DOI: 10.1111/bjh.19851

#### IN A NUTSHELL



# Different phenotypes with different endings—Telomere biology disorders and cancer predisposition with long telomeres

Sharon A. Savage<sup>1</sup> S | Alison A. Bertuch<sup>2</sup> | on behalf of Team Telomere and the Clinical Care Consortium for Telomere-Associated Ailments (CCCTAA)

<sup>1</sup>Clinical Genetics Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, Maryland, USA <sup>2</sup>Baylor College of Medicine, Houston,

Texas, USA

#### Correspondence

Sharon A. Savage, Clinical Genetics Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, 9609 Medical Center Drive, Bethesda, MD 20892-6772, USA. Email: savagesh@mail.nih.gov

#### **Funding information**

Division of Cancer Epidemiology and Genetics; NIH, Grant/Award Number: R01 HL131744

#### Summary

Rare germline pathogenic variants (GPVs) in genes essential in telomere length maintenance and function have been implicated in two broad classes of human disease. The telomere biology disorders (TBDs) are a spectrum of life-threatening conditions, including bone marrow failure, liver and lung disease, cancer and other complications caused by GPVs in telomere maintenance genes that result in short and/or dysfunctional telomeres and reduced cellular replicative capacity. In contrast, cancer predisposition with long telomeres (CPLT) is a disorder associated with elevated risk of a variety of cancers, primarily melanoma, thyroid cancer, sarcoma, glioma and lymphoproliferative neoplasms caused by GPVs in shelterin complex genes that lead to excessive telomere elongation and increased cellular replicative capacity. While telomeres are at the root of both disorders, the term TBD is used to convey the clinical phenotypes driven by critically short or otherwise dysfunctional telomeres and their biological consequences.

K E Y W O R D S cancer, genetics, telomere

Rare germline pathogenic variants (GPVs) in genes essential for telomere length maintenance (TLM) and function cause a broad spectrum of disorders. The biological consequences of these GPVs range from short or dysfunctional telomeres and reduced cellular replicative potential to long telomeres and increased cellular replicative capacity.

# DYSKERATOSIS CONGENITA WAS THE FIRST DISORDER TO LINK GERMLINE GENETICS, TELOMERE DYSFUNCTION AND HUMAN DISEASE

X-linked recessive GPVs in *DKC1* were the first identified connection between dyskeratosis congenita (DC) and very short telomeres, making DC the prototypic telomere biology

disorder (TBD).<sup>1,2</sup> DC is diagnosed clinically by the mucocutaneous triad of oral leukoplakia, nail dysplasia and abnormal skin pigmentation or the presence of two of the triad and bone marrow failure.<sup>3</sup> Individuals with DC are also at high risk of pulmonary fibrosis, acute myeloid leukaemia, myelodysplastic syndrome, head and neck squamous cell carcinoma (HNSCC), cryptogenic liver disease, oesophageal and lacrimal duct stenosis and avascular necrosis, among other complications.<sup>4–8</sup>

# TBDs ARE A SPECIFIC SPECTRUM OF ILLNESSES CAUSED BY TELOMERE DYSFUNCTION

Several subtypes of TBDs present early in childhood and are caused by GPVs in the same genes as DC. Features of

This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerives License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.

The complete list of Team Telomere and CCCTAA members and institutions is provided in the acknowledgements.

Published 2024. This article is a U.S. Government work and is in the public domain in the USA. British Journal of Haematology published by British Society for Haematology and John Wiley & Sons Ltd.



Hoyeraal–Hreidarsson syndrome include cerebellar hypoplasia, immunodeficiency and intrauterine growth restriction. Bilateral exudative retinopathy, intracranial calcifications and intrauterine growth restriction are features of Revesz syndrome and Coats plus.<sup>9–11</sup> Additionally, individuals with Coats plus typically have cerebral cysts, a tendency to fractures and telangiectasia-associated gastrointestinal bleeding.<sup>10</sup>

The identification of GPVs in TLM genes in individuals and families with only one or two clinical or overt features of DC (e.g. pulmonary fibrosis) and the development of lymphocyte telomere length (TL) measurement as a diagnostic test led to the recognition of variable penetrance and expressivity and the term 'telomere biology disorder'.<sup>12</sup> Individuals with TBDs generally have median lymphocyte TL <10th percentile for age, with the shortest telomeres (<1st percentile) correlating with earlier age at onset, autosomal or X-linked recessive or heterozygous *TINF2* PGVs.<sup>6,13</sup> GPVs in >17 genes are associated with TBDs.<sup>4–8</sup>

# TBD PHENOTYPES RESULT FROM LIMITED STEM CELL RENEWAL INDUCED BY CRITICALLY SHORT TELOMERES

Telomeres consist of kilobase pairs of TTAGGG repeats at chromosome ends coated with a six-protein complex called shelterin. They are essential for maintaining chromosomal integrity yet shorten with each cell division in cells lacking or with limited levels of telomerase (most human somatic cells). Cellular senescence or apoptosis is triggered when telomeres reach a critically short length (the Hayflick limit). The mechanisms causing short telomeres vary in TBDs.<sup>14</sup> In individuals without TBDs, in addition to age, telomere shortening is associated with oxidative stress such as from smoking or other lifestyle factors.<sup>15</sup> GPVs in components of the telomerase complex or proteins involved in the maturation of the telomerase RNA subunit compromise telomerase catalytic activity, thereby reducing the extension of TTAGGG repeats. Without affecting telomerase activity per se, GPVs in factors required for telomerase trafficking within the nucleus or its recruitment to telomeres also reduce TL. Alternatively, GPVs may impact factors required for telomere stability by impairing telomere replication. For TINF2 exon 6 GPVs, the precise molecular mechanism causing extremely short telomeres remains incompletely understood.

# SOME TBDs HAVE TELOMERE INSTABILITY WITHOUT GLOBALLY SHORT TELOMERES

TBDs may result from GPVs in the shelterin component *POT1* that alters the fill-in step of replication at the telomeric end, resulting in dysregulated telomere elongation,

instability and stochastic truncations.<sup>14</sup> Biallelic GPVs in *CTC1* and *STN1* similarly affect the structure of the telomere end and telomere stability, whereas those in *DCLRE1B* do so via a different mechanism.<sup>16</sup>

# A DISTINCT SET OF CANCER-PRONE INHERITED DISORDERS HAVE LONG TELOMERES

At the opposite end of the TL range are cancer-prone disorders caused by GPVs in some of the same genes as the TBDs but associated with TL >90th percentile for age, without typical TBD-related clinical features and with different effects on telomeres.<sup>15</sup> The first discovery of such GPVs were in *POT1* and associated with long telomeres in familial melanoma.<sup>17,18</sup> Subsequent studies added glioma, angiosarcoma (mainly cardiac) and chronic lymphocytic leukaemia to the cancer spectrum, leading to the designation of '*POT1* tumour predisposition (TPD)' as a specific syndrome.<sup>19</sup> Other sarcomas, thyroid cancer, Hodgkin lymphoma, myeloid malignancies and clonal haematopoiesis have been suggested part of the *POT1*-TPD spectrum.<sup>15,20,21</sup>

GPVs in shelterin components, *ACD*, *TERF2IP*, *TINF2* and *TERF1*, have also been associated with long telomeres and cancers seen in *POT1*-TPD. To date, GPVs in *TERF2*, the sixth shelterin protein, have not been described. *ACD* or *TERF2IP* GPVs are associated with familial melanoma.<sup>15</sup> *TINF2* GPVs were identified in individuals from cancer-prone families, including papillary thyroid cancer and multiple primary melanoma.<sup>15,22</sup> The association of sarcoma with shelterin proteins has also expanded to include *TERF1*, *TERF2IP* and *TINF2*.<sup>15</sup> Notably, although some of the genes with long telomere-GPVs are among those associated with TBDs, none of the individuals with shelterin complex GPVs and long telomeres have been reported to have TBD phenotypes.

# LONG TELOMERES CONFER A GREATER REPLICATIVE CAPACITY SINCE MORE CELL DIVISIONS ARE NEEDED BEFORE TELOMERES REACH A CRITICALLY SHORT LENGTH AND TRIGGER APOPTOSIS OR SENESCENCE

Cells with engineered heterozygous *POT1* or *TINF2* variants associated with familial cancer have excessive telomere elongation yet lack a defect in telomere end protection.<sup>23,24</sup> One reported mechanism is that *POT1* mutations weaken its interaction at the telomere, allowing for more telomerase access and telomere lengthening. Thus, the increased risk of cancer conferred by this class of variants is proposed to be via the greater proliferative capacity endowed by the long telomeres, increasing the population of cells that may acquire mutations to drive cancer progression over time.

# WE PROPOSE USING THE TERM 'CANCER PREDISPOSITION WITH LONG TELOMERES (CPLT)' TO DEFINE THE CONDITION CAUSED BY GPVs IN TELOMERE BIOLOGY GENES, TO DATE PRIMARILY IN THE SHELTERIN COMPLEX, ASSOCIATED WITH LONGER-THAN-AVERAGE FUNCTIONAL TELOMERES

This distinction from TBDs is important because CPLT is not associated with typical TBD clinical manifestations but with a distinct set of malignancies.

# THE TERM TBD IS USED TO REFER TO THE CONDITIONS THAT MANIFEST IN INDIVIDUALS WITH ABNORMALLY SHORT OR OTHERWISE DYSFUNCTIONAL TELOMERES

These conditions include the mucocutaneous triad of DC, bone marrow failure, pulmonary fibrosis, liver disease, HNSCC and additional features related to limited cell renewal capacity provoked by their telomeres. While most TBD-associated GPVs result in very short telomeres, some variants cause clinically significant telomere dysfunction in the context of TLs within the normal range; hence, short telomere syndromes as an alternative falls short as an allinclusive term, and we support the continued inclusion of *biology* in the TBD name.

# UNANSWERED QUESTIONS FOR THE FIELD INCLUDE

- Do common germline variants mediate TBD or CPLT phenotypes? Genome-wide association studies of telomere length in large population-based studies have identified numerous single nucleotide polymorphisms associated with telomere length and allowed for the creation of polygenic scores.<sup>25</sup> These have not been studied in individuals with highly penetrant TBD or CPLT germline variants but could contribute to phenotypic heterogeneity.
- How do somatic mutations affect phenotypes and outcomes? Limited studies suggest that somatic mutations in blood of individuals with TBDs is associated with haematopoietic rescue and with progression to MDS.<sup>21,26-29</sup> Additional large, longitudinal studies are required to understand the clinical consequences and to develop precision management approaches.
- What are the biological consequences of rare germline variants in TBDs and CPLT? Most of the variants in genes associated with TBDs and CPLTs have had limited studies of the biological consequences. Comprehensive

functional studies focused on disease-associated variants are required to thoroughly understand genotype-phenotype relationships and to improve clinical management. For some genes, such as *TERT*, in which a large proportion of the variants detected in patients are novel and classified as variants of uncertain significance, saturation mutagenesis approaches may be needed to broadly impact patient care.

#### AUTHOR CONTRIBUTIONS

SAS and AAB developed the concept and wrote the manuscript. All individuals listed in the acknowledgements read and approved the final version.

#### ACKNOWLEDGEMENTS

CCCTAA members endorsing this publication are listed below in alphabetical order.

Suneet Agarwal: Boston Children's Hospital and Harvard Medical School, Boston, MA, USA; Geraldine Aubert: Repeat Diagnostics, North Vancouver and BC Cancer, Vancouver, British Columbia, Canada; Fabian Beier: Department of Hematology, Oncology, Hemostaseology and Stem Cell Transplantation, Medical Faculty University Hospital Aachen, Aachen, Germany; Carmem Bonfim: Hospital Pequeno Principe, Curitiba, Brazil; Tracy M. Bryan: Children's Medical Research Institute, Faculty of Medicine and Health, University of Sydney, Westmead, NSW, Australia; Rodrigo T. Calado: University of São Paulo, São Paulo, Brazil; Vivian Y. Chang: University of California, Los Angeles, CA, USA; Jane E. Churpek: The University of Wisconsin-Madison, Madison, WI, USA; Edward W. Cowen: Dermatology Branch, National Institute of Arthritis and Musculoskeletal and Skin Diseases, National Institutes of Health, Bethesda, MD, USA; Courtney D. DiNardo: University of Texas MD Anderson Cancer Center, Houston, TX, USA; Carlo Dufour: IRCCS Istituto G. Gaslini Children's Hospital, Genova, Italy; Christen L. Ebens: University of Minnesota, Minneapolis, MN, USA; Lucy C. Fox: Peter MacCallum Cancer Centre, Melbourne, Australia; Neelam Giri: Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, MD, USA; Nicholas J. Gloude: University of California San Diego, Rady Children's Hospital, San Diego, CA, USA; Frederick Goldman: Children's of Alabama, University of Alabama at Birmingham, Birmingham, AL, USA; Emma M. Groarke: Hematology Branch, National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, MD, USA; Fernanda Gutierrez-Rodrigues: Hematology Branch, National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, MD, USA; F. Bradley Johnson: University of Pennsylvania School of Medicine, Philadelphia, PA, USA; Christian P. Kratz: Pediatric Hematology and Oncology, Hannover Medical School, Hannover, Germany; Abhishek Mangaonkar: Mayo Clinic, Rochester, MN, USA; Lisa J. McReynolds: Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, MD, USA; Maria Molina-Molina: University Hospital of Bellvitge,

L'Hospitalet de Llobregat, Spain; Kasiani C. Myers: Division of Bone Marrow Transplantation and Immune Deficiency, Cincinnati Children's Hospital Medical Centre and Department of Paediatrics, University of Cincinnati College of Medicine, Cincinnati, OH, USA; Taizo A. Nakano: Children's Hospital Colorado, Aurora, CO, USA; Adam S. Nelson: Sydney Children's Hospital, Randwick, MSW, Australia; Marena R. Niewisch: Pediatric Hematology and Oncology, Hannover Medical School, Hannover, Germany; Benjamin A. Raby: Boston Children's Hospital and Harvard Medical School, Boston, MA, USA; Christopher R. Reilly: Dana-Farber Cancer Institute and Harvard Medical School, Boston, MA, USA; Akiko Shimamura: Boston Children's Hospital and Harvard Medical School, Boston, MA, USA; Orna Steinberg-Shemer: Department of Hematology-Oncology, Schneider Children's Medical Center of Israel, Petach Tikva, Israel; Moon Ley Tung: University of Iowa, Iowa City, IA, USA; Marcin W. Wlodarski: St. Jude Children's Research Hospital, Memphis, TN, USA; Joanne Yacobovich: Tel Aviv Faculty of Medicine, Schneider Children's Medical Center of Israel and Schneider Children's Medical Center, Tel Aviv Faculty of Medical and Health Sciences, Tel Aviv, Israel.

Additional experts endorsing this manuscript.

Inderjeet Dokal: Blizard Institute, Queen Mary University of London, London, United Kingdom; Dirk Hockemeyer: University of California, Berkeley, Berkeley, CA, USA; Hilary J. Longhurst: Dyskeratosis Congenita Action (UK Charity no.1167150); Katie A. Stevens: Team Telomere, Coeur d'Alene, ID, USA; Hemanth Tummala: Center for Genomics and Child Health, Blizard Institute, Queen Mary University of London, London, United Kingdom; Tom J Vulliamy: Blizard Institute, Faculty of Medicine and Dentistry, Queen Mary University of London, London, United Kingdom.

#### FUNDING INFORMATION

The work of SAS is supported by the intramural research program of the Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health. The work of AAB is supported by R01 HL131744.

#### CONFLICT OF INTEREST STATEMENT

Team Telomere, Inc., is a non-profit family and patient support and advocacy organization. The CCCTAA is an international consortium of researchers and clinicians who collaborate to answer critical questions in the TBDs. Dr. Geraldine Aubert is employed by Repeat Diagnostics, a clinical laboratory specializing in telomere length measurement services. Drs. Alison Bertuch, Cristen Ebens and Kasiani Myers are consultants for a clinical trial sponsored by Elixirgen Therapeutics. Dr. Maria Molina-Molina has received funds from Boehringer Ingelheim, Ferrer and Roche for providing scientific advice unrelated to this work.

#### DATA AVAILABILITY STATEMENT

The data herein are based current scientific literature and referenced accordingly.

#### ORCID

Sharon A. Savage b https://orcid.org/0000-0001-6006-0740

#### TWITTER

Sharon A. Savage 🎔 sharonsavagemd

#### REFERENCES

- Heiss NS, Knight SW, Vulliamy TJ, Klauck SM, Wiemann S, Mason PJ, et al. X-linked dyskeratosis congenita is caused by mutations in a highly conserved gene with putative nucleolar functions. Nat Genet. 1998;19(1):32–8.
- Mitchell JR, Wood E, Collins K. A telomerase component is defective in the human disease dyskeratosis congenita. Nature. 1999;402(6761):551-5.
- Vulliamy TJ, Marrone A, Knight SW, Walne A, Mason PJ, Dokal I. Mutations in dyskeratosis congenita: their impact on telomere length and the diversity of clinical presentation. Blood. 2006;107(7):2680-5.
- Tummala H, Walne A, Dokal I. The biology and management of dyskeratosis congenita and related disorders of telomeres. Expert Rev Hematol. 2022;15:1–12.
- Alter BP, Giri N, Savage SA, Rosenberg PS. Cancer in the National Cancer Institute inherited bone marrow failure syndrome cohort after fifteen years of follow-up. Haematologica. 2018;103(1):30–9.
- Niewisch MR, Giri N, McReynolds LJ, Alsaggaf R, Bhala S, Alter BP, et al. Disease progression and clinical outcomes in telomere biology disorders. Blood. 2022;139(12):1807–19.
- Kam MLW, Nguyen TTT, Ngeow JYY. Telomere biology disorders. NPJ Genom Med. 2021;6(1):36.
- Armanios M. The role of telomeres in human disease. Annu Rev Genomics Hum Genet. 2022;23:363–81.
- 9. Revesz T, Fletcher S, al-Gazali LI, DeBuse P. Bilateral retinopathy, aplastic anaemia, and central nervous system abnormalities: a new syndrome? J Med Genet. 1992;29(9):673–5.
- Crow YJ, McMenamin J, Haenggeli CA, Hadley D, Tirupathi S, Treacy E, et al. Coats' plus: a progressive familial syndrome of bilateral Coats' disease, characteristic cerebral calcification, leukoencephalopathy, slow pre- and post-natal linear growth and defects of bone marrow and integument. Neuropediatrics. 2004;35(1):10–9.
- 11. Glousker G, Touzot F, Revy P, Tzfati Y, Savage SA. Unraveling the pathogenesis of Hoyeraal-Hreidarsson syndrome, a complex telomere biology disorder. Br J Haematol. 2015;170(4):457–71.
- 12. Savage SA, Bertuch AA. The genetics and clinical manifestations of telomere biology disorders. Genet Med. 2010;12(12):753–64.
- Alter BP, Rosenberg PS, Giri N, Baerlocher GM, Lansdorp PM, Savage SA. Telomere length is associated with disease severity and declines with age in dyskeratosis congenita. Haematologica. 2012;97(3):353–9.
- 14. Revy P, Kannengiesser C, Bertuch AA. Genetics of human telomere biology disorders. Nat Rev Genet. 2023;24(2):86–108.
- 15. Savage SA. Telomere length and cancer risk: finding goldilocks. Biogerontology. 2024;25(2):265–78.
- Sonmez C, Toia B, Eickhoff P, Matei AM, el Beyrouthy M, Wallner B, et al. DNA-PK controls Apollo's access to leading-end telomeres. Nucleic Acids Res. 2024;52(8):4313–27.
- Shi J, Yang XR, Ballew B, Rotunno M, Calista D, Fargnoli MC, et al. Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nat Genet. 2014;46(5):482–6.
- Robles-Espinoza CD, Harland M, Ramsay AJ, Aoude LG, Quesada V, Ding Z, et al. POT1 loss-of-function variants predispose to familial melanoma. Nat Genet. 2014;46(5):478–81.
- Henry ML, Osborne J, Else T. POT1 tumor predisposition. Adam MP, Mirzaa GM, Pagon RA, Wallace, SE, Bean, LJH, Gripp, KW, & Amemiya, A (Eds.). Seattle (WA): GeneReviews((R)); 1993.
- Lim TL, Lieberman DB, Davis AR, Loren AW, Hausler R, Bigdeli A, et al. Germline POT1 variants can predispose to myeloid and lymphoid neoplasms. Leukemia. 2022;36(1):283–7.

- DeBoy EA, Tassia MG, Schratz KE, Yan SM, Cosner ZL, McNally EJ, et al. Familial clonal hematopoiesis in a long telomere syndrome. N Engl J Med. 2023;388(26):2422–33.
- 22. He H, Li W, Comiskey DF, Liyanarachchi S, Nieminen TT, Wang Y, et al. A truncating germline mutation of TINF2 in individuals with thyroid cancer or melanoma results in longer telomeres. Thyroid. 2020;30(2):204–13.
- 23. Schmutz I, Mensenkamp AR, Takai KK, Haadsma M, Spruijt L, de Voer RM, et al. TINF2 is a haploinsufficient tumor suppressor that limits telomere length. elife. 2020;9:e61235.
- Kim WT, Hennick K, Johnson J, Finnerty B, Choo S, Short SB, et al. Cancer-associated POT1 mutations lead to telomere elongation without induction of a DNA damage response. EMBO J. 2021;40(12):e107346.
- Codd V, Wang Q, Allara E, Musicha C, Kaptoge S, Stoma S, et al. Polygenic basis and biomedical consequences of telomere length variation. Nat Genet. 2021;53(10):1425–33.
- Ferrer A, Lasho T, Fernandez JA, Steinauer NP, Simon RA, Finke CM, et al. Patients with telomere biology disorders show context specific somatic mosaic states with high frequency of U2AF1 variants. Am J Hematol. 2023;98(12):E357–E359.
- 27. Schratz KE, Gaysinskaya V, Cosner ZL, DeBoy EA, Xiang Z, Kasch-Semenza L, et al. Somatic reversion impacts myelodysplastic

syndromes and acute myeloid leukemia evolution in the short telomere disorders. J Clin Invest. 2021;131(18):e147598.

- Maryoung L, Yue Y, Young A, Newton CA, Barba C, van Oers NSC, et al. Somatic mutations in telomerase promoter counterbalance germline loss-of-function mutations. J Clin Invest. 2017;127(3):982–6.
- Gutierrez-Rodrigues F, Groarke EM, Thongon N, Rodriguez-Sevilla JJ, Bazzo Catto LF, Niewisch MR, et al. Clonal landscape and clinical outcomes of telomere biology disorders: somatic rescuing and cancer mutations. Blood. 2024. Online ahead of print. https://doi.org/10. 1182/blood.2024025023

**How to cite this article:** Savage SA, Bertuch AA. Different phenotypes with different endings— Telomere biology disorders and cancer predisposition with long telomeres. Br J Haematol. 2025;206(1): 69–73. <u>https://doi.org/10.1111/bjh.19851</u>