

عنوان مقاله:

A case of Frank-Ter Haar syndrome with a c.127C> T (p.Arg43Trp) mutation in SH3PXD2B gene

محل انتشار:

دومین کنگره بین المللی و دهمین همایش ملی نوروزنتیک ایران (سال: 1396)

تعداد صفحات اصل مقاله: 1

نویسندگان:

Pedram Khosravi - Medical Genetic laboratory, Shahid Akbarabad hospital, Iran University of Medical science, Tehran, Iran

Behnaz Karimi - Department of Genetics & Biotechnology, School of Biological Science, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran

Azadeh Shojaei - Department of Medical Genetics and Molecular Biology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran

Neda Asghari-Kollahi - Medical Genetic laboratory, Shahid Akbarabad hospital, Iran University of Medical science, Tehran, Iran

خلاصه مقاله:

Introduction: Frank-Ter Haar syndrome, is a rare severe progressive disease with a wide range of multisystemic disorders affecting the skin, bone, joints and heart. FTHS patients usually expire in infancy or in early childhood because of the cardiovascular anomalies and respiratory infections. Homozygous loss-of-function mutations in SH3PXD2B gene on 5q35.1 locus has been considered as one of the underlying causes of FTHS. **Patient and Method:** We studied a 5-year-old affected boy born of healthy consanguineous parents. The patient had a healthy sister and 2 affected siblings representing similar clinical symptoms including coarse face, prominent eyes, megalocornea, hypertelorism, congenital glaucoma, saddle nose, broad mouth, gingival hypertrophy, brachydactyly, camptodactyly, flexion deformity of fingers, severe mitral valve collapse, thoracolumbar kyphosis, lordosis and Thick skin. His 2 affected siblings have died at the age of 4 month and 17 years respectively due to respiratory infections. Exon 2, 5 and 10 of SH3PXD2B gene were analyzed by PCR-sequencing as hot spot mutations have been reported in these exons previously. **Result:** Mutation analysis revealed one homozygous c.127C> T (p.Arg43Trp) mutation in exon 2 of SH3PXD2B gene which is a known pathogenic mutation. **Conclusion:** Our results confirm that diagnosis of FTHS requires analysis of SH3PXD2B gene for which Sanger sequencing is still the most cost-effective method. If a negative result is obtained and the clinical evidence is strong, whole exome sequencing might be a better approach to take next.

کلمات کلیدی:

Frank-Ter Haar syndrome, SH3PXD2B, PCR sequencing, FTH

لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/745010>



