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Novel *TINF2* gene mutation in dyskeratosis congenita with extremely short telomeres: A case report

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Abstract

BACKGROUND

Dyskeratosis congenita is a rare disease characterized by bone marrow failure and a clinical triad of oral leukoplakia, nail dystrophy, and abnormal skin pigmentation. The genetics of dyskeratosis congenita include mutations in genes involved in telomere maintenance, including *TINF2*.

CASE SUMMARY

Here, we report a female patient who presented thrombocytopenia, anemia, reticulate hyperpigmentation, dystrophy in fingernails and toenails, and leukoplakia on the tongue. A histopathological study of the skin showed dyskeratocytes; however, a bone marrow biopsy revealed normal cell morphology. The patient was diagnosed with dyskeratosis congenita, but her family history did not reveal significant antecedents. Whole-exome sequencing showed a novel heterozygous punctual mutation in exon 6 from the *TINF2* gene, namely, NM_001099274.1:c.854delp.(Val285Alafs*32). An analysis of telomere length showed short telomeres relative to the patient's age.

CONCLUSION

The disease in this patient was caused by a germline novel mutation of *TINF2* in one of her parents.

INTRODUCTION

Dyskeratosis congenita is a rare genetic disease **whose prevalence in the general population has been estimated at nearly 1/1,000,000^[1]**. This disorder is characterized by bone marrow failure and a typical clinical triad comprised of oral leukoplakia, nail dystrophy, and abnormal skin pigmentation. The risk of aplastic anemia, myelodysplastic syndrome, and leukemia is elevated in patients with this condition^[2,3]. Other clinical findings in dyskeratosis congenita include pulmonary fibrosis, liver cirrhosis, and premature hair graying^[4]. The genetics of dyskeratosis congenita involve mutations in genes that govern the maintenance of telomeres; therefore, this disorder is marked, molecularly, by a progressive shortening of telomeres^[5,6]. The genes associated with dyskeratosis congenita are *DKC1*, *TERC*, *TERT*, *TINF2*, *RTEL1*, *PARN*, *ACD*, *NOP10*, *NHP2*, *TERT*, *USB1*, and *WRAP53*^[2,3,7] (**Table 1**). Pathogenic variants in any of these genes have been identified in most individuals who meet diagnostic criteria for dyskeratosis congenita^[3]. Because of this locus heterogeneity, there is a wide clinical variation among patients with this syndrome^[8]. Here, we report the case of a girl with dyskeratosis congenita who carries a previously undescribed germline mutation in the *TINF2* gene and an extremely short telomere length.

CASE PRESENTATION

Chief complaints

A 13-year-old Mexican female patient, height 151.0 cm and weight 48.0 kg, was found to have thrombocytopenia, anemia, abnormal skin pigmentation, dystrophic nails, and leukoplakia on the tongue.

History of present illness

The patient was the product of the second pregnancy of healthy nonconsanguineous parents (both parents were 31 years old at the time of birth). At the age of 5 years, she was detected to have thrombocytopenia and anemia (platelets $26,000/\text{mm}^3$ and hemoglobin 9.0 g/dL); peripheral blood cell smears showed normal morphology and no evidence of blasts. She was thought to have primary immune thrombocytopenia. Prednisone (1 mg/kg/d) was administered as therapy for 21 days. After the administration of prednisone, platelet and hemoglobin counts have fluctuated from $32,000/\text{mm}^3$ to $110,000/\text{mm}^3$ and 9.5 g/dL to 11.7 g/dL , respectively.

When the patient was 9 years old, she was suspected to have systemic lupus erythematosus and mixed connective tissue disease due to her nail dystrophy and neck pigmentation abnormalities, but an antinuclear antibody test was negative. Methotrexate was administered as prophylaxis regardless. Around this time, an esophagogram was performed due to her difficulty swallowing since childhood; this revealed esophageal stenosis requiring two endoscopies for dilation. At the age of 11, dyskeratosis congenita was suspected due to the progression of reticulate pigmentation to the entire upper trunk, the presence of leucoplakia on the tongue, and the evolution of fingernails and toenails dystrophy; a molecular study was subsequently performed.

History of past illness

The patient had no history of other significant diseases.

Personal and family history

The patient had a healthy older brother, and family history did not indicate any significant morbidities.

Physical examination

At the age of 6, the patient presented with microcephaly, reticulate pigmentation in the neck, neckline, and axillae, dystrophic nails on hands and feet (Figure 1A and 1B), and

lacrimal obstruction in the right eye. At the age of 11, she showed leukoplakia on the tongue (Figure 1C), and her reticulate pigmentation progressed to the entire upper trunk (Figure 1D).

Laboratory examinations

A histopathological study of the skin showed dyskeratocytes. Although previous peripheral blood smears showed normal leukocyte counts and the absence of blasts throughout the disease, a bone marrow biopsy was performed, which revealed normal cellularity.

Whole-exome sequencing

Whole-exome sequencing analysis was performed according to the manufacturer's protocol. DNA was enzymatically fragmented and hybridized with CentoXome™ (CENTOGENE, Rostock, Germany). Libraries were generated with Illumina-compatible adapters and ⁴sequenced on the Illumina platform (Illumina, Inc., San Diego, CA, USA). Sequenced readings were aligned to the hg19 version of the human genome (Genome Reference Consortium GRCh37) using validated software (Rostock, Germany). All variants reported in the *Human Gene Mutation Database* (HGMD®), ClinVar, and CentoMD, as well as those in which the frequency of the least common allele was less than ⁵1% in the Single Nucleotide Polymorphism database (dbSNP) and the Genome Aggregation Database (gnomAD) were considered. After analysis, a novel mutation, Chr14(GRCh37):g.24709832del NM_001099274.1:c.854delp. (Val285Alafs*32), was identified in exon 6 of the *TINF2* gene. This mutation was verified by Sanger sequencing. Bidirectional sequencing and comparison to the coding sequence of *TINF2* was performed (Figure 2). The reference sequence was NM_001099274.1.

Telomere analysis

To assess telomere length, ²genomic DNA was extracted from peripheral blood leukocytes using the Flexigene DNA kit (QIAGEN, Hilden, Germany) and qPCR was

¹ performed using the Absolute Human Telomere Length and Mitochondrial DNA Copy Number Dual Quantification qPCR kit (ScienCell Research Laboratories, San Diego, CA, USA) ¹ on a CFX96 Touch Real-Time PCR Detection System (Bio-Rad, Hercules, CA, USA) according to the supplier's recommendations. The analysis showed an absolute telomere length of 2.80 ± 0.09 kb.

Imaging examinations

Figure 1 Clinical findings in the patient. **A:** Dystrophic fingernails; **B:** Dystrophic toenails; **C:** White patches on the tongue representing leukoplakia; **D:** Upper trunk showing reticulate skin pigmentation.

Figure 2 Sequencing study. Plot showing the identification of the mutation in the *TINF2* gene (deletion of the T in the position 250; shaded area). Courtesy of Centogene AG, Rostock, Germany.

FINAL DIAGNOSIS

Based on clinical features and molecular analysis, the patient was diagnosed with dyskeratosis congenita.

TREATMENT

Prednisone (1 mg/kg/d) is administered as therapy for 21 days, whenever platelet count drops by nearly $30,000/\text{mm}^3$.

OUTCOME AND FOLLOW-UP

Hopefully, the patient has had a favorable evolution, as she has not developed aplastic anemia or bone marrow failure, although she is currently off medication.

DISCUSSION

Dyskeratosis congenita is caused more than 99% of the time by a germline mutation in one of the parents^[9], as was the case of our patient, who presented with the typical triad of this disease: dystrophy in fingernails and toenails, leukokeratosis plaques on the tongue, and reticulate skin pigmentation. Mutations in the *TINF2* gene (which encodes the TIN2 protein, a component of the shelterin telomere protection complex)^[2] represent the second most common cause of dyskeratosis congenita, accounting for approximately 12% of the cases, only after mutations in the *DKC1* gene (approximately 25%)^[1]. It is well known that patients with a mutation in the *TINF2* gene have a more severe course and a higher risk of developing aplastic anemia before the age of 10 years^[6]. To date, there are more than 200 punctual variations in the *TINF2* gene recorded in the ClinVar database. Most of them result in missense mutations, eight in nonsense, and almost twenty are frameshift mutations (**Table 2**), although some are associated with Revesz syndrome, a more severe variant of dyskeratosis congenita. Most pathogenic mutations occur in exon 6, principally between codons 280 and 288^[10]. The mutation detected in this patient was a deletion of a nucleotide (frameshift), which also occurred in exon 6, codon 285, and caused an amino acid change at position 285 and a stop codon 31 amino acids later.

While telomere shortening is a molecular feature of dyskeratosis congenita^[5], this is dramatic in patients with *TINF2* mutations^[11], as their telomere lengths are significantly shorter than those of patients with *DKC1* mutations^[6]. Our case showed an absolute telomere length of 2.80 ± 0.09 kb, which is considered very short relative to the patient's age. As a reference, a study performed on healthy young women aged 18 to 30 years showed an absolute telomere length of 4.59 ± 0.24 kb^[12]. TIN2 is important for telomere protection, and TIN2 deficiency increases the risk of telomeric DNA damage and consequent telomere shortening^[13-15]. Short telomeres are known to cause premature aging and increase the risk of developing cancer^[16]. Accordingly, patients with dyskeratosis congenita have a higher risk of developing bone marrow failure, acute leukemia, myelodysplastic syndrome, and squamous cell carcinoma of the head and neck^[3]. However, despite her extremely short telomere length, our patient has had a

favorable evolution, as she has not developed aplastic anemia or bone marrow failure, although she is currently off medication.

CONCLUSION

Since patients with mutations in the *TINF2* gene have a more severe course and a higher risk of developing aplastic anemia^[6], it is important to detect patients with such mutations to follow them more frequently, mainly through blood cytometry, and, if necessary, to provide some treatment, as has been done in this patient. In the meantime, she and her parents are hoping for an orphan or experimental drug that will impede the progression of the disease.

ACKNOWLEDGEMENTS

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