Screening for novel hexanucleotide repeat expansions at ALS- and FTD-associated loci

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ABSTRACT

Objective: To determine whether GGGGCC (G_4C_2) repeat expansions at loci other than *C9orf72* serve as common causes of amyotrophic lateral sclerosis (ALS).

Methods: We assessed G_4C_2 repeat number in 28 genes near known ALS and frontotemporal dementia (FTD) loci by repeat-primed PCR coupled with fluorescent fragment analysis in 199 patients with ALS (17 familial, 182 sporadic) and 136 healthy controls. We also obtained blood from patients with ALS4 for evaluation of repeats surrounding the *SETX* gene locus. *C9orf72* expansions were evaluated in parallel.

Results: Expansions of G_4C_2 repeats in *C9orf72* explained 8.8% of sporadic and 47% of familial ALS cases analyzed. Repeat variance was observed at one other locus, *RGS14*, but no large expansions were observed, and repeat sizes were not different between cases and controls. No G_4C_2 repeat expansions were identified at other ALS or FTD risk loci or in ALS4 cases.

Conclusions: G_4C_2 expansions near known ALS and FTD loci other than *C9orf72* are not a common cause of ALS. ***Neurol Genet* 2016;2:e71; doi: 10.1212/NXG.0000000000000071**

GLOSSARY

ALS = amyotrophic lateral sclerosis; **FTD** = frontotemporal dementia; **G_4C_2** = GGGGCC; **GWAS** = genome-wide association studies; **SNP** = single-nucleotide polymorphism.

A GGGGCC (G_4C_2) hexanucleotide repeat expansion in the first intron of *C9orf72* is the most common monogenic cause of amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD).[1,2] There are normally between 2 and 23 G_4C_2 repeats at this locus. The repeat expands to hundreds in affected individuals,[2] although 30 repeats may be sufficient to elicit G_4C_2-specific pathology.[3]

A growing body of evidence suggests that the *C9orf72* repeat elicits toxicity primarily through gain-of-function mechanisms that are independent of the genetic locus where the repeat resides. Specifically, *Drosophila* and mouse models of ALS with expression of the repeat outside its normal genomic context suggest that instability and expansion of G_4C_2 repeats elsewhere in the genome could also cause ALS or FTD. A precedent for this phenomenon is found in spinocerebellar ataxia, in which CAG repeat expansions in a diverse set of genes elicit overlapping clinical phenotypes.[4]

We therefore hypothesized that cryptic repeat expansions at loci other than *C9orf72* could also contribute to ALS and FTD pathogenesis. Using repeat-primed PCR assays, we evaluated whether G_4C_2 repeats near known ALS and FTD loci identified by linkage analysis or genome-wide association studies (GWAS) exhibited expansions in a cohort of patients with ALS and controls in the University of Michigan ALS Patient Biorepository. Our results confirm that repeat instability and large expansions at *C9orf72* are common in sporadic

Supplemental data at Neurology.org/ng

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ALS in the United States, but expansions at other disease-associated loci are rare in this population and are unlikely to be a common cause of ALS.

METHODS

Standard protocol approvals, registrations, and patient consents. This study was approved by the Institutional Review Board of the University of Michigan. Individual patients and controls who contributed these DNA samples provided written informed consent via representatives from the Coriell Institute, University of Michigan ALS Patient Biorepository, or individually to a member of the research group.

ALS and control patient cohorts and DNA isolation. DNA samples for repeat-primed PCR and genomic PCR were from the following sources: 1 μg of genomic DNA from 199 patients with ALS and 136 healthy controls from the University of Michigan ALS Patient Biorepository. Patients with ALS met the revised El Escorial criteria[5] and were recruited from the University of Michigan ALS Clinic; controls were recruited via the University of Michigan clinical trials Web site (https://umclinicalstudies.org/). Demographic data were analyzed using SAS9.5 software (SAS Institute Inc., Cary, NC) and summarized in table e-1 at Neurology.org/ng. Two hundred fifty nanograms of genomic DNA from 86 patients with sporadic ALS from Coriell Cell Repository panel #NDPT026 (Coriell Institute) was used for determination of *C9orf72* repeat status only. One hundred micrograms of genomic DNA from a patient with ALS4 and 1 non-ALS sibling from a previously reported large pedigree[6] was extracted from 4 mL of whole blood using a commercial DNA isolation kit (DNeasy Blood & Tissue kit; Qiagen, Netherlands). Genomic DNA from a second published ALS4 case with a family history[7] was extracted from patient fibroblast cells obtained from a collaborator's laboratory using the same kit.

Candidate gene selection. We performed a BLAST search (National Center for Biotechnology Information) against the human genome for G_4C_2 repeat sequences using a sequence of 5 G_4C_2 pure repeats (GGGGCCGGGGCCGGGGCCGGGGCCGGGGCC) as a start query. The identified repeat loci were overlaid with published genetic loci associated with ALS or FTD (see a recent review[8] and table 1). We constrained our analysis to repeat loci within 2 mega base pairs (Mb) of either the mapped critical region for an ALS or FTD candidate gene/locus or with single-nucleotide polymorphisms (SNPs) that achieved statistical significance on GWAS in sporadic ALS cohorts. Additional candidate repeats located more than 2 Mb outside of disease-associated loci were identified by requiring at least 3 pure repeats in a gene with abundant neuronal expression in brain based on BioGPS and Proteomic DB database analysis.[9,10] Three additional candidate genes with G_4C_2 repeats within the previously identified critical region of ALS4 but missed by our initial in silico analysis were added after we obtained access to case samples.

G_4C_2 repeat determination. G_4C_2 repeat numbers in the longer allele were determined by repeat-primed PCR as previously reported,[11] followed by capillary electrophoresis and fragment analysis. The primer sequences are included in table e-2. The individual reverse primers for each candidate gene were designed using Primer 3 tools (http://biotools.umassmed.edu/bioapps/primer3_www.cgi) and were labeled with either 6-FAM or 5-HEX fluorescent dye. The PCR products were diluted in highly deionized formamide (HiDi formamide; ThermoFisher Scientific, Waltham, WA) containing size standard ROX-1000 (BioVenture, TN). Fragment analysis was performed at the University of Michigan Sequencing Core facility on an ABI 3730 Sequencer. The data were analyzed using GeneMarker (SoftGenetics, PA) to determine the maximal repeat number.

Sanger sequencing. For samples with fewer than 35 G_4C_2 repeats in *C9orf72*, DNA flanking the repeat regions was PCR-amplified with the following primers: *C9orf72* forward: 5′-CCG CAG CCT GTA GCA AGC-3′ and *C9orf72* reverse: 5′-AGT CGC TAG AGG CGA AAG C-3′ using the same thermal cycling program as the repeat-primed PCR. The PCR products were gel purified and subjected to Sanger sequencing at the University of Michigan Sequencing Core facility to determine the exact repeat number.

For samples with a 31-nucleotide insertion in the *VAV2* gene, DNA flanking the repeat region was PCR-amplified with the following primers: VAV2 forward: 5′-GCC CAG GAC AGG AGG CCT CAG CA-3′ and VAV2 reverse: 5′- CTC AGG GCC GGG AGG AAG CAC CT-3′ using the same thermal cycling program as the repeat-primed PCR. The PCR products were gel-purified and subjected to Sanger sequencing as described above. For repeats at *Huwe1* and *RGS14*, PCR primers flanking the repeat regions were used to determine specific repeat sizes (see supplemental data).

Southern blot confirmation of repeat expansions at *C9orf72*. For Southern blot analysis, 25-μg aliquots of lymphoblast genomic DNA were obtained for 5 selected Coriell samples. Two additional lymphoblast cell lines were obtained from the Coriell Institute and were grown up to 15 million cells, and approximately 100 μg of lymphoblast genomic DNA was extracted using a DNA isolation kit. Ten fibroblast cell lines with G_4C_2 repeat expansion and 2 control fibroblast lines (1 ALS sample without expansion and 1 control) were obtained from the University of Michigan ALS Patient Biorepository and 100 μg of fibroblast genomic DNA was extracted from 15 million cells.

Statistical analysis. Two-tailed Fisher exact tests or χ^2 tests were performed to test for association of repeat length with ALS and to verify genotype frequencies in the *VAV2* gene. For *RGS14* repeat length, a 2-tailed nonparametric *t* test was performed to compare the median repeat size differences. For the correlation of *C9orf72* repeat size and patient age at onset of ALS, the Pearson correlation test was performed.

RESULTS

We first conducted an in silico experiment to identify all human genes containing at least 2 G_4C_2 repeats. Our rationale was that transcribed repeats at such loci could become unstable and lead to disease-causing expansions, unless the chromosomal context of the *C9orf72* repeat was critical to disease pathogenesis. Our initial analysis revealed that short G_4C_2 repeats are quite common in the human genome, with 344 identified as intragenic repeats. To narrow our window of potential sites of repeat expansion to a number that we could readily assay, we compared this in silico list of repeat loci with genetic loci implicated in ALS or FTD, either through critical region mapping in familial forms or by GWAS. We reasoned that utilization of GWAS conducted in patient populations similar to our cohort as well as known genetic loci in rare families (which have subsequently been shown to contribute

Table 1 G_4C_2 repeat loci evaluated in this study

Gene	Location	Repeat no.	ALS/FTD gene loci or SNP[a]	Different in ALS?
ARMC2	Intron	2	*FIG4/ALS11*	No
ATXN2	Coding	2	*ATXN2*	No
C8orf76	Intron	2	rs4581057, rs10106208	No
C9orf72	Intron	2–35	*C9orf72*	Yes
C16orf72	Intron	2	rs1551960, rs7185240	No
CACNA1G	Coding	2	rs8068533, rs1061947	No
DOCK1	Intron	2	rs7082776, rs4363506	No
GPR123	Intron	2–4	*OPTN/ALS12*	No
HUWE1[b]	Intron	12–14	*UBQLN2/ALS15*	No
ITPR3	Intron	3–4	rs9380343, rs963733	No
KMT2C	Intron	2	rs4725431, rs10260404	No
MBD2[c]	Coding	3	*ALS3*	No
NEURL1B	Intron	2	rs871503, rs4868146	No
PAPD5	Coding	3	rs12929266, rs1075875	No
PRRC2B	Coding	2	*SETX*/ALS4	No
SUPT5H	Coding	2	rs12327672, rs11669124, rs2287735	No
SYNM	Intron	3	rs931892, rs3803478	No
TAF4[d]	Coding	6	*VAPB/ALS8*	No
TPP1	Coding	2	rs2063082, rs16917433	No
TTC28	Intron	2	rs6005863, rs5762919	No
ZNF423[e]	Intron	4	rs1075875, rs1505112	No
BSN[f]	Coding	5	NA	No
GAS7	Intron	3	NA	No
RGS14	Intron	4–15	NA	No
STK39	Coding	3–5	rs13015447	No
PRRC2B	Coding	2	*SETX/ALS4*	No
PRRX2	Intron	3–5	*SETX/ALS*, rs395119	No
SURF4	Intron	2	*SETX*/ALS4	No
VAV2	Intron	2	*SETX*/ALS4	No

Abbreviations: ALS = amyotrophic lateral sclerosis; FTD = frontotemporal dementia; G_4C_2 = GGGGCC; GWAS = genome-wide association study; NA = not applicable; SNP = single-nucleotide polymorphism.

[a] G_4C_2 repeats found within 2 Mb of GWAS SNPs from references 12–14,28–36.

[b] *MBD2* has 2 separate G_4C_2 repeats that are 2 and 3 repeats long. Data shown for the 3-repeat region. The 2-repeat region was invariant.

[c] *TAF4* has 6 imperfect G_4C_2 repeats ($(C_2G_4)_3CCGGGC(C_2G_4)_2$).

[d] *ZNF423* has 2 separate G_4C_2 repeats that are 2 and 4 repeats long. Data are shown for the 4-repeat region. The 2-repeat region was invariant.

[e] *BSN* has 2 separate G_4C_2 repeats. One is 3 repeats long and the other has 5 imperfect repeats (CCGGGGCCGGGGCCGGGGCCCGGGCCGGGG). Data are shown for the 5-repeat region. The 3-repeat region was invariant.

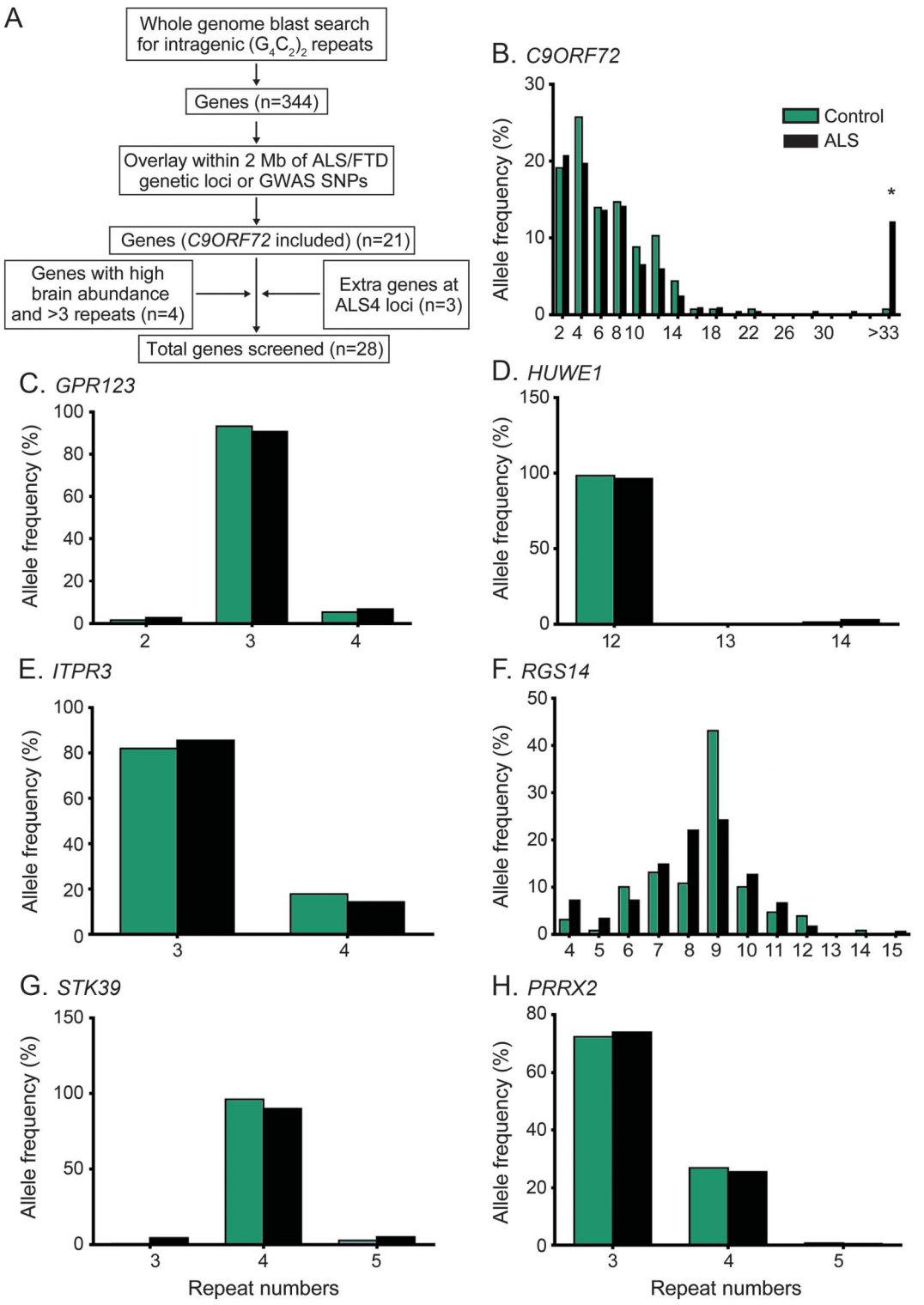
[f] *HUWE1* has 12 imperfect G_4C_2 repeats ($(C_2G_4)_3CCAGGG(C_2G_4)_4CCAGGGCCGGTG(C_2G_4)$).

to a percentage of sporadic cases) would identify most repeat expansions that confer a substantial contribution to the genetic burden of ALS in the United States. Consistent with this idea, the *C9orf72* locus was identified on multiple GWAS surveys in ALS and FTD in sporadic populations prior to identification of the causative repeat.[12–14] Using this approach, we identified 21 candidate genes, including *C9orf72*, containing at least 2 G_4C_2 repeats that are located within 2 Mb of known ALS-FTD loci or loci identified in GWAS by at least 2 associated SNPs (figure 1A).

We developed a modified fluorescent fragment analysis after repeat-primed PCR to evaluate instability at each of these loci, as previously described for *C9orf72* repeat expansions.[11] We also assessed repeat size at *C9orf72*. These assays were tested on control samples, and the actual repeat sizes were confirmed by standard PCR and Sanger sequencing. All 21 assays demonstrated accurate detection of repeat size, based on comparison with Sanger sequencing (data not shown). This assay readily detected G_4C_2 expansions at *C9orf72* in samples from ALS cases known to harbor the repeat.

We applied these assays to a sample collection from the University of Michigan ALS Patient Repository containing 199 ALS cases, of which 17 had a family history of ALS, and 136 healthy controls (University of Michigan). The demographic characteristics of this collection are shown in table e-1. Of note, there were no differences in the age at sample collection, sex composition, or racial/ethnic makeup between ALS cases and controls, and both cases and controls had similar frequencies of a family history of a non-ALS neurodegenerative condition (table e-1). In addition, we used samples from Coriell Cell Repository panel NDPT026, containing 86 sporadic ALS cases, for additional screening for repeat expansions in *C9orf72* (Coriell Institute). Consistent with published findings, we observed a wide variation of G_4C_2 repeat length at *C9orf72* in both cases and controls (table 1, table e-3, figure 1B). Pathogenic repeat expansions were observed in 47% of the familial cases and 8.8% (17/182) of sporadic ALS cases in the University of Michigan ALS Patient Repository (figure 1B and table e-3). *C9orf72* repeat expansions were observed at a similar frequency (6/86; 7.0%) in ALS samples from the Coriell Institute. To validate these findings and determine the actual repeat expansion size in cases with low repeat numbers, genomic PCR and selective Southern blotting analysis were performed. One sample contained exactly 32 repeats in the longer allele, which was confirmed by Sanger sequencing. Other samples exhibited a single band by genomic PCR reflecting the shorter, PCR-amplifiable allele. Southern blotting on genomic DNA extracted from patient-derived fibroblasts or lymphocytes in a subset of cases demonstrated a wide range of pathologic repeat expansion sizes from 200 to more than 1,500 repeats (figure e-1). Repeat expansion size from peripheral blood samples or cultured cells did not correlate with clinical age at onset (R = 0.173 in

Figure 1 G_4C_2 repeat numbers from controls and patients with ALS



(A) Flow chart of candidate genes selection for this study. (B–H) Graphs show the distribution of repeat sizes from ALS cases and controls for 7 genes. *Significant ($p < 0.05$) difference in the distribution of repeats larger than 33 times between cases and controls by Fisher exact test. ALS = amyotrophic lateral sclerosis; G_4C_2 = GGGGCC.

Pearson correlation test, $p = 0.572$, figure e-2), consistent with previous reports.[15]

In contrast to *C9orf72*, G_4C_2 repeats assayed at other loci exhibited little or no variance in repeat number in the University of Michigan ALS Patient Biorepository samples. Of the 20 novel repeats analyzed, 16 showed no variance at all across the cohort (80%). Four genes displayed small variations in repeat number (table 1), but none of these cases contained expansions of more than 2 repeats greater than the

prevalent alleles. The degree of repeat length variation was not significantly different between control and ALS groups, demonstrating a lack of association between repeat number variation and ALS/FTD in our cohort (figure 1, B–E, $p < 0.001$ for *C9orf72*, $p = 0.76$ for *GPR123*, $p = 0.69$ for *HUWE1*, $p = 0.374$ for ITPR3; χ^2 test for *C9orf72* and *ITPR3*, and Fisher exact test for *GPR123* and *HUWE1* used for the rest for different allele frequencies).

To expand the initial screening we selected 4 additional candidate genes that are highly expressed in brain and contain at least 3 G_4C_2 repeats in controls. In these candidate genes, no large repeat expansions were found in ALS or control groups (table 1, figure 1, F and G). However, an intronic repeat in *RGS14* displayed a much larger variation than those in other loci studied, with between 4 and 15 repeats present in both controls and ALS cases. The distribution of repeat lengths in *RGS14* was independent of clinical ALS (figure 1F) or *C9orf72* expansion status (control 8.49 ± 1.74 vs ALS 8.1 ± 1.93, $p = 0.082$, 2-tailed student t test).

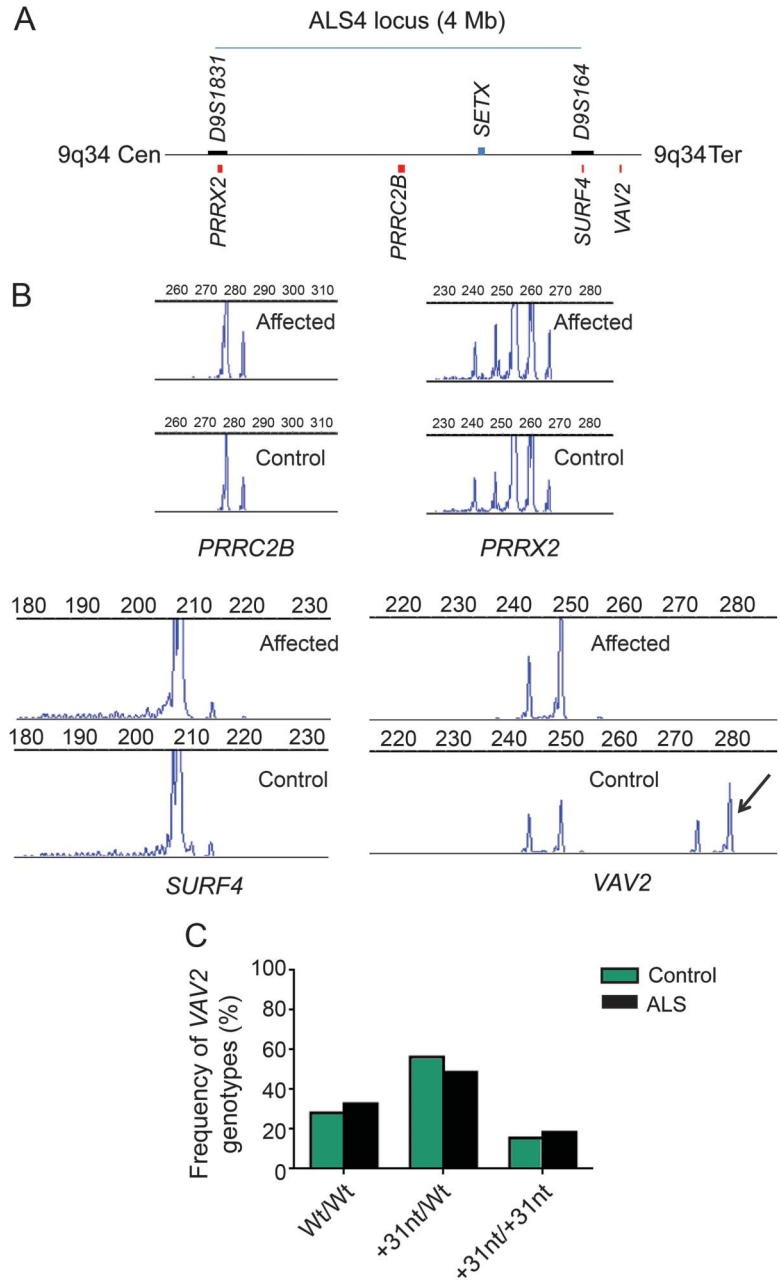
As a third approach, we examined additional loci harboring G_4C_2 repeats located near the ALS4 locus in patients with this disorder. ALS4 is a form of juvenile ALS with very slow progression that is thought to result from dominant mutations in *SETX*.[6] The mechanism of these dominant mutations is unclear, because recessive mutations in *SETX* cause a distinct neurodegenerative disorder, ataxia with oculomotor apraxia type 2, which does not include motor neuron degeneration.[16] Within the critical region defined by linkage analysis,[6] there are 4 genes containing short G_4C_2 repeats: *PRRX2*, *PCCR2B*, *SURF4*, and *VAV2* (figure 2A). To investigate whether a cryptic repeat expansion might provide an alternative explanation for the ALS4 phenotype, we analyzed repeat numbers in 2 patients with ALS4 and an unaffected control from 2 previously described ALS4 families.[6,7] No repeat expansions were observed (figure 2B). Of these 4 loci, only 1 (*PRRC2B*) was included in our initial repeat screen in the University of Michigan ALS Patient Repository. Assessment of the additional 3 loci in this larger cohort identified no repeat expansions, only a minor repeat length variance in gene *PRRX2* (table 1, figure 1H). We did observe an amplicon length variant of 31 bp in *VAV2* by fragment analysis in the *ALS4* family (figure 2B). Sanger sequencing identified it as a 31-bp intronic insertion in the longer allele that contains an imperfect duplication of intronic sequence (GCCGGGGCCGTGTGGCCCTCACGCAGTGACC). This insertion was common in controls and ALS cases in the University of Michigan ALS Patient Biorepository panel (figure 2C), and appears to be nonpathogenic ($p = 0.398$, χ^2 test).

DISCUSSION G_4C_2 repeat expansions in *C9orf72* are the most common known cause of ALS and FTD. Here we tested whether G_4C_2 repeat instability at other loci could be a common cause of ALS. Our results confirmed that G_4C_2 repeat expansions and instability are common at the *C9orf72* locus in both familial and sporadic ALS cases in 2 patient cohorts (University of Michigan ALS Patient Repository and the NDPT026 ALS collection from Coriell). However, for 27 other genomic loci that harbor G_4C_2 repeats, no pathogenic G_4C_2 expansions were identified. Thus, repeat instability at these alternative loci are unlikely to be major contributors to the genetic burden in ALS in the United States.

This study is not exhaustive in the number of repeat loci assayed or the number of patient and familial cohorts examined. Therefore, we cannot rule out G_4C_2 repeat expansions as rare causes of ALS. For practical reasons, we assayed fewer than 10% of the G_4C_2 repeats located near protein-coding genes and a much smaller fraction of the GC-rich repeats in the human genome. Specifically, we focused our analysis on repeats located adjacent to loci already implicated in ALS or FTD. Our rationale for this choice was that utilization of GWAS conducted in similar patient populations as well as known genetic loci in rare families (which have subsequently been shown to contribute to a percentage of sporadic cases) would colocalize with repeat expansions that confer a substantial contribution to the genetic burden of ALS in the United States. Consistent with this idea, the *C9orf72* locus was identified on multiple GWAS surveys in ALS and FTD in sporadic populations prior to identification of the causative repeat. Moreover, we reasoned that cryptic repeat expansions might have escaped identification during the initial analyses of these loci, several of which lack an identified causative gene or a clear pathogenic mechanism for the currently implicated gene. As such, our findings that none of these alternative loci harbor repeat expansions in 199 ALS cases suggest that G_4C_2 repeat expansions at non-*C9orf72* loci are unlikely to be a common cause of ALS in our patient population, given that most common highly penetrant mutations would be detected by this approach. However, it is important to acknowledge that for highly penetrant loci identified in familial ALS cases, it might be necessary to examine the original published cohorts, which might carry rare or private mutations. We took this step for ALS4 and found no G_4C_2 repeat instability at 4 neighboring loci. Application of this approach to other isolated pedigrees could more definitively rule out expansions at these genetically implicated loci.

The lack of G_4C_2 repeat expansions at alternative gene loci suggests that there could be something about the *C9orf72* locus that promotes instability. The vast majority (75%) of the other hexanucleotide repeats studied here exhibited no variation among

Figure 2 Analysis of G_4C_2 repeats near the *ALS4* locus



(A) Schematic of the *ALS4* locus defined by chromosome markers *D9S1831* and *D9S164* (black boxes)[6] drawn to scale showing the location of 4 G_4C_2 repeat-containing genes (red boxes) and the proposed disease-causing gene *SETX* (blue box). (B) Chromatograms showing the G_4C_2 repeat peaks in the 4 G_4C_2 repeat-containing genes from an affected ALS4 case and a control sibling. One control had a 31-bp insertion in the *VAV2* gene (double peak marked with an arrow). (C) Genotypes of controls and ALS cases in the University of Michigan ALS Patient Biorepository for the 31-bp insertion in gene *VAV2*. Both groups had a similar distribution of genotypes carrying the 31-bp insertion allele. ALS = amyotrophic lateral sclerosis; Cen = centromere; G_4C_2 = GGGGCC; nt = nucleotide; Ter = telomere; Wt = wild type.

335 individuals, and variance in repeat size was largely absent from the 1,000-genome database for the 321 intragenic G_4C_2 repeat loci not assayed (data not shown). With one exception, the repeat size variants observed were limited to 1 or 2 repeats. Studies in vitro suggest that stretches of G_4C_2 as short as 4 repeats are capable of forming intramolecular G quadruplexes, which might contribute to repeat instability through activation of DNA mismatch repair pathways and mistemplating.[17] In general, our data are consistent with this threshold, since only genes with at least 4 repeats had variation of more than 1 repeat. However, some of the G_4C_2 repeats we studied were larger than this threshold but were invariant, suggesting that the length of the repeat is insufficient to explain instability. While future work will be needed to determine which factors drive selective instability, it may reflect specific aspects of the GC-rich sequence surrounding the repeat at the *C9orf72* loci. This concept is supported by the finding that all pathologic repeat expansions at *C9orf72* observed to date have occurred on a single haplotype background.[18]

Our approach here focused solely on the role of G_4C_2 repeat expansions in ALS. However, G_4C_2 repeat expansions in genes other than *C9orf72* may be enriched in neurologic disorders other than ALS. Phenotypes of polyglutamine disorders associated with CAG repeat expansions, for example, are not all the same.[19] In this context, it is interesting to note that the *C9orf72* repeat expansion exhibits neurologic symptoms in addition to motor neuron disease and frontotemporal cognitive dysfunction, which are still being explored.[11,20]

We observed noteworthy repeat instability in both cases and controls in one other gene: a G_4C_2 intronic repeat in *RGS14* with a mean repeat length of 9 and a range of 4–14 repeats. *RGS14* encodes a member of the regulator of G-protein signaling family of proteins. It is highly expressed in the developing brain and has known functions in hippocampal learning and synaptic plasticity.[21] Although we observed no association between the size of this repeat and clinical ALS, our study cannot rule out a role for expansion in rare ALS families or other racial/ethnic populations. As such, reevaluation of this locus may be worthy of further study in familial ALS, FTD, and other neurodegenerative disorders.

Other repeat expansions are implicated in causing or modifying motor neuron disease phenotypes. A GGCCTG repeat expansion in *NOP56* causes spinocerebellar ataxia type 36[22] and has motor neuron disease as a clinical feature. Moderate CAG repeat expansions (encoding polyglutamine) in *ATXN2*[23] and GCG repeat expansions (encoding polyalanine) in *NIP1A*[24] are associated with an increased risk of ALS. However, other known pathogenic CAG and CGG repeat expansions do not influence the risk of ALS or FTD, suggesting that the observed effects may be gene specific rather than repeat sequence specific.[25–27]

We screened 28 loci harboring G_4C_2 repeats near known ALS/FTD loci in 199 patients with ALS and

did not find pathogenic repeat expansions other than that previously reported in *C9orf72*. While future studies in larger cohorts and select families are still needed, our results suggest that G_4C_2 repeat expansions outside the *C9orf72* gene are not a common cause of ALS, supporting the importance of identifying *cis* elements that explain the genetic instability at the *C9orf72* locus.

AUTHOR CONTRIBUTIONS

F.H., M.H.M., D.Z., B.C.C., and P.K.T. conceptualized and designed the study. F.H., J.M.J., and C.F.-R. performed the experiments. F.H., J.M.J., M.H.M., B.C.C., and P.K.T. analyzed the data. M.H.M., E.L.F., S.A.G., and B.C.C. provided patient samples. F.H. and P.K.T. wrote the manuscript. All authors revised the manuscript.

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