



Idiopathic Hypogonadotropic Hypogonadism due to a GNRH1 Mutation

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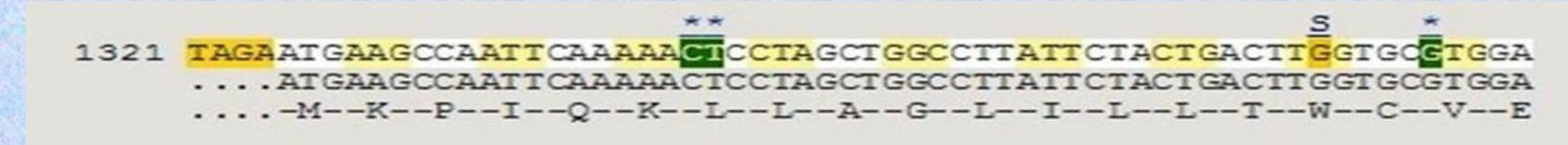
Background: Idiopathic hypogonadotropic hypogonadism may be normosmic (nIHH) or it may be associated with anosmia, which is known as Kallmann syndrome (KS). First mutation *GNRH1* was described in 2009 in patients with nIHH.

Mutations of the human GNRH1 gene are a very rare cause of nIHH, with only six mutations so far described.

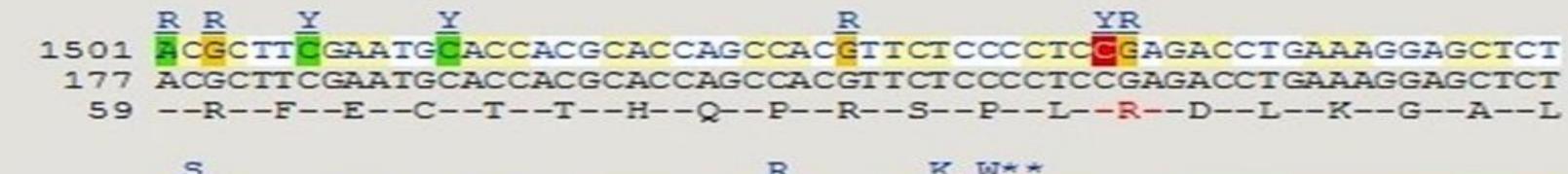
Case: The proband is a 11.3-year-old boy who first presented at age 1 with micropenis and cryptorchidism. His past medical history is unremarkable except for a bilateral orchidopexy surgery at the age of two years. His parents are healthy cousins. The proband's height and weight are 149 cm (50th-75th percentile) and 84.5 kg (>95 percentile), respectively. His pubic and axillary hair are at Tanner stage 4 and 2, respectively. His testes are 1 mL bilaterally in the scrotum. His stretched penile length was 3.6 cm. Chromosome analysis revealed a 46,XY karyotype. Pelvic ultrasonography confirmed the absence of müllerian structures and the presence of both gonads with features of normal testes in the scrotum. His bone age is 11years.

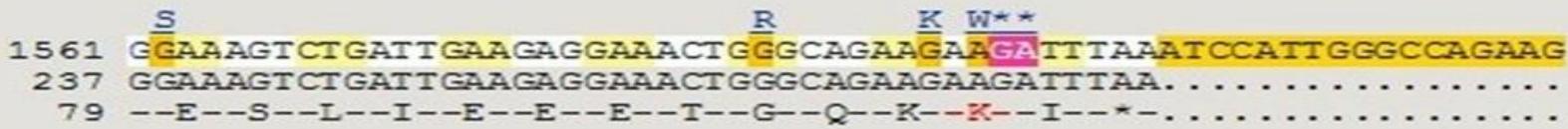
Results: Genetic analysis of this patient identified a homozygous deletion (c.87delA) leading to a frameshift mutation

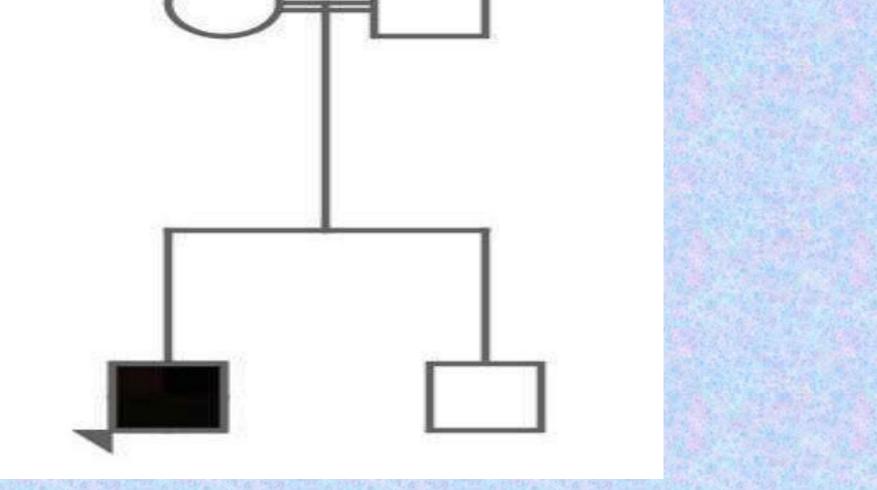
(p.G29GfsX12) in GNRH1.



K S K 1441 AAATTTGATTGATTCTTTCCAAGAGATAGTCAAAGAGGTTGGTCAACTGGCAGAAACCCA 117 AAATTTGATTGATTCTTTCCAAGAGATAGTCAAAGAGGTTGGTCAACTGGCAGAAACCCA 39 --N--L--I--D--S--F--Q--E--I--V--K--E--V--G--Q--L--A--E--T--Q







Whole exome sequencing data

	Α	B	С	D	E	F	G	Н	1	J	К	L	М	N	0		Q R	S	T
1	#chr_name	chr_start	chr_end	ref_base	alt_base 🔽	hom_het	snp_qual	tot_depth 💌	alt_depth	region 🖸	gene 🔽	📔 change 💽	annotation	JbSNP135	NP135_co	10No 11	De SCS (CLN 💽	OMIM 🔽
40498	chr08	25246481	25246481	G	A	hom	17.8	2	2	intronic	DOCK5			rs2709602	rs2709602	0.883 0.9	90 .		•
40499	chr08	25247587	25247587	G	Т	hom	23.5	4	4	intronic	DOCK5		•	rs1000798	rs1000798	0.498 0.5	53 .		•
40500	chr08	25257531	25257531	A	G	hom	222	41	41	intronic	DOCK5	•/		rs3763520	rs3763520	0.517 0.5	52 .		•
40501	chr08	25267622	25267622	A	G	hom	222	73	73	exonic	DOCK5	synonymous_SNV	DOCK5:NM_024940:exon51:c.A5412G:p.P1804P,	rs2709618	rs2709618	0.510 0.5	54 .		
40502	chr08	25280666	25280666	A	С	hom	148	36	36	intronic	GNRH1			rs2709608	rs2709608	0.960 0.9	97 .		•
40503	chr08	25280760	25280760	T		hom	214	49	49	exonic	GNRH1	frameshift_deletion	GNRH1:NM_001083111:exon2:c.87delA:p.G29fs,GNRH1:NM_000825:exon1:c.87delA:p.G29fs						
40504	chr08	25280800	25280800	С	G	hom	222	48	48	exonic	GNRH1		GNRH1:NM_001083111:exon2:c.G47C:p.W16S,GNRH1:NM_000825:exon1:c.G47C:p.W16S,		rs6185	0.249 0.2	27 .		•
40505	chr08	25287556	25287556	A	G	hom	150	71	71	intronic	KCTD9			rs965130	rs965130	0.508 0.5	55 .		•
40506	chr08	25317691	25317691	A	Т	hom	222	98	98	intronic	CDCA2			rs6987936	rs6987936	0.956 0.9	97 .		2
40507	the second se	25323777	25323777	Т	С	hom	222	53	53	exonic	CDCA2	synonymous_SNV	CDCA2:NM_152562:exon5:c.T474C:p.N158N,	rs10108752	rs10108752	0.952 0.9	96.		•
40508	chr08	25363864	25363864	G	A	hom	35.1	6	6	intronic	CDCA2			rs146273040		0.002 0.0	. 00		

Conclusion: We here described a frameshift *GNRH1* mutation which is predicted to lead a total failure of GnRH synthesis. This mutation was previously reported by Chan et al. Comparison of phenotypes show no difference. *GNRH1* mutation in IHH are indeed very rare as we found only one mutation among 30 families with identified causative mutations. These rare patients offer a unique opportunity to study the effects of human GnRH deficiency.