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Whole-genome and long-read sequencing identify a novel mechanism in RFC1 resulting in CANVAS syndrome

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Whole-Genome and Long-Read Sequencing Identify a Novel Mechanism in RFC1 Resulting in **CANVAS Syndrome**

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Abstract

Objectives

Cerebellar ataxia with neuropathy and bilateral vestibular areflexia syndrome (CANVAS) results from biallelic intronic pentanucleotide repeats in RFC1. We describe an adult male proband with progressive imbalance, cerebellar atrophy, somatosensory neuronopathy, and absence of peripheral vestibular function for whom clinical testing demonstrated a heterozygous RFC1 expansion consistent with an unaffected carrier.

Methods

We performed whole-genome sequencing (WGS) on peripheral blood DNA samples from the proband and his unaffected mother. We performed DNA long-read sequencing and synthesized complementary DNA from RNA using peripheral blood from the proband.

Results

WGS confirmed the maternally inherited RFC1 expansion and identified a rare, nonsense RFC1 variant: c.C1147T; p.R383X in the proband but not the maternal DNA sample. RFC1 variants were confirmed in trans with long-read sequencing. Functional studies demonstrated the absence of complementary DNA (cDNA) transcript from the c.C1147T; p.R383X variant supporting nonsense-mediated decay of this transcript.

Discussion

We report an adult with CANVAS due to compound heterozygous pathogenic *RFC1* variants: the pathogenic intronic pentanucleotide expansion confirmed in *trans* with a nonsense variant. This report represents a novel molecular mechanism for CANVAS. Sequencing for RFC1 should be considered for adults meeting clinical criteria for the CANVAS phenotype if only a heterozygous pathogenic RFC1 expansion is identified.

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Undiagnosed Disease Network (UDN) coinvestigators are listed in Appendix 2 at the end of the article.

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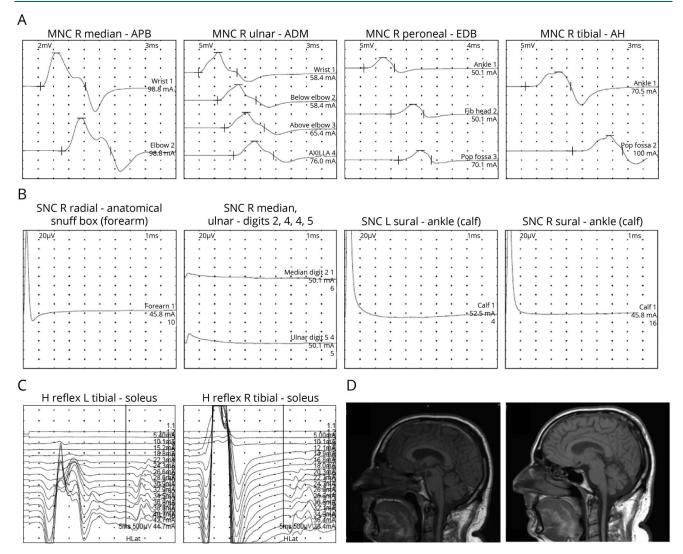
Cerebellar ataxia with neuropathy and bilateral vestibular areflexia syndrome (CANVAS) (MIM #614575) is a rare, adult-onset, neurodegenerative disorder attributed to biallelic intronic pentanucleotide expansions in *RFC1*, which encodes replication factor *C*, subunit 1,¹ the largest subunit of a DNA polymerase accessory protein important for DNA replication and repair. The mechanism by which biallelic intronic pentanucleotide repeats in *RFC1* result in neurologic disease is unknown but is unlikely to result from decreased expression of *RFC1*.² Here, we report an adult meeting clinical criteria for CANVAS³ who was identified to be compound heterozygous for the *RFC1* expansion in *trans* with a nonsense variant, thereby identifying a new molecular mechanism for CANVAS.

Case Report

A 49-year-old man presented with a 5-year history of imbalance, most prominent in the absence of visual feedback and when walking on uneven ground. He reported a dry cough of 7-year duration. He endorsed symptoms consistent with oscillopsia but denied diplopia. He denied sensory loss, weakness, vertigo, change in hearing, or tinnitus. His mother reported vertigo and muscle cramps, and he has 3 healthy full siblings and 3 healthy children.

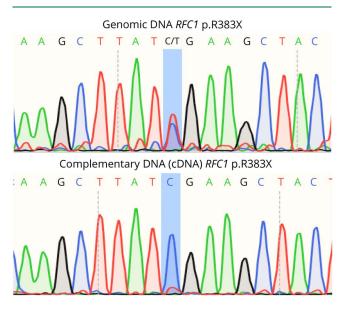
His neurologic examination demonstrated abnormal bilateral head impulse tests (large catch-up saccades bilaterally), downbeat nystagmus at the extremes of horizontal gaze,

Figure 1 Electrodiagnostic Studies and Brain MRI



(A) MNC, (B) antidromic SNC, and (C) tibial H-reflexes at age 49 years demonstrate diffuse loss of sensory responses with preserved motor responses and normal EMG, consistent with sensory neuronopathy. The preserved tibial H-reflexes, while atypical for most neuronopathies, have been identified as a unique attribute of neuronopathy associated with cerebellar ataxia with neuropathy and bilateral vestibular areflexia syndrome. (D) Sagittal T1-weighted MRI of the brain at age 44 years (left) and at age 49 years demonstrates interval development of mild cerebellar atrophy. ADM = abductor digiti minimi; AH = abductor hallucis; APB = abductor pollicis brevis; EDB = extensor digitorum brevis; MNC = motor nerve conduction; SNC = sensory nerve conduction.

Figure 2 Sanger Sequencing Files of the *RFC1* c.C1147T; p.R383X Variant Location (Blue Highlighted Box) in Genomic DNA and Complementary DNA



The presence of the heterozygous variant in genomic DNA is shown by 2 peaks (C/T), whereas only the wild-type peak (C) is seen in cDNA supporting nonsense-mediated decay of the transcript containing the *RFC1* c.C1147T; p.R383X nonsense variant. cDNA = complementary DNA.

panmodal sensory deficits in all limbs, and a positive Romberg sign. Reflexes were brisk throughout but symmetric. There was no appendicular ataxia. Stance in natural position was slightly wide, measuring 14 cm at the medial malleoli. He was unable to tandem but was otherwise steady on his feet.

Prior evaluations including brain MRI and extensive clinical laboratory testing were nondiagnostic. Electrodiagnostics showed diffusely absent sensory responses with normal motor studies and normal EMG, consistent with sensory neuronopathy (Figure 1, A–C). The cerebellum appeared smaller (mild atrophy) on subsequent brain MRI (Figure 1D). Vestibular testing demonstrated near absence of peripheral vestibular function bilaterally, with concurrent central features of abnormal optokinetic reflexes and side-to-side differences in quantitative measurements of smooth pursuits on videonystagmography. Because of clinical suspicion for CANVAS, clinical testing for the pathogenic RFC1 intronic expansion was performed and demonstrated that the proband was heterozygous, consistent with an unaffected carrier.

Methods

Standard Protocol Approvals, Registrations, and Patient Consents

This study was approved by the Washington University Human Research Protection Office. We obtained written informed consent from the proband and his mother as part of the Undiagnosed Disease Network (Supplement, links.lww. com/NXG/A552).

Sequencing

We performed whole-genome sequencing (WGS) on peripheral blood DNA from the proband and his mother. We used PacBio long-read sequencing (\sim 20 kb reads, Pacific-Biosciences) to phase *RFC1* variants. We synthesized complementary DNA (cDNA) from RNA using proband peripheral blood.

Results

WGS confirmed the maternally inherited *RFC1* intronic pentanucleotide expansion and identified a *RFC1* nonsense variant c.C1147T; p.R383X in the proband that was not present in the maternal sample. Long-read sequencing confirmed the expansion (~600 AAGGG repeats), and phasing demonstrated that the *RFC1* variants are in *trans* (eFigure 1, links.lww.com/NXG/A552). The c.C1147T; p.R383X variant is extremely rare (gnomAD-v.3.1.2,⁴ minor allele frequency 0.000007). Comparison of Sanger sequencing results for genomic and cDNA supported nonsense-mediated decay of the c.C1147T; p.R383X transcript (Figure 2). Alternative repeat disorders with ataxia and predicted damaging variants in *PNPLA6* and *ELF2* were excluded.^{5,6}

Discussion

Adults with CANVAS typically display progressive ataxia from cerebellar dysfunction, vestibulopathy, and somatosensory deficits, deemed the CANVAS diagnostic triad.^{1,7} Additional symptoms include chronic spasmodic cough, orthostatic hypotension, neuropathic pain, autonomic dysfunction, and sensory neuronopathy with preserved or even brisk reflexes.^{1,7}

The molecular etiology of CANVAS was identified in affected unrelated adults using linkage analysis, exome/genome sequencing, and Sanger sequencing of long-range PCR products.² Affected adults were homozygous for a pentanucleotide intronic repeat, AAGGG(n) in *RFC1*, ranging in size from 400 to 2,000 repeats across families and stable within families.² Most affected individuals had \sim 1,000 repeats with no association between repeat size and age at onset.² This RFC1 intronic expansion has been identified in diverse populations with an estimated carrier frequency of 0.7%-6.8%, with increased frequencies among certain ethnic groups.^{1,8} The biallelic RFC1 expansion is present in \sim 90% of individuals with the CANVAS triad and has been identified in individuals with related neurologic phenotypes including late-onset ataxia, peripheral neuropathy, and cerebellar dysfunction.^{1,9} Our report demonstrates a novel mechanism for CANVAS with the identification of a nonsense variant in trans with the pathogenic RFC1 expansion. RFC1 sequencing should be considered if only a heterozygous pathogenic RFC1 expansion is identified in an adult meeting clinical criteria for CANVAS.

Given the high carrier frequencies for the pathogenic *RFC1* expansion and the expanding number of neurologic disorders associated with *RFC1*,⁸ the finding of this report may have implications for other neurodegenerative diseases.

Study Funding

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Disclosure

P. Dickson receives research support from Genzyme and M6P Therapeutics and is a consultant to Mandos, LLC. All other authors have no financial relationships to disclose. Full disclosure form information provided by the authors is available with the full text of this article at Neurology.org/NG.

Publication History

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Appendix 2 (continued)

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Appendix 2 (continued)

Appendix 2 (continued)					
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Pacific Northwest	Coinvestigator	Project administration
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Stanford	Genetic Project counselor administra	
Stanford	Study Project coordinator administra	
Stanford	Clinician, adults Project administra	
Stanford	Bioinformatician	Project administration
	Pacific Northwest Pacific Northwest Pacific Northwest Pacific Northwest Pacific Northwest Pacific Northwest Pacific Northwest Pacific Northwest Pacific Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford Stanford	Pacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestPediatric rheumatologistPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestCoinvestigatorPacific NorthwestPediatric geneticistStanfordPrincipal investigatorStanfordPrincipal investigatorStanfordStudy coordinator/ licensed Spanish interpreter/ curatorStanfordStudy coordinator/ licensed Spanish interpreter/ curatorStanfordLaboratory technicianStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanfordStudy coordinatorStanford<

Appendix 2 (continued)				
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Irma Gutierrez	UCLA	Study coordinator	Project administration	
Alden Huang	UCLA	Sequencing interpretation	Project administration	

Appendix 2 (continued)					
Name	Location	Role	Contribution		
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Bryan C. Mak	UCLA	Site coordinator and genetic counselor	Project administration		
Martin G. Martin	UCLA	Coinvestigator	Project administration		
Julian A. Martínez- Agosto	UCLA	Principal investigator	Project administration		
Elisabeth McGee	UCLA	Research nurse	Project administration		
Stanley F. Nelson	UCLA	Principal investigator	Project administration		
Shirley Nieves- Rodriguez	UCLA	Graduate student researcher	Project administration		
Christina G.S. Palmer	UCLA	Principal investigator	Project administration		
Jeanette C. Papp	UCLA	Coinvestigator	Project administration		
Neil H. Parker	UCLA	Coinvestigator	Project administration		
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Rebecca H. Signer	UCLA	Site coordinator and genetic counselor	Project administration		
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Jijun Wan	UCLA	Research assistant	Project administration		
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Jeremy D. Woods	UCLA	Medical fellow	Project administration		
Justin Alvey	University of Utah	Coinvestigator	Project administration		
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Jim Bale	University of Utah	Coinvestigator	Project administration		
John Bohnsack	University of Utah	Coinvestigator	Project administration		
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Name	Location	Role	Contribution	
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Laura Pace	University of Utah	Coinvestigator	Project administratior	
Nicola Longo	University of Utah	Coinvestigator	Project administratior	
Gabor Marth	University of Utah	Bioinformatician	Project administratior	
Paolo Moretti	University of Utah	Coinvestigator	Project administration	
Aaron Quinlan	University of Utah	Bioinformatician	Project administration	
Matt Velinder	University of Utah	Bioinformatician	Project administratior	
Dave Viskochil	University of Utah	Coinvestigator	Project administration	
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Rong Mao	University of Utah/ARUP	Molecular geneticist	Project administratior	
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Elly Brokamp	Vanderbilt	Genetic counselor	Project administratior	
Laura Duncan	Vanderbilt	Genetic counselor	Project administratior	
Rizwan Hamid	Vanderbilt	Principal investigator	Project administration	
Jennifer Kennedy	Vanderbilt	Genetic counselor	Project administratior	
Mary Kozuira	Vanderbilt	Nurse practitioner	Project administratior	
John H. Newman	Vanderbilt	Principal investigator	Project administration	
John A. Phillips III	Vanderbilt	Principal investigator	Project administration	
Lynette Rives	Vanderbilt	Lab Manager	Project administration	
Amy K. Robertson	Vanderbilt	Nurse practitioner	Project administratior	
Emily Solem	Vanderbilt	Genetic counselor	Project administratior	
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Name	Location	Role	Contribution
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Dana Kiley	Washington University Clinical	Research coordinator	Project administration
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Dustin Baldridge	Washington University Clinical & Model Organism Screening Core	Coinvestigator	Project administration
Stephen Pak	Washington University Model Organism Screening Core	Coinvestigator	Project administration
Timothy Schedl	Washington University Model Organism Screening Core	Principal investigator	Project administration

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Name	Location	Role	Contribution	
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Lilianna Solnica- Krezel	Washington University Model Organism Screening Core	Principal investigator	Project administration	

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