Repeat-Associated Non-AUG Translation of AGAGGG Repeats that Cause X-Linked Dystonia-Parkinsonism

Charles Jourdan Reyes, PhD,[1]
Katsura Asano, PhD,[2,3,4] Peter K. Todd, MD, PhD,[5,6]
Christine Klein, MD,[1] and Aleksandar Rakovic, PhD[1*]

[1]Institute of Neurogenetics, University of Lübeck, Lübeck
[2]Molecular Cellular and Developmental Biology Program, Division of Biology, Kansas State University, Manhattan, Kansas, USA
[3]Laboratory of Translational Control Study, Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan [4]Hiroshima Research Center for Healthy Aging, Hiroshima University, Hiroshima, Japan [5]Department of Neurology, University of Michigan Medical School, Ann Arbor, Michigan, USA [6]Veterans Affairs Medical Center, Ann Arbor, Michigan, USA

ABSTRACT: Background: X-linked dystonia-parkinsonism (XDP) is a neurodegenerative disorder caused by the intronic insertion of a SINE-VNTR-*Alu* (SVA) retrotransposon carrying an $(AGAGGG)_n$ repeat expansion in the *TAF1* gene. The molecular mechanisms by which this mutation causes neurodegeneration remain elusive. **Objectives:** We investigated whether $(AGAGGG)_n$ repeats undergo repeat-associated non-AUG (RAN) translation, a pathogenic mechanism common among repeat expansion diseases. **Methods:** XDP-specific RAN translation reporter plasmids were generated, transfected in HEK293 cells, and putative dipeptide repeat proteins (DPRs) were detected by Western blotting. Immunocytochemistry was performed in COS-7 cells to determine the subcellular localization of one DPR. **Results:** We detected putative DPRs from two reading frames, supporting the translation of poly-(Glu-Gly) and poly-(Arg-Glu) species. XDP RAN translation initiates within the $(AGAGGG)_n$ sequence and poly-(Glu-Gly) DPRs formed nuclear inclusions in transfected cells.

Conclusions: In summary, our work provides the first *in-vitro* proof of principle that the XDP-linked $(AGAGGG)_n$ repeat expansions can undergo RAN translation. © 2022 The Authors. *Movement Disorders* published by Wiley Periodicals LLC on behalf of International Parkinson and Movement Disorder Society

Key Words: X-linked dystonia-parkinsonism; RAN translation; repeat expansion; SVA retrotransposon; Dipeptide repeat proteins; TAF1

DNA tandem repeats are the most unstable portions of the human genome.[1] Their expansion causes more than 50 genetic diseases,[1] most of which are neurological.[2] How these dynamic mutations elicit neurodegeneration are variable dependent on the location of the repeats within genes and their impact on transcription and translation. Historically, non-coding repeat expansions were thought to cause disease exclusively by host gene loss of function or RNA-mediated toxicity.[3] However, repeats can also support non-canonical translation in the absence of an AUG start codon through a process known as repeat-associated non-AUG (RAN) translation.[4] RAN translation generates aggregation-prone proteins from multiple reading frames, contributing to the pathogenesis of at least 10 repeat expansion disorders.[3]

X-linked dystonia-parkinsonism (XDP) is a hereditary neurodegenerative disorder with a clear genetic etiology, but ill-defined pathophysiology. XDP involves a progressive neuronal loss in the striatum and neuroanatomic alterations in the cortex and cerebellum.[5-7] Recent genetic findings converge on the notion that the age-related penetrance and expressivity of XDP are modified by an $(AGAGGG)_n$ hexanucleotide repeat expansion within a SINE-VNTR-*Alu* (SVA) retrotransposon inserted in the sense strand (and $[CCCTCT]_n$ in the antisense orientation) of the *TAF1* gene.[8,9] Repeat length ranged from 30 to 55 in patients and showed a significant inverse correlation with age at disease onset (range, 22–67 years).[9] *TAF1* loss of function (LoF) was proposed as the primary mechanism causing striatal neurodegeneration in XDP.[10,11] However, *TAF1* LoF in rodents' brains failed to recapitulate the specific pattern of striatal neurodegeneration in this rare disease.[12,13] Moreover, somatic expansions of the hexanucleotide repeat mentioned above were found to occur at greater levels in the brain relative to the blood of XDP patients, hinting at the possible contribution of other repeat-mediated pathogenic processes in XDP.[14-16] This study investigated the potential of the XDP-linked

(AGAGGG)$_n$ repeat expansion to undergo RAN translation as a possible contributor to disease pathogenesis.

Methods

Development of XDP-Specific RAN Translation Reporter Plasmids

Detailed procedures for generating XDP-specific RAN translation reporter plasmids are found in the Supporting Data (including Supplementary Table S1).

Mammalian Cell Culture, Transfection Conditions, and Western Blot Analysis

Human embryonic kidney 293 (HEK293) cells were maintained in Dulbecco's modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS) and 1% penicillin/streptomycin (Gibco, Grand Island, NY) at 37°C in the presence of 5% CO_2. For transfection, cells were seeded in 6-well plates at 2.0×10^6 cells per well and transfected using a mixture of 5 μg of plasmid DNA, 20 μL FuGENE HD transfection reagent (Promega, Madison, WI), and 300 μL of sterile Opti-MEM 24 h post-seeding. Cells were then lysed 24 h after transfection with radioimmunoprecipitation assay (RIPA) buffer (Pierce, Rockford, IL). The protein concentration was determined using the Pierce BCA protein assay kit (Thermo Scientific, Waltham, MA) immediately before Western blot analysis.

For Western blot analysis, 10 μg of protein was prepared in 1x NuPAGE LDS sample buffer (Thermo Scientific) and electrophoresed in 1.0-mm, 10-well NuPAGE 4%–12% Bis-Tris protein gels (Thermo Scientific, Waltham, MA) at 150 V for 90 min. Proteins were transferred to a nitrocellulose membrane at 32 V for 60 min. Visualization was carried out using the SuperSignal West Pico PLUS Chemiluminescent Substrate (Thermo Scientific, Waltham, MA), the ChemiDoc MP Imaging System (Bio-Rad Laboratories, Hercules, CA), and the appropriate antibodies in Supplementary Table S2.

Immunocytochemical Staining and Apoptosis Assay

COS-7 cells were seeded on coverslips and carefully placed in 24-well plates. After 24 h, each well was transfected using 33 μL of the aforementioned transfection mixture. Twenty-four hours post-transfection, cells were fixed in 4.0% formaldehyde for 15 min and permeabilized with 0.1% Triton X-100. Blocking was performed using 4.0% normal goat serum in phosphate buffered saline (PBS) for 1 h. Immunofluorescence staining was done using a primary antibody against FLAG (1:100; Sigma-Aldrich). The appropriate secondary antibody was used (Goat anti-mouse IgG Alexa Fluor 594, 1:1000, Invitrogen). Coverslips were viewed using an LSM710 confocal microscope (Zeiss, Oberkochen, Germany). Apoptosis was assayed using a TUNEL Apoptosis Assay Kit (Roche Life Science, Basel, Switzerland) according to the manufacturer's protocol. TUNEL-positive cells were counted in 10 randomly chosen viewing fields each containing at least 20 cells. Coverslips were viewed using an LSM710 confocal microscope (Zeiss, Oberkochen, Germany) under 40× magnification.

Data Sharing

The authors confirm that the data supporting the findings of this study are available within the article and its supplementary material.

Results

The (AGAGGG)$_n$ Sequence Is RAN-Translated in Two Reading Frames

Based on the hexanucleotide repeat motif located within the XDP-causing intronic SVA retrotransposon, a maximum of three dipeptide repeat proteins (DPRs) could potentially cause neurodegeneration if the XDP-associated repeats undergo RAN translation (Fig. 1A). We designed a series of XDP-specific RAN translation reporter plasmids by inserting the TAF1 SVA retrotransposon bearing either 30 or 54 repeats, the lowest and one of the highest repeat lengths detected in our cohort of patients,[9] into a previously described RAN translation reporter (GGG-nLuc-3xFLAG) (Supporting Data).[17,18] Such constructs harbor the nanoluciferase (nLuc)-coding sequence without the canonical AUG start codon followed by a 3xFLAG sequence, therefore, producing fusion proteins initiated only from the upstream sequence (Fig. 1B). These reporter plasmids have been previously used to elucidate how RAN translation is regulated in the context of the C9ORF72 and FMR1 repeat expansions causing amyotrophic lateral sclerosis/frontotemporal dementia (ALS-FTD) and fragile X tremor ataxia syndrome (FXTAS), respectively.[17,18]

Western blot analysis of cell lysates derived from HEK293 cells transfected with the RAN translation reporters (Supplementary Table S2) was performed using a FLAG-specific antibody to investigate whether translation could initiate from within the TAF1 SVA retrotransposon sequence. We observed that the AUG-nLuc-3xFLAG fusion protein was at its expected molecular weight of ~22 kDa. No band was detected in reading frame 1 (RF1), demonstrating the absence of a poly-(Arg-Gly) product. Conversely, bands representing higher molecular weight products were detected in cells expressing either RF2 or RF3,
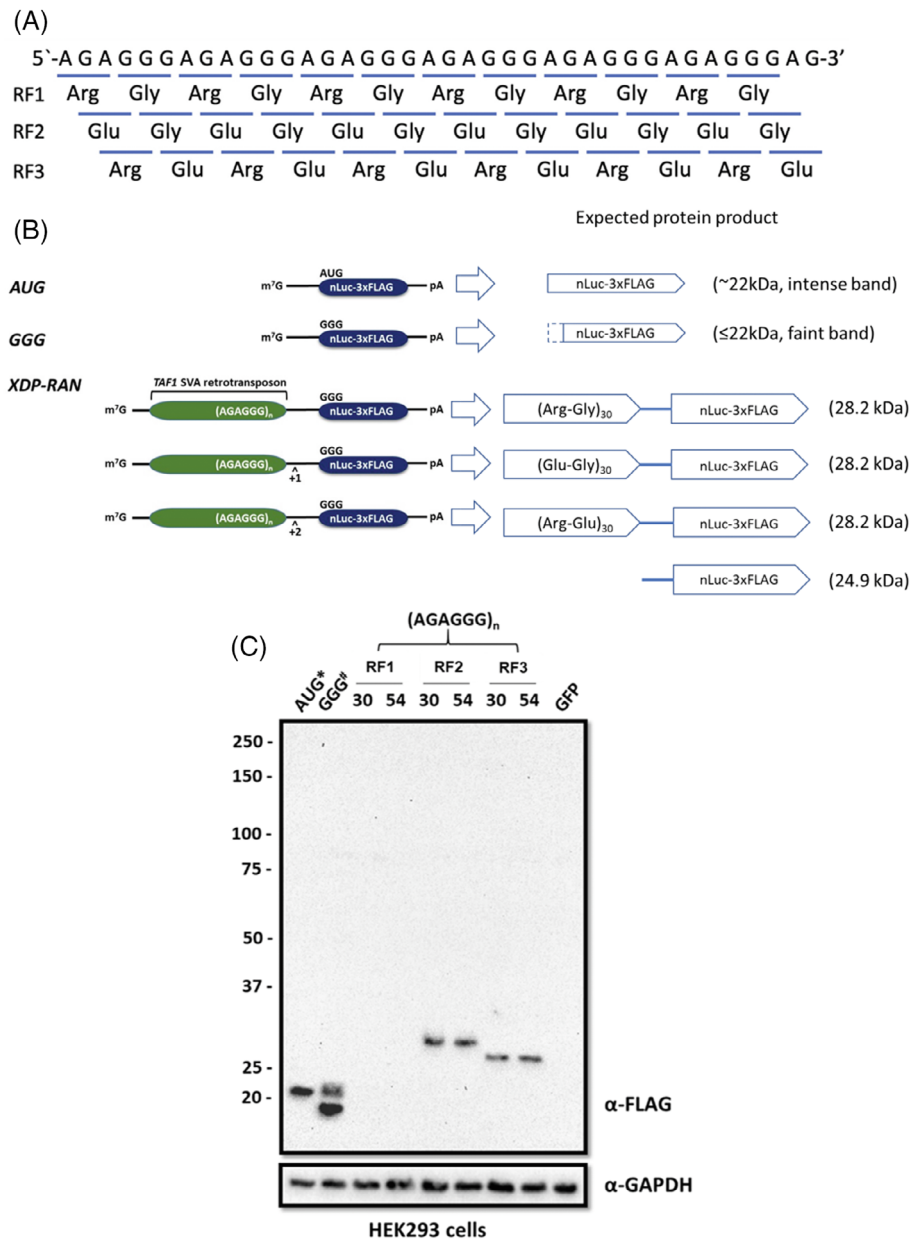
FIG. 1. Development of repeat-associated non-AUG (RAN) translation-specific reporter plasmids for X-linked dystonia-parkinsonism (XDP). (**A**) Schematic depiction of the putative dipeptide repeat proteins (DPRs) generated by RAN translation of the $(AGAGGG)_n$ repeats in the three alternate reading frames (RF1, RF2, and RF3). (**B**) Plasmids were designed by inserting the *TAF1* SVA retrotransposon bearing 30 or 54 AGAGGG repeats upstream of a mutant nanoluciferase (nLuc) with the canonical AUG start site replaced by a GGG codon. The SVA was inserted in 3 different reading frames (RF1, RF2, and RF3) relative to the repeat sequence. A C-terminal 3xFLAG tag is available for Western blot detection. m7G = 7-methylguanosine cap; pA = poly(A) tail. (**C**) Western blot analysis using a FLAG-specific antibody in HEK293 cells transfected with XDP-specific RAN translation reporter plasmids carrying 30 or 54 repeats indicates that the $(AGAGGG)_n$ sequence is translated in RF2 and RF3, forming putative poly-(Glu-Gly) and poly-(Arg-Glu) DPRs. No band was detected in RF1 (poly-[Arg-Gly]) reading frame. In addition, no apparent molecular weight increase was observed between 30- and 54-repeat constructs. GAPDH was used as a loading control. *One-hundredth of the AUG control plasmid was used to avoid overexposure on western blots. #Smaller molecular weight proteins derived from initiation within the nLuc tag coding sequence were observed in the GGG control. A GFP-expressing vector (pmaxGFP) was used to determine successful transfection.

supporting the translation of poly-(Glu-Gly) and poly-(Arg-Glu) DPRs, respectively (Fig. 1C). In both reading frames, no repeat length-dependent shift in molecular weight and slower migrating proteins accumulating in the stacking gel were observed between 30- and 54-repeat plasmids.

RAN Translation Initiates within the $(AGAGGG)_n$ Sequence

Depending on the sequence context, RAN translation can initiate from near-cognate start codons upstream of the repeats or within the repeat motif forming a secondary structure such as a hairpin
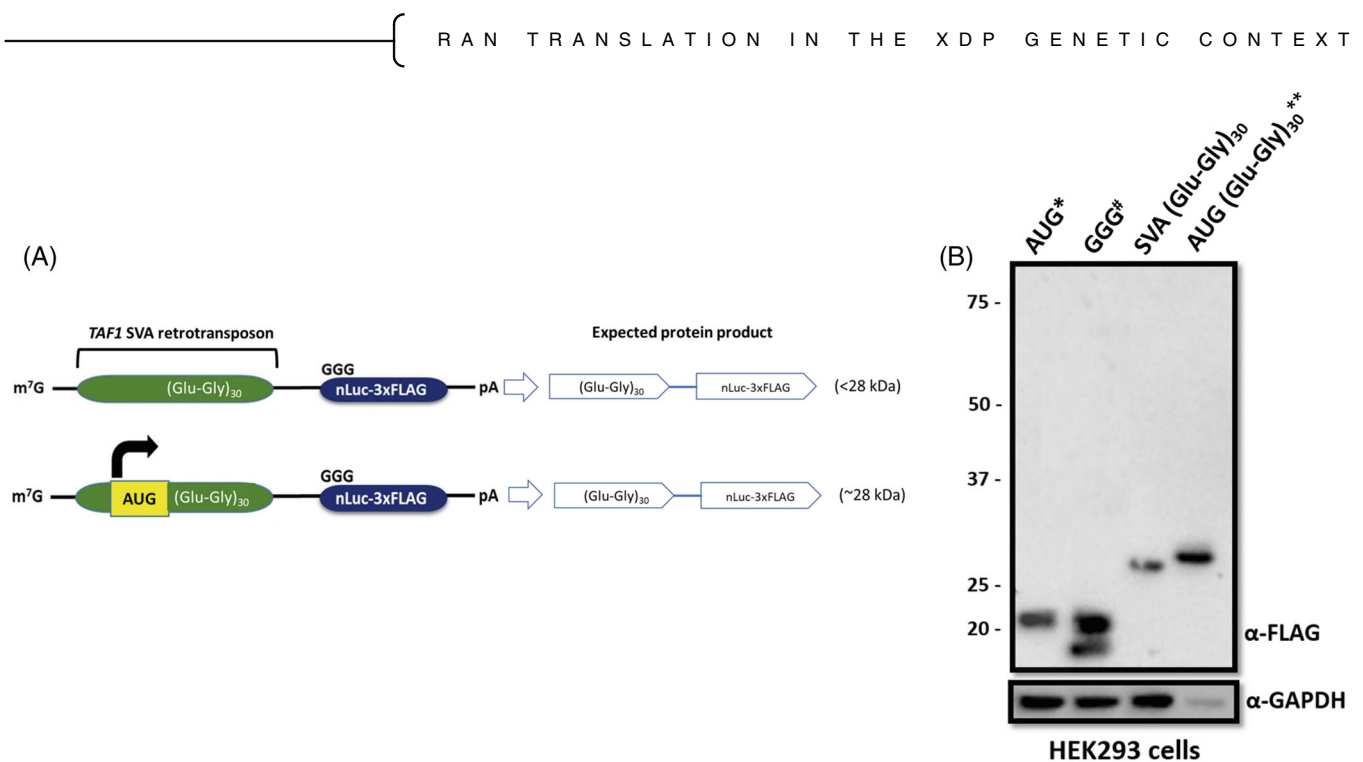
FIG. 2. Repeat-associated non-AUG (RAN) translation initiates within the $(AGAGGG)_n$ repeat sequence. **(A)** Translation initiation was forced upstream of the repeat sequence by artificially introducing an AUG start codon in good Kozak sequence context (yellow box) in the reading frame 2 (RF2). **(B)** Western blot analysis using a FLAG-specific antibody in HEK293 cells transfected with 30-repeat constructs in the native or AUG-initiated context. GAPDH was used as a loading control. *One-hundredth of the AUG control plasmid was used to avoid overexposure on Western blots. #Smaller molecular weight proteins derived from initiation within the nanoluciferase (nLuc) tag coding sequence were observed in the GGG control. **The cell lysate was diluted 10-fold to avoid signal saturation on Western blots.

or G-quadruplex.[17] The molecular weight of the bands (Supplementary Table S3) and the absence of a repeat length-dependent increase in molecular weight between 30- and 54-repeat constructs in both reading frames suggested that RAN translation initiates within the $(AGAGGG)_n$ sequence. To verify this hypothesis, translation was forced to begin directly upstream of the hexanucleotide repeats by introducing an AUG start codon in a good Kozak sequence context in RF2 (Fig. 2A). HEK293 cells were transfected with 30-repeat plasmids in the native and AUG-initiated sequence contexts. Western blotting using the same FLAG-specific antibody showed that the AUG-initiated plasmid produced a higher molecular weight protein than the original plasmid, supporting the proposed mechanism for translation initiation (Fig. 2B).

Poly-(Glu-Gly) Has a Propensity to Form Nuclear Inclusions

Immunocytochemical staining was performed in COS-7 cells to determine the subcellular localization of the poly-(Glu-Gly) DPR. In contrast to the AUG-nLuc-3xFLAG fusion protein, which was widely distributed throughout the nucleus and the cytoplasm, poly-(Glu-Gly) was primarily localized in the nucleus, where it showed a tendency to form inclusions (Fig. S1A).

However, poly-(Glu-Gly) did not induce apoptosis in our model system (Fig. S1B).

Discussion

Although two independent genome-editing studies have established that the SVA retrotransposon insertion in *TAF1* causes XDP,[19,20] the pathogenic mechanisms linking this genetic etiology to neurodegeneration in this rare disease remain unsettled. An essential clue to this longstanding issue was the observation that a polymorphic hexanucleotide repeat within this pathogenic insertion correlates with clinical disease manifestation and somatically expands in patients' brains,[8,9,14,15] implying that XDP may share causal pathways with other diseases caused by unstable repeat expansions.[16] By developing XDP-specific RAN translation reporters, our work provides the first *in-vitro* proof of principle that the XDP-associated hexanucleotide repeat is translated into proteins. Importantly, we offer evidence that RAN translation initiates from within the $(AGAGGG)_n$ repeat, not the upstream sequence. Consistent with this notion, the *TAF1* SVA retrotransposon possessed intrinsic promoter activity,[8] and SVA transcription has been confirmed to initiate from within the hexamer.[21,22] Furthermore, a similar regulatory mechanism was

recently reported for a 68-bp repeat expansion in *WDR7*, which is transcribed into microRNAs at regular repeat length intervals.[23]

This study reports the potential translation of poly-(Glu-Gly) and poly-(Arg-Glu) DPRs in XDP. To our knowledge, poly-(Glu-Gly) and poly-(Arg-Glu) DPRs have not been reported for any other repeat expansion disorder. Nevertheless, arginine-rich DPRs were the most toxic proteins produced in *C9ORF72*-mediated ALS-FTD, causing neurodegeneration by blocking global protein translation[24,25] and disrupting nucleocytoplasmic transport.[26] In particular, poly-(Gly-Arg) DPRs accumulated in clinically affected brain regions[27] and caused TDP-43 cytoplasmic mislocalization and aggregation,[28] the main pathological hallmark of ALS-FTD. Because the toxicity of protein aggregates is linked to their specific pathophysiology,[26,29,30] functional studies are warranted to elucidate the unique cellular pathways disrupted by these putative DPRs in endogenous disease models of XDP.

Our study also encountered some technical limitations. In line with previous observations on FXTAS, RAN translation of the XDP-specific $(AGAGGG)_n$ repeats was highly inefficient, showing <1% efficiency relative to canonical AUG translation.[31] Furthermore, the near-cognate AGG initiation codon, which repeatedly occurs within the $(AGAGGG)_n$ repeat motif, did not show significantly higher expression levels than the GGG-nLuc-3xFLAG negative control in a prior investigation.[32] These limitations precluded us from directly detecting the nLuc tag via luciferase assays, immunofluorescence, and immunocytochemistry. RAN translation is a highly inefficient process relative to canonical AUG translation, and the slow accumulation of toxic proteins has been linked to the age-associated penetrance of these diseases.[17,31] However, cellular stress triggered by protein misfolding can promote RAN translation while suppressing global AUG translation.[18,33] Furthermore, DPR toxicity can synergize with RNA-mediated toxicity mediated by G-quadruplexes[34] and host gene loss of function to drive progressive neurodegeneration.[35] Therefore, the subtle build-up of DPRs in aging neurons over time, in concert with other disease-causing pathways, may lead to late-onset neuronal death seen in patients with XDP.[7]

Collectively, our findings support the notion that RAN translation is possible in the context of the XDP-linked $(AGAGGG)_n$ repeat expansion. Our work provides the impetus for investigating the pathological significance of proteotoxicity in this devastating neurological disease. ∎

Data Availability Statement

The authors confirm that the data supporting the findings of this study are available within the article and its supplementary material.

References

1. Depienne C, Mandel J. 30 years of repeat expansion disorders: what have we learned and what are the remaining challenges? Am J Hum Genet 2021;108(5):764–785. https://doi.org/10.1016/j.ajhg.2021.03.011

2. Paulson H. Repeat Expansion Diseases. Vol. 147. 1st ed. Amsterdam, The Netherlands: Elsevier B. V; 2018 https://doi.org/10.1016/B978-0-444-63233-3.00009-9.

3. Malik I, Kelley CP, Wang ET, Todd PK. Molecular mechanisms underlying nucleotide repeat expansion disorders. Nat Rev Mol Cell Biol 2021;22(9):589–607. https://doi.org/10.1038/s41580-021-00382-6

4. Zu T, Gibbens B, Doty NS, et al. Non-ATG-initiated translation directed by microsatellite expansions. Proc Natl Acad Sci U S A 2011;108(1):260–265. https://doi.org/10.1073/pnas.1013343108

5. Goto S, Lee LV, Munoz EL, et al. Functional anatomy of the basal ganglia in X-linked recessive dystonia-parkinsonism. Ann Neurol 2005;58(1):7–17. https://doi.org/10.1002/ana.20513

6. Arasaratnam CJ, Singh-Bains MK, Waldvogel HJ, Faull RLM. Neuroimaging and neuropathology studies of X-linked dystonia parkinsonism. Neurobiol Dis 2021;148:105186. https://doi.org/10.1016/j.nbd.2020.105186

7. Hanssen H, Heldmann M, Prasuhn J, et al. Basal ganglia and cerebellar pathology in X-linked dystonia-parkinsonism. Brain 2018;141(10):2995–3008. https://doi.org/10.1093/brain/awy222

8. Bragg DC, Mangkalaphiban K, Vaine CA, et al. Disease onset in X-linked dystonia-parkinsonism correlates with expansion of a hexameric repeat within an SVA retrotransposon in TAF1. Proc Natl Acad Sci 2017;114(51):E11020–E11028. https://doi.org/10.1073/pnas.1712526114

9. Westenberger A, Reyes CJ, Saranza G, et al. A hexanucleotide repeat modifies expressivity of X-linked dystonia parkinsonism. Ann Neurol 2019;85(6):812–822. https://doi.org/10.1002/ana.25488

10. Makino S, Kaji R, Ando S, et al. Reduced neuron-specific expression of the TAF1 gene is associated with X-linked dystonia-parkinsonism. Am J Hum Genet 2007;80(3):393–406. https://doi.org/10.1086/512129

11. Sako W, Morigaki R, Kaji R, et al. Identification and localization of a neuron-specific isoform of TAF1 in rat brain: implications for neuropathology of DYT3 dystonia. Neuroscience 2011;189:100–107. https://doi.org/10.1016/j.neuroscience.2011.05.031

12. Janakiraman U, Yu J, Moutal A, et al. TAF1-gene editing alters the morphology and function of the cerebellum and cerebral cortex. Neurobiol Dis 2019;132(June):104539. https://doi.org/10.1016/j.nbd.2019.104539

13. Cirnaru M, Creus-Muncunill J, Nelson S, et al. Striatal cholinergic dysregulation after neonatal decrease in X-linked dystonia parkinsonism-related <scp>TAF1</scp> isoforms. Mov Disord 2021;36(12):2780–2794. https://doi.org/10.1002/mds.28750

14. Reyes CJ, Laabs BH, Schaake S, et al. Brain regional differences in hexanucleotide repeat length in X-linked dystonia-parkinsonism using Nanopore sequencing. Neurol Genet 2021;7(4):e608. https://doi.org/10.1212/NXG.0000000000000608

15. Campion LN, Mejia Maza A, Yadav R, et al. Tissue-specific and repeat length-dependent somatic instability of the X-linked dystonia parkinsonism-associated CCCTCT repeat. Acta Neuropathol Commun 2022;10(1):49. https://doi.org/10.1186/s40478-022-01349-0

16. Bragg DC, Sharma N, Ozelius LJ. X-linked dystonia-parkinsonism: recent advances. Curr Opin Neurol 2019;32(4):604–609. https://doi.org/10.1097/WCO.0000000000000708

17. Kearse MG, Green KM, Krans A, et al. CGG repeat-associated non-AUG translation utilizes a cap-dependent scanning mechanism of initiation to produce toxic proteins short article CGG repeat-associated non-AUG translation utilizes a cap-dependent scanning mechanism of initiation to produce toxi. Mol Cell 2016;62(2):314–322. https://doi.org/10.1016/j.molcel.2016.02.034

18. Green KM, Glineburg MR, Kearse MG, et al. RAN translation at C9orf72-associated repeat expansions is selectively enhanced by the integrated stress response. Nat Commun 2017;8(1):2005. https://doi.org/10.1038/s41467-017-02200-0

19. Aneichyk T, Hendriks WT, Yadav R, et al. Dissecting the causal mechanism of X-linked dystonia-parkinsonism by integrating genome and transcriptome assembly a Mendelian form of dystonia arises from altered splicing and intron retention within a general transcription factor. Dissecting the causal. Cell 2018;172:897–909. https://doi.org/10.1016/j.cell.2018.02.011

20. Rakovic A, Domingo A, Grütz K, et al. Genome editing in induced pluripotent stem cells rescues TAF1 levels in X-linked dystonia-parkinsonism. Mov Disord 2018;33(7):1108–1118. https://doi.org/10.1002/mds.27441

21. Hancks DC, Kazazian HH. Roles for retrotransposon insertions in human disease. Mob DNA 2016;7(1):9. https://doi.org/10.1186/s13100-016-0065-9

22. Damert A, Raiz J, Horn AV, et al. 5′-Transducing SVA retrotransposon groups spread efficiently throughout the human genome. Genome Res 2009;19(11):1992–2008. https://doi.org/10.1101/gr.093435.109

23. Course MM, Gudsnuk K, Smukowski SN, et al. Evolution of a human-specific tandem repeat associated with ALS. Am J Hum Genet 2020;107(3):445–460. https://doi.org/10.1016/j.ajhg.2020.07.004

24. Zhang YJ, Gendron TF, Ebbert MTW, et al. Poly(GR) impairs protein translation and stress granule dynamics in C9orf72-associated frontotemporal dementia and amyotrophic lateral sclerosis. Nat Med 2018;24(8):1136–1142. https://doi.org/10.1038/s41591-018-0071-1

25. Moens TG, Niccoli T, Wilson KM, et al. C9orf72 arginine-rich dipeptide proteins interact with ribosomal proteins in vivo to induce a toxic translational arrest that is rescued by eIF1A. Acta Neuropathol 2019;137(3):487–500. https://doi.org/10.1007/s00401-018-1946-4

26. Jovičič A, Mertens J, Boeynaems S, et al. Modifiers of C9orf72 dipeptide repeat toxicity connect nucleocytoplasmic transport defects to FTD/ALS. Nat Neurosci 2015;18(9):1226–1229. https://doi.org/10.1038/nn.4085

27. Saberi S, Stauffer JE, Jiang J, et al. Sense-encoded poly-GR dipeptide repeat proteins correlate to neurodegeneration and uniquely co-localize with TDP-43 in dendrites of repeat-expanded C9orf72 amyotrophic lateral sclerosis. Acta Neuropathol 2018;135(3):459–474. https://doi.org/10.1007/s00401-017-1793-8

28. Cook CN, Wu Y, Odeh HM, et al. C9orf72 poly(GR) aggregation induces TDP-43 proteinopathy. Sci Transl Med 2020;12(559):eabb3774. https://doi.org/10.1126/scitranslmed.abb3774

29. Johnson BS, McCaffery JM, Lindquist S, Gitler AD. A yeast TDP-43 proteinopathy model: exploring the molecular determinants of TDP-43 aggregation and cellular toxicity. Proc Natl Acad Sci U S A 2008;105(17):6439–6444. https://doi.org/10.1073/pnas.0802082105

30. Gitler AD, Chesi A, Geddie ML, et al. α-Synuclein is part of a diverse and highly conserved interaction network that includes PARK9 and manganese toxicity. Nat Genet 2009;41(3):308–315. https://doi.org/10.1038/ng.300

31. Singh CR, Glineburg MR, Moore C, et al. Human oncoprotein 5MP suppresses general and repeat-associated non-AUG translation via eIF3 by a common mechanism. Cell Rep 2021;36(2):109376. https://doi.org/10.1016/j.celrep.2021.109376

32. Kearse MG, Goldman DH, Choi J, et al. Ribosome queuing enables non-AUG translation to be resistant to multiple protein synthesis inhibitors. Genes Dev 2019;33(13–14):871–885. https://doi.org/10.1101/gad.324715.119

33. Cheng W, Wang S, Mestre AA, et al. C9ORF72 GGGGCC repeat-associated non-AUG translation is upregulated by stress through eIF2α phosphorylation. Nat Commun 2018;9(1):51. https://doi.org/10.1038/s41467-017-02495-z

34. Asamitsu S, Yabuki Y, Ikenoshita S, et al. CGG repeat RNA G-quadruplexes interact with FMRpolyG to cause neuronal dysfunction in fragile X-related tremor/ataxia syndrome. Sci Adv 2021;7(3):1–15. https://doi.org/10.1126/sciadv.abd9440

35. Shi Y, Lin S, Staats KA, et al. Haploinsufficiency leads to neurodegeneration in C9ORF72 ALS/FTD human induced motor neurons. Nat Med 2018;24(3):313–325. https://doi.org/10.1038/nm.4490

Supporting Data

Additional Supporting Information may be found in the online version of this article at the publisher's web-site.

Magnetic Resonance–Guided Focused Ultrasound Thalamotomy May Spare Dopaminergic Therapy in Early-Stage Tremor-Dominant Parkinson's Disease: A Pilot Study

Nico Golfrè Andreasi, MD,[1] Roberto Cilia, MD,[1*]
Luigi Michele Romito, PhD,[1] Salvatore Bonvegna, MD,[1]
Giulia Straccia, MD,[1] Antonio Emanuele Elia, PhD,[1]
Alessio Novelli, MD,[1] Giuseppe Messina, MD,[2]
Giovanni Tringali, MD,[2] Vincenzo Levi, MD,[2]
Grazia Devigili, PhD,[1] Sara Rinaldo, Tch,[1]
Valentina Gasparini, MD,[1] Marina Grisoli, MD,[3]
Mario Stanziano, MD,[3,4] Francesco Ghielmetti, MSc,[5]
Sara Prioni, MSc,[6] Elisa Bocchi, MSc,[6]
Paolo Amami, MSc,[6]
Sylvie Hélène Marie Jeanne Piacentini, PhD,[6]
Elisa Francesca Maria Ciceri, MD,[7]
Maria Grazia Bruzzone, MD,[3] and
Roberto Eleopra, MD[1]

*Correspondence to: Dr. Roberto Cilia, Fondazione IRCCS Istituto Neurologico Carlo Besta, Department of Clinical Neurosciences, Parkinson and Movement Disorders Unit, via G. Celoria 11, 20133 Milan, Italy; E-mail: roberto.cilia@istituto-besta.it