

A new mutation in IHH gene causing severe short stature

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Background

IHH gene, located on long arm of chromosome 2, is a member of Hedgehog family and plays a role in endochondral ossification, according to its expression in prehypertrophic chondrocytes.

Heterozygous mutation in *IHH* are known to cause Brachydactyly A-1, in which the typical clinical features are bilaterally shortening or absence of the middle phalanges of most digits of hands and feet, shortness of 1st proximal bone and short stature; although short stature is considered part of BDA1, in most reported cases is not always present or irrelevant compared to the stature of unaffected relatives.

Case presentation

A girl of 11 years and 7 months was referred to our clinic for short stature. She was born from unrelated parents at 40 weeks of a pregnancy complicated by threats of abortion, birth parameters were weight 2.7 kg (-1.85DS), length 48 cm (-1.32DS), head circumference 35 cm (0.53DS).

The mother's height was 150.2 cm (-2.1 DS), the father's height was 166.1 cm (-1.6 DS), target height 151.6 cm (-1.8DS). After one year of life she had a poor growth, psychomotor development was normal, menarche occurred at 11 years.

At the first visit she showed height 129.1 cm (-2.9 SDS), sitting height 65.6 cm, sitting height/ height ratio 0.51 (-0.65DS), armspan 127.5 cm, armspan/height ratio 0.98, head circumference 49 cm (-2.7SDS), weight 30.8 kg (-1.64DS), BMI 18.5 (-0.34DS), pubertal stage PH4 B3, cubitus valgus and scoliosis. The karyotype, thyroid function and IGF1 were normal, *SHOX* gene defects were excluded, hand radiograph showed adult bone age.

Considering the poor height prognosis given the very advanced bone age, we performed a whole exome sequencing analysis (NGS) by a panel including 254 genes causing short stature.

The NGS analysis revealed a new mutation in *IHH* gene, exon3:c.G1045A:p.A349T, that was confirmed by Sanger sequencing, the same mutation was found in the mother. Our mutation is located in the C-terminal domain of *IHH* protein.

The prediction software SIFT, Polyphen and Mutation Tester confirmed the pathogenicity of the identified variant.

Discussion

Recently Vasques et al. found heterozygous mutations in *IHH* in children and adults with short stature without specific skeletal signs of BDA1, adding *IHH* defects among genetic causes of short stature. In this report the mean height SDS was in Brazilian children (twelve subjects) -2.6 +/-0.9DS and in Spanish children (five subjects) -3.2 +/-0.6DS, in adults the mean height SDS (ten Brazilian and four Spanish) was -3 +/-1.1 DS.

Our case is in line with this findings but with a more remarkable short stature (height 129.4 cm, -5.6 SDS considering adult bone age); hand radiograph of patient showed no classical features of BDA1, but an overtubulation of distal phalanges.

Conclusion

Our case confirms the role of *IHH* gene in short stature and add new phenotypic features: very short stature, SGA, very mild radiographic features and great phenotypic variability in the same family.

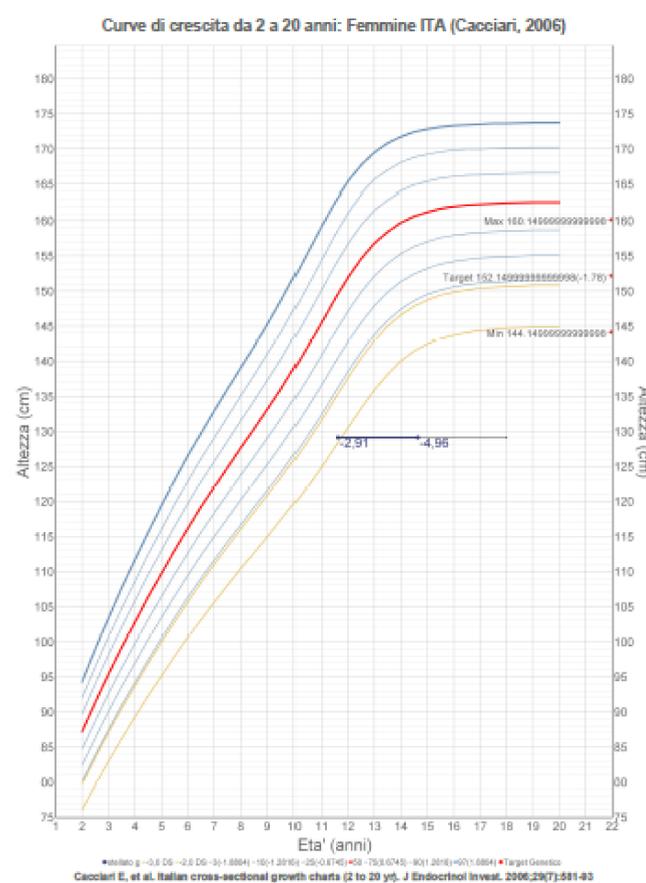


Figure 1. Patient's growth chart.

References

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No conflict of interest to declare

P2-P268