritin (mcg/mL)</td>
<td>63</td>
<td>56</td>
<td>103</td>
</tr>
<tr>
<td>Testicular volume (mL)</td>
<td>12</td>
<td>10</td>
<td>-</td>
</tr>
<tr>
<td>Ovarian volume (mL)</td>
<td>-</td>
<td>-</td>
<td>&lt;10</td>
</tr>
<tr>
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<td>3-mm Rathke's cyst</td>
<td>Normal</td>
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<tr>
<td>Olfactometry**</td>
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<td>Normal</td>
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<tr>
<td>Associated features</td>
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<td>None</td>
<td>None</td>
</tr>
</tbody>
</table>

**GA111P01**

Table 1. Clinical, biological and genetic characterization of patients.

<table>
<thead>
<tr>
<th>Genetic data</th>
<th></th>
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<tr>
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<td>NA</td>
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<td>normal</td>
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</tr>
<tr>
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</tr>
<tr>
<td>GNRH1 promoter</td>
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<td>normal</td>
<td>normal</td>
</tr>
<tr>
<td>GNRH1 exon 1</td>
<td>normal</td>
<td>normal</td>
<td>normal</td>
</tr>
<tr>
<td>GNRH1 intron 1</td>
<td>normal</td>
<td>normal</td>
<td>normal</td>
</tr>
</tbody>
</table>

**Subjective olfactometry was performed by a computed-assisted validated test (35).**

**Prop v.1.0b predicted that this missense did not abolish proconvertase-dependent cleavage site for pre-pro-GnRH maturation into the decapeptide (amino-acids 24 to 33).**

Alignment with orthologs revealed conservation of arginine in position 8 of GnRH in mammals (Fig 1). This amino acid exchange was classified as deleterious by various in silico prediction tools (see methods section). More importantly, experiments on the substitution of arginine 8 with a variety of amino acids demonstrate that it is crucial for binding and signaling [10]. Arginine 8 was further shown by mutagenesis studies in the GnRH-R that it interacted with an acidic residue in the extracellular loop three of the mouse (glutamate 320) and the human (aspartate 302) GnRH-Rs [8,9].

In vitro molecular characterization

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Dose-response curves generated from SRE-coupled luciferase were indistinguishable from WT GnRH administered alone (Fig 3A).
After pulsatile administration of each ligand at 90-minute frequency, WT GnRH was more potent than R31C GnRH to induce luciferase activity coupled to SRE reporter gene. Combination of WT and R31C was not able to impair luciferase activity when compared to WT alone (Fig. S2).

Treatment of LbetaT2 and GnRH-R-expressing HEK293T cells with 10 nM WT GnRH in combination with 10 nM R31C GnRH induced similar kinetics of ERK1/2 phosphorylation compared to 10 nM WT alone (Fig. 4A). Increasing the dose of R31C GnRH from 10 nM to 300 nM in the presence of 10 nM WT GnRH did not reduce ERK1/2 phosphorylation at 5 minutes exposure (Fig. 4B). Calcium peak and area under the curve after treatment with the combination of 10 nM GnRH and 10 nM mutant peptide was indistinguishable from WT GnRH alone (Fig. 5). IP dose-response curve with equal concentrations of WT and R31C peptides was indistinguishable from WT GnRH alone.
This indicates that a full range of doses of R31C GnRH does not influence the ability of WT to bind and activate the GnRH-R. R31C GnRH was also unable to influence the stimulation of \(lhb\) transcription (Fig. 7A) or LH secretion (Fig. 7B) from LbetaT2 cells by WT GnRH.

**Discussion**

\textit{GNRH1} mutations are a very rare cause of nCHH [5–7,11,12]. The \textit{GNRH1} p.R31C mutation is the only description of an amino acid change in GnRH. Yet this mutation has been described in nine individuals in four separate families. This mutation was first reported in association with nCHH in heterozygosis and a dominant inheritance was postulated [6], contrasting with the previously described recessive transmission of the frame shift mutation, which fails to transcribe the GnRH sequence [5]. Some nCHH individuals with the R31C mutation concomitantly had variations in other nCHH genes perhaps suggesting oligogenism. More recently, the R31C mutation was reported in a girl with no variations in other nCHH and Kallmann Syndrome-related genes [7]. This is of interest since this study analyzed all known genes associated with nCHH and Kallmann Syndrome aiming to establish the prevalence of oligogenism in these syndromes. This mutation was considered not sufficient to explain the phenotype because of the heterozygous inheritance [7]. In the present study, we have found the same mutation in three additional nCHH patients from two unrelated families and unrelated to the previously described families with the R31C mutation. Although sex steroid and gonadotropin levels undoubtedly related to CHH, more-than 4 mL testicular volume in patients at presentation suggested a residual functional activity of hypothalamic-pituitary-gonadal axis, probably reflecting heterozygosity.

The identification of this recurrent mutation in four unrelated families, the finding of a \textit{de novo} event in one family and the location of the nucleotide base change within a CpG islet are three consistent arguments for a mutational «hot spot». As interest, this amino acid is the most variable among vertebrate and invertebrate GnRHs [1–4]. The R31C GnRH mutation has never been identified in controls and segregation with the phenotype has been found in all affected families (see Table 2). Furthermore, this nucleotide base change has not been identified in 5989 individuals from the Exome Sequencing Project (ESP) cohort (NHLBI GO, Seattle, WA; URL: http://evs.gs.washington.edu/EVS; October, 2012). Thus, this implies that this missense mutation is likely responsible for the nCHH phenotype. However, although the R31C GnRH had very low activity in receptor binding, SRE-luciferase, IP, \(Ca^{2+}\), ERK1/2 signaling and in \(lhb\) gene expression and LH secretion, we were unable to demonstrate any dominant negative effect on WT GnRH activities.

Previous genetic studies established that \textit{GNRH1} loss of function mutations lead to an autosomal recessive nCHH. Thus we first searched for another genetic event at \textit{GNRH1} locus. This was excluded by an exhaustive analysis of the entire sequence of intron 1 present in the hypothalamic primary transcript, the sequence of the upstream and downstream \textit{GNRH1} promoters and the cDNA coding regions [13,14]. We also ruled out oligogenism by sequencing the main genes associated with nCHH and Kallmann Syndrome [15–17], although \textit{WDR11}, \textit{CHD7} and \textit{SEMA3A}, other genes known to be associated with CHH, have not been analyzed. Furthermore, we cannot entirely exclude the contribution of a gene not known to be associated with CHH. Next generation
sequencing methods could be helpful to find a possible second genetic defect.

In order to investigate the possible mechanisms whereby R31C GnRH might influence the actions of WT GnRH, as it is apparently the case in the patients, we set about first examining the activity of the R31C GnRH in receptor binding and variety of signaling pathways, as well as its ability to stimulate LH release. We then examined its ability to affect WT GnRH actions in these systems. R31C GnRH had a binding affinity of more than 100-fold lower than that of WT GnRH. Consistent with this observation, R31C GnRH had similar reductions in potency (increased EC-50 values) in stimulation of SRE-luciferase and IP generation. However, R31C GnRH was able to elicit the same maximal stimulation of SRE-luciferase and IP, clearly demonstrating that it is a full agonist in recruiting these signaling pathways. This indicates that it has no antagonistic activity and it is therefore unlikely to explain the phenotype of the heterozygous patients. Supporting these observations, R31C peptide determined weaker responses in contrast to those of WT GnRH in ERK1/2 phosphorylation, Ca2+ mobilization, lhb transcription and LH secretion.

Further studies confirmed our interpretation that R31C GnRH does not antagonize WT GnRH actions at the receptor level. When R31C GnRH, at concentrations varying from $10^{-10}$ M to $10^{-6}$ M, was added in combination with WT GnRH at $10^{-9}$ M in various experiments, it failed to have any impact on receptor binding, SRE-luciferase, IP generation and Ca2+ signaling or on lhb transcription and LH secretion. These findings are in accordance with our understanding of structure-activity relations of GnRH analogs and their interaction with the GnRH-R. Arginine 8 is crucial for the correct conformation of mammalian GnRH and for its binding to the receptor [1–4]. In particular arginine 8 has been demonstrated to be crucial for the interaction with the aspartate 302 of the human GnRH-R and the glutamate 301 of the mouse GnRH-R [8,9,18].

The mode of inheritance, apparently dominant in four families, is thus not explained by a simple negative dominance in the parameters that we have measured. There are other possibilities that were not investigated here. Firstly, the mutant peptide may interact with molecules within the GnRH neuron to impair activity or induce toxicity, thereby reducing WT GnRH secretion. Aberrant transcription products might be retained in the endoplasmic reticulum or could act as neurotoxic agents, as already demonstrated for pro-dynorphin in ataxia [19] or arginine-vasopressin variants in diabetes insipidus [20]. Another

![Graph showing calcium kinetics](image-url)
possibility is that, in GnRH neurons, the R31C GnRH precursor forms an aberrant intermolecular disulfide bridge with the WT GnRH precursor, which disrupts correct folding of the molecule leading to detection by surveillance proteins and trafficking to lysosomes for degradation of both peptides. In addition, the heterodimer may be resistant to processing.

Although a wide range of cellular models was used, they do not necessarily reflect *in vivo* events. Despite abundant literature, the molecular mechanisms underlying GnRH-R down-regulation and pulse deciphering remain currently poorly understood [21–23]. It is of note that SRE-luciferase activity was not impaired after four pulses at 90-minute frequency (Fig. S2). Nevertheless a slow and progressive loss of pituitary response to mutant GnRH might require a longer pulsatile exposure. In this context, a transgenic mouse model may shed light on the mechanism of the dominant negative effect [24].

In conclusion, together with our report, four nCHH families carrying R31C *GNRH1* heterozygous mutations have been identified. As this is a putative «hot spot» mutation it is likely to be identified in other nCHH families. The families harboring the R31C mutation are of great interest for reproductive sciences since the pathophysiology is not explained by *in vitro* experiments. There is herein an obvious opportunity to study novel aspects of GnRH signaling *in vivo* and/or to identify novel genes modulating GnRH reproductive function.

**Materials and Methods**

**Patients**

From a cohort of 410 patients with congenital hypogonadism we screened for a panel of mutations including *GNRH1* (see below). The study was approved by the Paris Sud University Hospital ethics committee and complied with human research guidelines as stated in the Declaration of Helsinki. Patients gave their written informed consent before genetic analysis and hormone studies.

**Hormone assays**

Serum LH, FSH, inhibin B, plasma testosterone and estradiol concentrations were measured by immunoradiometric, enzyme-linked immunoabsorbent, or radioimmuno-assays [25] as reported in Table 1.

**Genetic testing**

Genomic DNA was isolated from white blood cells (WBC). Direct genomic sequencing of *GNRH1* was performed by sequencing all exons and exon-introns junctions (NG_016457.1), up-stream and down-stream promoter encompassing 1100 bp before start site of transcription (Fig. S3). Direct genomic sequencing of coding exons and intron-exon junctions of *GNRHR1, KISS1, GPR54, NELF, TAC3, TACR3, FGFR1, PROK2* and *PROKR2* was performed as previously described [26]. PCR primers were designed by Primer Blast (http://www.ncbi.nlm.nih.gov/tools/primer-blast/) [26]. PCR and sequencing products were purified on a Biomek NXP-96 Laboratory Automation Workstation (Beckman Coulter, Villepinte, France) with Agencourt Ampure XP and Agencourt Cleanseq (Beckman Coulter Genomics, Danvers, MA). Sequencing products were analyzed with an automated capillary sequencer (ABI PRISM 3130xl Genetic Analyzer; Applied Biosystems, Foster City, CA). Electropherogram-derived sequences were compared with NCBI references using SeqScape Software 2.6 (Applied Biosystems, Foster City, CA).
Molecular Characterization of the GnRH R31C mutant

Peptide custom and stability. “Wild type” (pGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH2) and “R31C” (pGlu-His-Trp-Ser-Tyr-Gly-Leu-Cys-Pro-Gly-NH2) mutant GnRH were synthesized by a custom peptide manufacturer (Eurogentec, Liège, Belgium). Molecular weight was confirmed by MALDI-TOF and purity was assessed at ~95% by the manufacturer. Lyophilized products were suspended in sterile water in order to obtain 0.1 mM aliquots and conserved frozen at ~150°C.

LC-MS/MS was performed with Quattro-LCZ triple quadrupole mass spectrometer equipped with the orthogonal electrospray source (Micromass, Manchester, UK) to analyze peptides stability in solution. Peptides solutions (water and cell culture medium) were incubated 24-h at room temperature for these stability studies.

In silico prediction of peptide cleavage was performed by means of Prop v.1.0b ProPeptide Cleavage Site (http://www.cbs.dtu.dk/services/ProP).

Prediction of protein function after selective amino acid substitution was obtained by means of Alamut® (Interactive Biosoftware, Rouen, France), AlginGVD (http://agvd.iarc.fr/agvd_inupt.php/), Polyphen2 (http://genetics.bwh.harvard.edu/pph2/), SIFT (http://sift.jcvi.org/) and PANTHER Coding SNP Analysis tool (http://www.pantherdb.org/tools/csnpScoreForm.jsp).

Cell lines

Various cell lines were used for the experiments. HEK293T (ATCC CRL-11268) and COS-7 (ATCC CRL-1651), which do not express GnRH-R, were used after transient transfection with the Trizol® reagent (Invitrogen, Cergy Pontoise, France). RT-PCR and direct cDNA sequencing was performed as previously reported [26,27]. Complete CDS of GNRH1 transcripts (NM_0001083111.1 and NM_000825.3) were analyzed with primers for RT-PCR and sequencing in Table S1.

Microsatellites genotyping was performed to confirm filiation (Powerplex 16 System®, Promega, Madison, WI).

Total RNA was extracted from cells (WBC or cells in culture) with the Trizol® reagent (Invitrogen, Cergy Pontoise, France). RT-PCR and direct cDNA sequencing was performed as previously reported [26,27]. Complete CDS of GNRH1 transcripts (NM_0001083111.1 and NM_000825.3) were analyzed with primers for RT-PCR and sequencing in Table S1.

Table 2. Recurrence of c.91C>T (p.R31C) GNRH1 base change in subjects from CHH families and in healthy controls.

<table>
<thead>
<tr>
<th>Authors</th>
<th>Reference Year</th>
<th>CHH</th>
<th>Healthy Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vagenakis et al. [11]</td>
<td>2005</td>
<td>0/26</td>
<td>NA</td>
</tr>
<tr>
<td>Chan et al. [6]</td>
<td>2009</td>
<td>4/310</td>
<td>0/192</td>
</tr>
<tr>
<td>Topaloglu et al. [36]</td>
<td>2009</td>
<td>0/50</td>
<td>0/100</td>
</tr>
<tr>
<td>Quaynor SD. et al. [7]</td>
<td>2011</td>
<td>2/48</td>
<td>0/188</td>
</tr>
<tr>
<td>Current study</td>
<td>2013</td>
<td>3/410</td>
<td>0/545</td>
</tr>
<tr>
<td>Total</td>
<td>9/844</td>
<td>0/1025</td>
<td></td>
</tr>
</tbody>
</table>

NA: not applicable; ***p<0.0001 by Fisher’s test between CHH patients and healthy controls. a: the mother of the female propositus has been represented as a carrier but no clinical data are reported. b: 120 CHH patients and 345 healthy subjects have been added to previously published data [5].

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The high affinity GnRH analog, [His5, D-Tyr6]-GnRH was radio-iodinated as previously described [29] and purified using Sephadex chromatography [30]. COS-7 cells were transiently transfected with a human GNRHR (Missouri S&T cDNA Resource Center, Rolla, MO). Murine gonadotrope LbetaT2 cells were kindly provided by Dr. Mellon laboratory [28]. These cells endogenously express GnRH-R and are able to express gonadotropin subunit transcripts and to secrete mature LH glycoprotein after GnRH treatment [28].

Competition radioligand binding assays

The high affinity GnRH analog, [His5, D-Tyr6]-GnRH was radio-iodinated as previously described [29] and purified using Sephadex chromatography [30]. COS-7 cells were transiently transfected with a human GNRHR-RNA construct containing the human GNRHR-R1I carboxy-terminal to enhance expression [31] using 6 µg of DNA and 30 µl FuGene HD (Promega Corporation, Madison, WI) per 10 cm dish and seeded into 12-well plates. Two days after transfection cells were washed with HEPES-DMEM containing 0.1% bovine serum albumin (2×1 ml, HEPES-DMEM-BSA) and incubated with [125I- [His5, D-Tyr6]]-GnRH (100,000 CPM per well) and various concentrations of WT GnRH or R31C GnRH (4 h, 4°C) in a total volume of 0.5 ml. Cells were washed with phosphate-buffered saline (2×1 ml) and lysed with NaOH (1 ml, 0.1 M). Cell-bound radioactivity was counted in a gamma counter and IC-50 values were calculated using Graphpad Prism (GraphPad Software Inc, San Diego).

To determine whether R31C GnRH binds covalently to the GnRH-R, transfected COS-7 cells were incubated with WT GnRH (10−8 M), R31C GnRH (10−7 M) or HEPES-DMEM-BSA alone (2 h, 4°C), washed with HEPES-DMEM-BSA (1 ml) and incubated in HEPES-DMEM-BSA (5 ml, 1 h, 4°C) to allow
dissociation of non-covalently bound peptide, before the binding assay was performed as above.

**Serum Responsive Element (SRE) luciferase assay**

Luc2P/SRE/Hygro plasmid (Promega, Madison, WI) was used to test luciferase production in response to MAP kinase activation as a reporter gene system. HEK293T cells (1.2 x 10^6 cells/well) were seeded 72 h before testing in high-glucose Dulbecco’s minimal essential medium (DMEM, Invitrogen, Cergy Pontoise, France) containing 2 mM glutamine, 100 IU/mL penicillin, 100 mg/mL streptomycin, and 10% heat-inactivated fetal calf serum at 37°C in 96-well plates. Twenty-four hours before testing, cells were co-transfected in serum free OptiMEM, using Lipofectamine 2000 (Invitrogen, Cergy Pontoise, France) with the plasmids for human GnRH receptor, luc2P/SRE/Hygro and pMIR-REPORT™ beta-galactosidase vector (Applied Biosystems, Foster City, CA). WT GnRH, R31C, WT+R31C or vehicle were added at different dilutions (from 10^-10 to 10^-6 M). After 5 h-incubation cells were harvested and assayed for luciferase activities as previously described [32], using a luminometer (Victor, Perkin Elmer, Waltham, MA). To standardize for transfection efficiency, the relative light units were normalized by the galactosidase activity at optical density. EC-50 and Emax values were calculated using GraphPad Prism (GraphPad Software Inc).

**Inositol phosphate (IP) accumulation**

COS-7 cells were transiently transfected by electroporation with human GnRH-R DNA (10 μg/15 cm dish), seeded into 12-well plates and radiolabelled by overnight incubation with myo-[3H]Insitol (0.5 μCi/well, American Radiolabeled Chemicals, St Louis, MO). Radiolabelled cells were washed and incubated (30 min, 37°C) in IP medium (HEPES-DMEM-BSA supplemented with 10 mM LiCl), then stimulated (60 min, 37°C) with various concentrations of WT GnRH or R31C GnRH or equal concentrations of WT GnRH and R31C GnRH. Incubations were stopped by removal of the medium and cells were lysed by addition of formic acid (1 ml, 10 mM). IP were extracted from cell lysates using Dowex 1 X8-200 chromatography and counted using a liquid scintillation counter (Packard). EC-50 and Emax values were calculated using Graphpad Prism (GraphPad Software Inc) [33].

**ERK1/2 Western blot**

LbetaT2 cells were starved overnight in serum-free DMEM. The test day cells were exposed to 10 nM WT, R31C, the combination of 10 nM of each peptide or vehicle during five hours. Cell culture supernatants were collected and rapidly stored at −80°C. In cell culture media, LH concentration was measured using a previously described ELISA method [34] with reagents supplied by Dr. Parlow (National Hormone and Peptide Program, Harbor-UCLA Medical Center, Torrance, CA). The minimum detectable LH concentration was 0.2 ng/ml, and the interassay coefficient of variation was less than 10%.

**Supporting Information**

**Figure S1** Peptide stability on mass spectrometry-coupled electrospray (Quattro-LC). Peptides were measured in aqueous solution at pH 7 and starved overnight at 37°C. WT and R31C decapeptides are found at the expected molecular weights (1181.6 and 1128.5, respectively). Formation of smaller fragments was absent in WT and negligible in R31C. Formation of R31C dimers was absent.

**Gene expression study**

LbetaT2 cells were grown at 10^6/well in 6-well plates and starved in serum-free DMEM 18 h before tests. After 5 hours incubation with 10 nM WT, R31C, the combination of 10 nM WT +10 nM R31C peptides or vehicle, cells were washed with 1 x PBS and total RNA isolated using Trizol® (Invitrogen, Germany). Lhβ (murine LH beta subunit) transcript was quantified by realtime RT-PCR, using an ABI Step One Sequence Detector (Applied Biosystem, Foster City, CA) as previously described [27]. Primers are provided in Table S1.

**Statistical analyses**

Only nonparametric tests were used. Friedman’s test was used to compare three or more matched groups and Kruskall-Wallis test for unmatched groups. These analyses were followed by Dunn’s post comparison test. Differences were significant when p<0.05 (**p<0.01, ***p<0.001). Statistical analyses were performed using GraphPad Prism version 5.0d (GraphPad Software Inc., San Diego, CA).

**Figure S2** Luciferase activity after pulsatile exposure. HEK293T cells were transiently transfected with GNRHR and SRE-coupled luciferase reporter gene, and then exposed to four 90 min-spaced pulses of 10 nM WT, 10 nM R31C and 10+10 nM WT+R31C. After 5 minutes exposure to each ligand, cells were washed, and a subsequent pulse was given 90 minutes after. Five hours after the last pulse, cells were harvested for luciferase assay. Luciferase activity arbitrary units obtained by luminometry (a.l.u.) are shown as ratio on beta-galactosidase activity by optical density (used as transfection efficiency internal control). This experience was conducted three times (n = 8 replicates for each experiment).

**Figure S3** Genomic localization of human GNRH1 and related transcription and translation products. Two main regulatory regions are located upstream the transcription start site: the proximal promoter mainly regulates hypothalamic transcript, whereas the distal promoter controls a longer GNRH1 transcript (retaining entire intron 1 sequence) in the extra-cerebral tissues. Amino acids are represented by letters from the international nomenclature. In the prepropeptide GnRH, functional domains
are represented for the signal peptide (23 amino acids, blue), decapetide GnRH (purple), and GnRH-associated peptide (GAP) (56 amino acids, green) (adapted from Bouligand et al., NEJM, 2009).

(PPT)

Table S1 Primer sets used for experiments. (DOC)

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Author Contributions

Conceived and designed the experiments: LM JB JY AGM. Performed the experiments: LB RPM CAF MG RP ML JCT. Analyzed the data: LM JB RR. Contributed reagents/materials/analysis tools: FA PB AC ML TB. Wrote the paper: LM JB JY.