Analysis of the WDR11 gene in patients with isolated hypogonadotropic hypogonadism with and without olfactory abnormalities

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INTRODUCTION

- The WDR11 gene was recently involved in the pathogenesis of isolated hypogonadotropic hypogonadism (IHH).
- In 2010, Kim et al. (1) identified five different heterozygous missense WDR11 rare variants in 6 of 201 IHH patients (5 normosmic IHH and 1 Kallmann Syndrome), which were absent in more than 400 controls.
- Studies in animal models demonstrated that WDR11 interacts with EMX1, a homeodomain transcription factor involved in the development of olfactory neurons and the missense alterations reduced or abolished this interaction (1).
- However, since this first description, no other mutations in this gene were associated with the IHH phenotype (2-4).

OBJECTIVE

- To investigate the presence of WDR11 rare variants in patients with isolated hypogonadotropic hypogonadism (IHH) with and without olfactory defects.

METHODS

- Genomic DNA extraction from peripheral leukocytes
- PCR amplification of the 29 exons and intron-exon boundary regions of the WDR11, using specific intronic primers pairs
- Sanger sequencing and comparison to the reference DNA sequence available at NCBI: NM_018117.11

RESULTS

- No rare variants were identified in the patients studied.
- Only the following known polymorphisms were identified:
  - rs35692153
  - rs7899928
  - rs1652277
  - rs149486212
  - rs12268298
  - rs151162552
  - rs117848117

CONCLUSIONS

- These results suggest that WDR11 rare variants are not a common cause of IHH.
- The role of this gene in the pathogenesis needs to be further investigated.

REFERENCES


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