Novel *POFUT1* mutation in patient with flexural and acral hyperpigmented reticulated macules presenting in adolescence



Maija Kiuru, MD, PhD,^{a,b} Jessica R. Terrell, BA,^a Farzam Gorouhi, MD,^{a,c} and John D. McPherson, PhD^d Sacramento, California

Key words: acral hyperpigmentation; Dowling-Degos disease; dyschromia; genodermatosis; *KRT5*; mutation; *POFUT1*; *POGLUT1* reticulate pigmentary disorder.

INTRODUCTION

Dowling-Degos disease (DDD) is an autosomal dominant pigmentary disorder characterized by reticular hyperpigmentation, hypopigmentation, and hyperkeratotic papules of the flexures, including the neck, axillae, antecubital fossae, inframammary area and groin, and acral sites typically presenting between ages 20 and 50.¹ The clinical presentation is variable and is partly attributable to mutations causing DDD, including loss-of-function mutations in *KRT5*, *POGLUT1*, or *POFUT1*, involved in melanin synthesis and transport.¹⁻⁴ Here we report a case of DDD presenting in adolescence with prominent acral hyperpigmentation caused by a novel hetero-zygous truncating mutation and potential modifying single nucleotide polymorphism (SNP) in *POFUT1*.

CASE REPORT

A 27-year-old woman of Asian descent presented with hyperpigmented macules since adolescence on ventral wrists (Fig 1, *A*), ankles (Fig 1, *B*), dorsal hands and feet, face, neck, and axillae and hypopigmented macules on the ankles. Family history was notable for similar macules in the patient's mother, maternal aunt, and grandmother.

Genomic DNA was extracted from the patient's peripheral blood. Whole exome sequencing found a heterozygous truncating mutation, NM_015352.1:c. 342delC (NP_056167.1:p.Thr115fs) in *POFUT1* (Fig 2).⁵ An SNP, NP_056167.1:p.Met251Val in *POFUT1*, was also present, but no other pathogenic mutations

Conflicts of interest: None disclosed.

Abbreviations used:

DDD: Dowling-Degos disease SNP: single nucleotide polymorphism

were found in *KRT5*, *POGLUT1*, *ADAM10*, or *ADAR*. Together, the findings confirmed a diagnosis of DDD.

DISCUSSION

DDD, caused by mutations in KRT5, POGLUT1, or *POFUT1*, has a variable clinical presentation, which is likely related to the heterogeneity of the mutation landscape.^{6,7} The phenotype of DDD caused by *POFUT1* mutations appears particularly complex.¹ Similar to other reported cases, our patient showed prominent acral involvement but lacked hyperkeratotic papules, erythematous macules, palmar pits, or interrupted dermatoglyphics.¹ The frameshift mutation described here results in a truncated and likely dysfunctional POFUT1 protein. These proteins are thus far the most common type of mutation described in POFUT1 and include 9 other truncating mutations on POFUT1.6 It is possible that the POFUT1 SNP identified in our patient may contribute to the phenotype given it is likely to impact POFUT1 function as determined by several prediction tools of genomic variants, SIFT, PolyPhen-2, and CADD.⁸⁻¹⁰ This SNP is rare in all populations with the exception of those of East Asian descent, 0.004 to 8 versus 0.04

From the Departments of Dermatology,^a Pathology and Laboratory Medicine,^b and Biochemistry and Molecular Medicine,^d University of California, Davis and The Permanente Medical Group, South Sacramento Medical Center.^c

Funding sources: Dr Kiuru's involvement in this article is in part supported by the Dermatology Foundation, through Career Development Award in Dermatopathology and National Institute of Arthritis and Musculoskeletal and Skin Diseases of the National Institutes of Health under award number K23 AR074530-01A1.

Correspondence to: Maija Kiuru, MD, PhD, Department of Dermatology, University of California, Davis, 3301 C Street Suite 1400, Sacramento, CA 95816. E-mail: mkiuru@ucdavis.edu. JAAD Case Reports 2020;6:334-6.

²³⁵²⁻⁵¹²⁶

^{© 2020} by the American Academy of Dermatology, Inc. Published by Elsevier, Inc. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/ 4.0/).

https://doi.org/10.1016/j.jdcr.2020.02.016



A, Hyperpigmented macules of the ventral wrists

B, Hyperpigmented macules of the ankles

Fig 1. A, Hyperpigmented macules of the ventral wrists. B, Hyperpigmented macules of the ankles.



Fig 2. The heterozygous frameshift *POFUT1* mutation NM_015352.1:c.342delC (NP_056167. 1:p.Thr115fs) identified in the patient through whole-exome sequencing (Integrative Genomics Viewer v2.3.93; GRCh38).⁵

to 0.05, respectively. Our study highlights the phenotypic heterogeneity seen in DDD, particularly when it is caused by mutations in *POFUT1* and a potential modifying SNP.

Distribution of skin lesions, associated clinical findings, and age of onset can be helpful in differentiating DDD from other inherited reticulate pigmentary disorders, including reticulate acropigmentation of Kitamura, dyschromatosis symmetrica hereditaria (reticulate acropigmentation of Dohi), dyschromatosis universalis hereditaria, X-linked reticulate pigmentary disorder, epidermolysis bullosa simplex with mottled pigmentation, dermatopathia pigmentosa reticularis, and dyskeratosis congenita,¹ but given the phenotypic variability, genetic testing is needed to confirm the diagnosis. Early recognition and genetic testing are important for patient counseling. The treatment of DDD remains difficult with limited efficacy of therapies such as hydroquinone, retinoids, or adapalene. Laser treatments, such as erbium- yttrium aluminum garnet and intense pulsed light, show some promise.¹ Further studies are needed to ascertain the pathogenesis of this group of diseases for development of targeted treatment options.

REFERENCES

- Zhang J, Li M, Yao Z. Updated review of genetic reticulate pigmentary disorders. Br J Dermatol. 2017;177(4):945-959.
- Betz RC, Planko L, Eigelshoven S, et al. Loss-of-function mutations in the keratin 5 gene lead to Dowling-Degos disease. Am J Hum Genet. 2006;78(3):510-519.
- Basmanav FB, Oprisoreanu AM, Pasternack SM, et al. Mutations in POGLUT1, encoding protein O-glucosyltransferase 1, cause autosomal-dominant Dowling-Degos disease. Am J Hum Genet. 2014;94(1):135-143.
- Li M, Cheng R, Liang J, et al. Mutations in POFUT1, encoding protein O-fucosyltransferase 1, cause generalized Dowling-Degos disease. Am J Hum Genet. 2013;92(6):895-903.

- Robinson JT, Thorvaldsdottir H, Wenger AM, Zehir A, Mesirov JP. Variant review with the integrative genomics viewer. *Cancer Res.* 2017;77(21):e31-e34.
- 6. Zhong W, Liu J, Wang H, et al. Atypical presentation of Dowling-Degos disease with novel and recurrent mutations in POFUT1. *Clin Exp Dermatol.* 2018;43(8):937-939.
- 7. Li CR, Brooks YS, Jia WX, et al. Pathogenicity of POFUT1 mutations in two Chinese families with Dowling-Degos disease. *J Eur Acad Dermatol Venereol.* 2016;30(10):e79-e81.
- Sim NL, Kumar P, Hu J, Henikoff S, Schneider G, Ng PC. SIFT web server: predicting effects of amino acid substitutions on proteins. *Nucleic Acids Res*. 2012;40(Web Server issue):W452-W457.
- **9.** Adzhubei IA, Schmidt S, Peshkin L, et al. A method and server for predicting damaging missense mutations. *Nat Methods*. 2010;7(4):248-249.
- Rentzsch P, Witten D, Cooper GM, Shendure J, Kircher M. CADD: predicting the deleteriousness of variants throughout the human genome. *Nucleic Acids Res.* 2019;47(D1):D886-D894.