Expanding Clinical Spectrum of C9ORF72-Related Disorders and Promising Therapeutic Strategies

A Review

Sarah Breevoort, MD, PhD, Summer Gibson, MD, Karla Figueroa, MS, Mark Bromberg, MD, PhD, and Stefan Pulst, MD, Dr med

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Abstract

In 2011, a pathogenic hexanucleotide repeat expansion in the C9ORF72 gene was discovered to be the leading genetic cause of amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD). Before this, the C9ORF72 gene and its protein were unknown. The repeat expansion was found to cause both haploinsufficiency and gain of toxicity through aggregating RNA products and dipeptide repeat proteins. A worldwide effort was then initiated to define C9ORF72 ALS/FTD and unravel the pathogenic mechanism for the development of therapeutic options. A decade later, C9ORF72 genetic testing is readily available. There is now an increasing appreciation that C9ORF72 not only is the leading genetic cause of ALS/FTD but may contribute to a spectrum of disorders. This article reviews what is currently known about the C9ORF72 expansion and how C9ORF72 expansion manifests in ALS, FTD, psychiatric disorders, and movement disorders. With therapeutic strategies fast approaching the clinic, earlier recognition of possible C9ORF72 expansion related disorders is even more paramount to improve patient care.

From the Department of Neurology, University of Utah, Salt Lake City.

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Before the identification of the C9ORF72 gene in 2011, it had been known for some time that a gene or genes associated with frontotemporal dementia (FTD)—amyotrophic lateral sclerosis (ALS) resided on human chromosome 9 using genetic linkage analysis in pedigrees segregating ALS or FTD or both phenotypes. Mok et al. described a ~140-kb risk haplotype on chromosome 9p21 that was shared by chromosome 9p-linked families and showed significant association with FTD and ALS in several populations. The presence of the same haplotype across multiple families suggested that most individuals carried the same pathogenic variant. Finding the haplotype in individuals with ALS or FTD also supported the notion that the same mutation could cause disparate phenotypes.

Two groups identified the disease-causing chromosome 9p mutation using different approaches and succeeded simultaneously. The collaborative group led by Rademakers performed detailed sequencing of the C9ORF72 gene and identified a polymorphic GGGGCC (G4C2) hexanucleotide repeat (HRE) located between the 2 noncoding C9ORF72 exons 1a and 1b. Analysis of this HRE in samples from members of a family with autosomal dominant ALS/FTD showed an aberrant segregation pattern with all affected individuals appearing homozygous. They suspected that lack of segregation was due to the presence of an unamplifiable repeat expansion and developed a repeat-primed PCR (RP-PCR) method (see below) designed to detect expanded G4C2 repeats. The presence of repeat expansions was detected by RP-PCR in all affected family members, but not in unaffected relatives, which was subsequently confirmed by Southern blot analysis. The maximum size of the repeat in controls was 23 units, whereas in affected individuals, it was estimated at 700 or more repeats.

The collaborative group led by Traynor used an approach that emphasized enrichment of the chromosome 9p region followed by massive parallel sequencing. Enrichment techniques encompassed flow sorting of chromosome 9 or enrichment of the target region using 43,000 custom oligonucleotide baits covering a total of 2.58 MB in the chromosome 9p FTD/ALS locus. Subsequent manual alignment of sequence reads in the target region identified the HRE in the C9ORF72 gene. Defining a pathogenic expansion as >30 repeats, they found that 113 of 402 ALS cases and 2 of 478 controls from Finland had an expanded repeat using rp-PCR analysis. None of the African samples carried >15 G4C2 repeats (average: 3; range: 0–15) providing the first suggestion that repeat alleles may differ in specific populations. In Finish familial ALS cases, 52 (46.4%) had the expansion. Independently confirming the pathogenic role of the G4C2 repeat in FTD, they also found a 29% occurrence of expanded repeats in Finnish FTD cases. Indeed, C9ORF72-ALS frequency varies widely based on ethnicity and geographic region and is most common in European and North American populations, accounting for about 40% of ALS cases with a family history of ALS and 8% of ALS without a family history; in contrast, it is rarely found in Asian populations. A recent study in 140 South Africans with sporadic ALS identified 10 cases (7%) of pathogenic C9ORF72 expansions: 4 White and 6 Cape mixed Africans—ancestry derived from European settlers, Indigenous tribes, and Indian Islanders, among others. This regional variance, increased risk among those with a family history—along with the common haplotype—suggests a single common founder, who originated from Finland. Modeling estimates have dated this founder to around 500 AD, which closely coincides with the beginning of the Viking invasions from Finland. Alternatively, a competing hypothesis is that the identified common haplotype contributes instability to the C9ORF72 region; thus, the region itself predisposes to the creation of expansion. A recent study of 593 patients with ALS in India discovered the presence of C9 expansion in 3.2% (19/593) of patients with ALS where 47.4% (9/19) positive cases belonged to the eastern region of India. The common haplotype was present in 11 of the 19 cases. Although pathogenic C9 expansions appear to be most prevalent in individuals of European ancestry, recent work supports the need for increased testing in more diverse populations.

Pathogenesis of C9ORF72 Expansion

C9ORF72 Expansion and Morphologic Findings

Mechanisms of neuronal dysfunction in the setting of C9ORF72 expansion are currently not clear. Pathologically, in most, but not all, patients with C9ORF72 ALS/FTD, aggregation of TAR DNA-binding protein 43 (TDP-43) occurs in clinically correlated cortical and spinal motor neurons and the frontal cortex. The histopathologically unique TDP-43 subtypes A and B are the predominant inclusions found in C9ORF72 patients. TDP-43 is primarily nuclear; however, in patients with ALS/FTD, posttranslationally altered TDP-43 proteins are found to aggregate the cytoplasm. A pathologic...
link between abnormal TDP-43 and C9ORF72 expansion is currently under extensive investigation. The collaborative study group led by Rothstein recently provided evidence that nuclear accumulation of CHMP7, a critical mediator of nuclear pore complex (NPC) function, is sufficient to cause TDP-43 mislocalization to the cytoplasm and subsequent dysfunction. Impaired nuclear export of CHMP7 led to reduced expression of NPC components and contributed to TDP-43 mislocalization, dysfunction, and downstream deficits in neuronal survival. CHMP7 expression was also found to be elevated in post-mortem neuronal tissue of patients with C9ORF72 ALS.

Approximately 50%–60% of patients with ALS will develop frontotemporal dysfunction, ranging from dementia (FTD) to one or more problems with neuropsychological, language, or speech function. These are collectively known as the frontotemporal spectrum disorders of ALS and are discussed in greater detail below. Anatomically, sporadic FTD and C9ORF72-FTSD have similar morphologic changes in the brain, with atrophy of the anterior insula, anterior cingulate, amygdala, and striatum; those with C9ORF72-FTSD, however, display more involvement of the medial pulvinar thalamus. Increased cerebellar atrophy has also been shown in C9ORF72-FTSD and ALS, though less consistently.

Pathogenesis and Allele Size

There is debate surrounding both the pathogenic allele size for C9ORF72-ALS and the correlation of size of the expansion and disease severity. Pathologic expansions are typically hundreds to thousands of repeats in length, although disease has been seen with smaller expansions. Alleles with greater than 30 repeats are generally considered pathogenic for C9ORF72-ALS; yet, although relatively rare, intermediate-length alleles of 20–30 repeats may increase the risk for C9ORF72-ALS and parkinsonism. C9ORF72 expansion size has been suggested to correlate with age at onset of ALS—a common feature in many neurologic repeat expansion diseases—other studies, however, have failed to demonstrate this. One of the confounding factors for both of these debates is the somatic instability of the expansion, specifically that the repeat size is highly variable from tissue to tissue, often with a significant increase in size in the CNS in comparison to blood-derived DNA, which most studies are based on. A second factor is the variety of testing modalities that make determining the size of the expansion often unreliable or incomparable.

The secondary structure of the C9ORF72 expansion has been shown to contribute to expansion and contraction of repeat lengths and cause cell-to-cell transmission of dipeptide repeat proteins (DPRs), which are found in aggregates throughout the CNS of C9ORF72 patients. Conceivably, then, just a small population of cells with pathogenic C9ORF72 expansions could be present in the CNS and initiate the disease process. Such somatic variations would be missed by routine blood DNA testing that evaluates germline cells. A recent report found no evidence of C9ORF72 expansion in spinal cord tissue of patients with ALS negative for C9ORF72 expansions, providing further support that normal C9ORF72 expansions are stable and expansion instability occurs only when restricted to expanded alleles. Repeat length variability in tissues of patients with very large C9ORF72 expansions has been reported, but as these studies suggest pathogenic expansions likely occur in most if not all cells. It remains unclear whether an exact number of repeats trigger disease or whether other factors are more important than repeat length.

Pathophysiology of C9ORF72 Expansion

Several mechanisms are hypothesized to explain C9ORF72 expansion pathogenesis, with RNA toxicity and repeat-associated non-ATG (RAN) translation being the 2 major ones (Figure 1B and Figure 1C), and loss of C9ORF72 function likely of lesser importance (Figure 1D). C9ORF72 transcript levels and protein expression are decreased in patients with C9ORF72 ALS/FTD, yet, neurodegenerative features are not found in loss of function models. C9ORF72 expansion occurs within an intron and therefore undergoes canonical transcription. Toxic gain of function occurs when expansion RNA transcripts block the transcription of other genes by sequestering RNA-binding proteins. Products from RAN translation of C9ORF72 expansion can also exert deleterious effects on cellular processes. First discovered in spinocerebellar ataxia type 8 and myotonic dystrophy (DM1), RAN translation is now known to occur in many microsatellite expansion–related diseases, including C9ORF72-ALS/FTD. RAN translation begins in hairpin forming expansion regions independent of the canonical ATG start codon. Multiple RAN products can be produced from different reading frames as expansion mutations are often bidirectionally transcribed. RAN proteins can cause cytoplasmic mislocalization and block splicing of genes related to mitochondrial, neuronal, and pre-mRNA splicing function. In addition, they can disrupt the ubiquitin proteosome system, form aggregates trapping macromolecular complexes, and cause vesicle and endoplasmic reticulum membrane deformation. The contribution of individual RAN proteins to disease is unclear. C9ORF72-RAN protein expression is toxic in zebrafish and induces neurodegeneration in mice. In particular, the arginine-containing proteins (polyPR and polyGR) show the greatest toxicity. These C9ORF72-RAN toxicity studies used repeat lengths of fewer than 90 units, whereas human C9ORF72 disease often involves repeat lengths in the hundreds to thousands. Continued investigation is necessary to better define the structure and pathogenesis of C9ORF72-RAN proteins.

C9ORF72 Expansion and Nuclear Transport

Compositional changes to the NPC occur early in C9ORF72 disease with associated reduction in NPC expression and cytoplasmic mislocalization of componentry. Critical in maintaining overall cellular function, disruption of the NPC and nuclear export influences neuronal viability and is a common feature in neurodegenerative disorders. C9ORF72 expansion disrupts nucleocytoplasmic transport either via...
direct interaction of C9ORF72 RNA fragments with nuclear pore proteins or through RAN protein disruption of the NPC. PolyPR-containing RAN proteins bind to regions enriched in phenylalanine/glycine repeats within the complex, thereby plugging the pore and blocking nuclear export. Whether nuclear transport deficits are a cause or consequence of other cellular events in C9ORF72 disease is actively being investigated.

**C9ORF72 Testing Methods**

Clinical testing for C9ORF72 has been available since 2012. Reliable and consistent analysis of the C9ORF72 expansion across multiple laboratories, however, has proven to be problematic with a high incidence of both false-positive and negative test results. The characterization of the C9ORF72 expansion is complex due to its GC-rich DNA region and the presence of sequence variations at the 3’ end of the repeat region. This creates a challenge for utilization of conventional PCR-based fragment analysis, and therefore, at a minimum, a combination of gene-specific and RP-PCR is needed for the assessment of large repeat expansions. RP-PCR was first developed in 1996 as an approach to detect the CAG repeat expansion in the DMPK gene that causes DM1. RP-PCR is essentially a 3-primer PCR, where one primer flanks the repeat, another is complementary to the repeat with a tail, and a third binds within the repeat region. This generates a heterogeneous mixture of fragments differing in size by 1 repeat that are then analyzed via capillary electrophoresis (CE) (Figure 2). Because of CE size constraints, the maximum fragment size that can be analyzed by PCR is 145 repeats in length, anything larger must be evaluated with Southern blot. The capability to size larger repeats makes Southern blot the advocated gold standard; however, it is may not detect small or intermediate expansion, and few laboratories offer it. Interpretation of expansion size is inconsistent among laboratories with cutoffs for normal, intermediate, and...
expanded alleles varying significantly. Most laboratories do not report allele sizes within the normal range due to inability to detect fewer than 25, and what constitutes a pathogenic allele size may vary from lab to lab. (Figure 3). Amplicon-length analysis using primers flanking the repeat motif can resolve ambiguous cases where sequence variants interfere with PCR results. Combining amplicon-length analysis and bidirectional 5′ and 3′ RP-PCR is recommended for greatest sensitivity and specificity. Several laboratories offering certified C9ORF72 testing are listed in the Table.

**Recommendations for C9ORF72 Genetic Testing**

Clinician surveys reveal a growing consensus (~93%) to offer genetic testing to patients with familial ALS. Whether to extend testing in cases of sporadic ALS is less clear. With the growing availability of clinical trials for C9ORF72-ALS, and very recently FTD, testing should be offered to any patient diagnosed with either condition, particularly of European ancestry. Recent studies identified the C9ORF72 expansion as accounting for 75%–79% of pathogenic variants in ALS. It
is becoming increasingly evident, therefore, that at least in US clinics, the prevalence of pathogenic variants in genes other than C9ORF72 may be much lower than originally thought. Presymptomatic testing may be considered for adult relatives of patients with C9ORF72 disease, but only when combined with extensive genetic counseling and psychological assessment. The limitations of testing should be emphasized as the penetrance of C9ORF72-related disease remains unclear. A few studies report a penetrance of 80%–90% by age 80 years, yet others report a much lower rate. Clinical guidelines for C9ORF72 testing in both sporadic and familial ALS/FTD might allow us to better understand the incidence of C9ORF72 expansion in our diverse population and guide decision making for testing affected persons of non-European descent, in which the incidence rates are likely significantly lower.

**C9ORF72 ALS**

Clinically, patients with C9ORF72 ALS are relatively indistinguishable from nonexpanded patients, with a few exceptions. One of the most obvious is the increased risk among patients with a family history of ALS or FTD, particularly in those of Caucasian ethnicity. A second exception is the coexistence of cognitive and behavioral impairment—most commonly behavioral variant FTD (FTDbv), which is seen in about 50%. There is a reported increased risk of bulbar-onset ALS (up to 40%), although this has not been supported in all cohorts. The age at onset ranges from the 2nd to the 9th decades, with a peaked age-related prevalence in the 5th decade. Penetration is high, although incomplete, and is estimated to be 80%–90% by age 80 years. Duration of disease (from onset to death) is comparable to that of patients with ALS without C9ORF72 expansions, although on average, death occurs earlier by 1.8 years.

**Nonmotor Symptoms in ALS**

The most common nonmotor symptom in patients with ALS is bvFTD. The other FTD subtypes, semantic and progressive aphasia, are uncommon in patients with ALS. FTDbv is diagnosed clinically based on established criteria and is characterized by progressive deterioration of personality, social norms, and cognition. Ultimately, FTD is caused by frontotemporal lobar degeneration (FTLD), which is a pathologic diagnosis based on the presence of proteinaceous inclusions containing either tau or TDP-43 proteins found in neural tissue at autopsy. Frontotemporal lobe spectrum disorder (FTSD) represents a lesser degree of symptoms, manifesting as apathy, disinhibition, compulsivity, loss of empathy, and executive dysfunction. Screening tests for elements of FTD/FTSD have been developed for use in ALS clinics.

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Abbreviation: RP-PCR = repeat-primed PCR.

*a Reference normal >30.

*b Maximum reportable sizing 65 repeats.

*c Can provide size up to 145 repeats.

*d Sizing accuracy expected to be ±1 repeat alleles greater than or equal to 31 repeats.

*e Reference range: normal <21 repeats.

*f Assay designed to only detect pathogenic expansions.
1–5 years before onset of ALS although has been observed in population-based studies. Other symptoms include drug use/abuse and suicide. All are present a long period before onset of weakness.\textsuperscript{\text{e15}} Similarities also exist between symptoms of bvFTD and those in autism spectrum disorder (ASD), including social isolation, obsessive compulsion, inflexibility, and stereotypy of speech.\textsuperscript{\text{e16}}

Whether there is an increased incidence of nonmotor symptoms in patients with ALS and relatives with C9ORF72 expansions, particularly psychiatric symptoms, is difficult to answer with precision. Although C9ORF72 expansion is the most common genetic abnormality associated with ALS, the percentage is only moderately high and varies among populations; thus, the number of patients and families available for study is relatively small.\textsuperscript{\text{e14,e17}} C9ORF72 expansion size varies among patients with ALS. There is also variable expression of expansion size within different tissues from a patient (blood and brain). There does not appear to be a phenotypic correlation with expansion number and ALS or FTD/FTSD.\textsuperscript{\text{17}}

When investigating the incidence of dementia in family members, the type of dementia is not commonly assessed rigorously for type. In both patients and family members, psychiatric symptoms can be missed as they are frequently not diagnosed. Furthermore, the incidence of any psychiatric disorder in the general population is relatively high, and methods of query for these disorders vary, making comparisons among studies and robust generalizations difficult.

**C9ORF72 Expansions in Patients With ALS and FTD/FTSD and Families**

Nonmotor symptoms occur in patients with ALS with and without C9ORF72 expansions. In a study of 60 patients with ALS and FTD, \textasciitilde 20\% had repeat expansions, and 80\% had normal repeat numbers.\textsuperscript{\text{e18}} The associations below are considered statistically significant.

An Australian study involving 89 patients with the diagnosis of FTD and ALS and 1,414 first- and second-degree relatives found the following associations: among patients with FTD, 32\% had a family member with ASD, whereas only 9\% with ALS had an affected family member. Comparing other psychiatric disorders, in patients with FTD or ALS, there were no differences in the percentages of family members with a psychotic, mood, or bipolar disorder or risk of suicide. Family members of patients with FTD and patients with ALS were more likely to have any psychiatric disorder if the family had C9ORF72 expansions.\textsuperscript{\text{e19}}

In a study of 127 patients with ALS and 2,116 first- and second-degree relatives from an Irish ALS registry, the following were noted: 61\% of patients with ALS reported greater than one first- and second-degree relative with psychiatric symptoms, in contrast to 38.6\% in a control population. Among families with greater than 3 affected family members, the diagnostic breakdown was schizophrenia, suicide, autism, and alcoholism. All patients with ALS with a C9ORF72 expansion had 1 family member with psychiatric diagnoses, and in those with 3 or more affected members with psychiatric diagnoses, only 20.7\% had an expansion. The data support a strong connection between ALS and psychiatric disorders, but the presence of a C9ORF72 expansion did not associate with greater numbers of affected family members. Of note, depression was not overrepresented in patients with ALS.\textsuperscript{\text{e16}}

A study based on a Scottish national motor neuron disease (ALS) registry used a uniform 4-generation family history to assess dementias and psychiatric disorders in the patient and family and also included assessment for frontotemporal lobe dysfunction.\textsuperscript{\text{e19}} Determination of C9ORF72 repeat expansion was available for 84.9\% (256/305), and 9.3\% had disease-causing expansions. Among the patients with ALS, FTD was identified in 5.6\% and FTSD in 51.1\%, with apathy the most common behavioral change in 29.7\%. A family history of dementia was reported in 29\% (76/266). The above associations were not linked with C9ORF72 status, and cognitive and psychiatric features in patients and family members were felt to represent a general overlap or continuum with these conditions and ALS.

**Movement Disorders**

Initial studies of patients with C9ORF72 ALS/FTD noted the presence of additional motor symptoms with parkinsonian features, suggesting that C9ORF72 expansion could cause a more heterogeneous syndrome.\textsuperscript{\text{e20,e22}} Movement disorders occur frequently in patients with C9ORF72 expansion and can precede the diagnosis of ALS/FTD. Movement disorders can also be the initial or sole manifestation of C9ORF72 expansion.\textsuperscript{\text{e23}} Parkinsonism is a prevalent (\textasciitilde 40\%) feature of C9ORF72-ALS/FTD, particularly in those with bvFTD where prevalence can increase to 75\%.\textsuperscript{\text{e20}} C9ORF72 expansion–associated movement disorders are clinically heterogeneous and frequently found in combination. Tremor and parkinsonism were the most frequent movement disorders reported in a recent cohort study.\textsuperscript{\text{e23}} Although there are no consensus guidelines, several studies provide support for testing for C9ORF72 expansion in persons presenting with parkinsonism, tremor, distal myoclonus, cervical dystonia, and chorea with orofacial involvement in the setting of familial neurodegenerative conditions.

**C9ORF72 Expansion Carriers, Typical Parkinson Disease, and Parkinsonism**

There is no evidence that C9ORF72 positivity (as defined by >60 repeat units) contributes a significant risk for Parkinson disease (PD). Yet, several studies have shown an increased risk associated with intermediate repeat expansions (20–30 units).\textsuperscript{\text{e24,e25}} The clinical significance of this finding is limited due to the relatively small number of cases, and further studies are needed to explore this correlation. Likely, there are...
disease-modifying genetic and environmental factors present that may partially explain the inconclusive link between C9ORF72 expansion number and PD. Of interest, patients with PD with intermediate expansions appear to be quite Dopa responsive, which is not the case in most C9ORF72 patients harboring larger expansions and displaying parkinsonian features as part of a more complex phenotype.\textsuperscript{e20,e24,e26}

Patients with C9ORF72-FTD/ALS who develop parkinsonism often present with the typical symptoms of asymmetric-onset akinetic rigidity with prominent bradykiniesia and little or no tremor.\textsuperscript{e20,e28} On average, patients with C9ORF72-FTD/ALS with parkinsonism present at a younger age (~52 years), with parkinsonian signs typically manifesting in the first 2 years of disease and even earlier in familial FTD/ALS cases.\textsuperscript{e4,e20,e28} In a review of 45 C9ORF72 patients with parkinsonism, the syndrome consisted of hypokinetic rigidity without resting tremor (61%) with both asymmetric (59%) and symmetric (41%) distributions. Additional features included upper motor neuron signs (60%), lower motor neuron signs (36%), cognitive dysfunction (85%), behavior/personality changes (55%), and psychiatric symptoms (29%). Family history yielded evidence of ALS (31%) and FTD (21%).\textsuperscript{e28}

Among the few histopathologically confirmed studies, the presence of parkinsonism in C9ORF72 patient correlated with TDP-43 and p62 pathology within the basal ganglia. Across 2 large studies of autopsy-proven PD (pooled sample size >800 patients), just 1 C9ORF72 expansion carrier (>30 units) had both typical PD (diffuse Lewy bodies throughout the neocortex and TDP-43 pathology with FTLD) and C9ORF72-mediated pathology consisting of p62-positive, TDP-43-negative neuronal cytoplasmic inclusions in the hippocampus and cerebellar granule cells.\textsuperscript{e26,e29} The distinct pathology in the substantia nigra in these cases suggests a unique mechanism for C9ORF72-mediated parkinsonism.\textsuperscript{e29,e30}

**C9ORF72 and Atypical Parkinsonian Syndromes**

The prevalence of C9ORF72 expansion in atypical parkinsonian syndromes is difficult to determine based on only a few case reports and small cohort studies. C9ORF72 expansion has been found in patients with dementia with Lewy bodies, corticobasal syndrome, and progressive supranuclear palsy. It has been suggested, however, that these cases constitute incomplete diagnoses as ALS/FTD signs are often absent in the beginning.\textsuperscript{e27,e28,e31}

C9ORF72 expansion is now recognized as the leading genetic cause of Huntington-like (Huntington disease [HD]-like) disease, which is clinically indistinguishable from HD but without the diagnostic CAG repeat expansion in the HTT gene.\textsuperscript{e32,e33} Further neuropathologic studies elucidating whether C9ORF72-mediated pathology occurs in HD-related brain regions are needed; however, there does not appear to be a causal relationship between C9ORF72 expansion and HD. That C9ORF72 expansion can cause HD-like disease does support the findings that atypical movement disorders including chorea, dystonia, tremor, myoclonus, and rigidity can be present among C9ORF72 expansion carriers.\textsuperscript{e33} With limited cases, it is unclear if there is age-related penetrance or disease anticipation. It is feasible that even intermediate-length C9ORF72 expansions can interact with repeats of other genes, thereby altering the phenotypic presentation of HD and other repeat disorders.\textsuperscript{e34-e37} Conversely, the repeats of other disease-causing expansions can interact with and influence the C9ORF72 phenotype.\textsuperscript{e36}

**C9ORF72 Mouse Models**

There are several mouse models probing the pathogenic mechanism of C9ORF72 expansion. As discussed previously, the pathogenesis of C9ORF72 expansion is thought to be due to loss of C9ORF72 function, gain of toxicity from expansion RNA, or via products of RAN translation. Likely, there is a synergetic effect among these processes, which may also be disease or tissue specific given the heterogeneity that is observed across similar repeat lengths.

**Gain of Toxicity Models**

Transgenic mouse models carrying the intronic C9orf72 expansion have been generated by several groups.\textsuperscript{e35,e38,e39} Although all develop molecular characteristics of ALS/FTD, only 2 models reported behavioral and pathologic phenotypes.\textsuperscript{e35,e40} The model background appears to exert influential effects on phenotype. In the C57 black 6 (C57Bl/6) background C9orf72 expansion resulted in age-dependent cognitive deficits and mild hippocampal neuronal loss at 12 months. Conversely, on the Friend Virus B NIH Jackson (FVB/NJ) background C9orf72 expansion resulted in length and dose-dependent phenotypes, including motor dysfunction and ALS/FTD neurodegenerative features.\textsuperscript{e40} Consistent with human disease, there is variable penetrance in these animals, with some developing acute disease (~30%) and others showing milder, slowly progressing phenotypes (~40%) or no detectable phenotype (~25%). End-stage, acutely affected mice had severe hippocampal and cortical degeneration, weakness, and paralysis of one or both hindlimbs. Motor neuron loss, neuroinflammation, gait abnormalities, decreased survival, and aggregation of RAN proteins were detectable in both acutely and slowly progressing mice.\textsuperscript{e40} These mice (FVB C9-500) were deposited at The Jackson Laboratory (JAX) in 2017 and are available to the research community. To note, follow-up studies with these mice have shown disparate phenotypes, including the absence of survival and motor deficits,\textsuperscript{e41} with this difference being ascribed to differing research methods.\textsuperscript{e42} A recent study did show a robust ALS/FTD phenotype in this JAX FVB C9-500 cohort that was prevented with an antibody against the poly-GA dipeptide RAN proteins. This study provides support not only for the relevance of this model for study but also that RAN protein pathology is a driving mechanism for C9ORF72.
Other groups have now also reported decreased survival and similar findings in these JAX FVB C9-500. Loss of Function Models

Loss of C9orf72 in zebrafish and Caenorhabditis elegans causes motor deficits, whereas there is no neurodegenerative phenotype in mice with reduced or eliminated expression of C9orf72. Decreased lifespan is seen in these animals resulting from age-dependent abnormalities independent of the nervous system, including splenomegaly and lymph node enlargement. The selective elimination of C9ORF72 from neurons and glial cells, at least in mice, does not cause motor neuron degeneration, motor deficits, or disease. An unresolved question has been whether reduced C9ORF72 production from the affected allele synergizes with gain of toxicity mechanisms from repeat expansion to drive disease. To better understand this, one group developed a cohort of mice in which neither, one, or both endogenous C9orf72 alleles are inactivated and express transgenes encoding either 66 repeats or a 450 repeat-containing C9orf72 gene that does not encode the C9ORF72 protein. Reduction or elimination of C9ORF72 protein resulted in early accumulation of DPR proteins, cognitive deficits, and hippocampal neural degeneration. Both genotypes in the reduction or absence of C9ORF72 had reduced lifespan. These studies support the ALS/FTD C9ORF72 model that pathogenesis is a result of reduced C9ORF72 function synergizing with repeat-dependent gain of toxicity (Figure 4).

Clinical Trials

There are several compounds that have entered the pipeline and are progressing toward clinical use. Most of these therapeutics use antisense oligonucleotides (ASOs) targeting the sequences adjacent to the HRE in the first intron of the C9ORF72 pre-mRNA. Doing so can direct degradation of repeat-containing RNAs, without lowering the level of C9ORF72 protein encoding mRNA. A phase 1b/2a trial (FOCUS-C9) is currently investigating the safety and tolerability of an ASO selectively targeting transcriptional variants containing the HRE expansion (G4C2), thereby sparing C9ORF72 protein. The study has recently been opened to patients with C9ORF72 ALS/FTD. Preclinical work demonstrated knock down of repeat-containing transcripts in the spinal cord and cortex and knock down of 80% of DPRs in the...
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The pathogenic mechanism of disease. It is the most frequent phenocopy of Huntington C9ORF72. While there does not appear to be an association between C9ORF72 pathogenic expansion and Parkinson disease, it is the most frequent phenocopy of Huntington disease.

There is growing recognition that in addition to ALS/FTD, C9ORF72 expansion likely contributes to a spectrum of disorders. Movement disorders, particularly parkinsonism, are frequently observed in C9ORF72 expansion carriers and can precede the onset of ALS/FTD symptoms or present in isolation. While there does not appear to be a link between C9ORF72 expansion and Parkinson disease, the most common genetic cause of ALS/FTD in European and North American populations, with the haplotype likely arising from a single founder. Recent studies, however, highlight the importance of recruiting a more diverse population of affected individuals to better understand the worldwide prevalence and geographic variance.

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The pathogenic mechanism of C9ORF72 expansion is actively being explored in various animal models. RNA toxicity and products of RAN translation are thought to be leading contributors; however, recent findings suggest reduction in C9ORF72 synergizes with gain of toxicity from repeat expansion to cause early accumulation of DPR proteins and neural degeneration.

With commercial testing widely available, consensus guidelines would help establish consistent repeat length interpretations and address genetic testing and counseling for patients and families with both familial and sporadic disease. As C9ORF72 expansion targeted therapies are approaching clinical approval, the offer and decision to test is even more important.

Expansion targeting therapies are expected to enter the clinic in the next few years with several studies having recently opened to patients with C9ORF72 ALS/FTD. These opportunities represent an exciting time for the study of C9ORF72 disease and highlight the importance to continue to advance our understanding of the mechanism, prevalence, and natural history of C9ORF72-related disorders.

**Study Funding**

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**Disclosure**

The authors report no disclosure relevant to this manuscript. Go to Neurology.org/NG for full disclosure.

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**Highlights**

C9ORF72 expansion is the most common genetic cause of ALS/FTD in European and North American populations, with the haplotype likely arising from a single founder. Recent studies, however, highlight the importance of recruiting a more diverse population of affected individuals to better understand the worldwide prevalence and geographic variance.

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**Appendix Authors**

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<thead>
<tr>
<th>Name</th>
<th>Location</th>
<th>Contribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sarah Breevoort, MD, PhD</td>
<td>Department of Neurology, University of Utah, Salt Lake City, UT</td>
<td>Drafting/revision of the manuscript for content, including medical writing for content; major role in the acquisition of data; and study concept or design</td>
</tr>
<tr>
<td>Summer Gibson, MD</td>
<td>Department of Neurology, University of Utah, Salt Lake City, UT</td>
<td>Drafting/revision of the manuscript for content, including medical writing for content; major role in the acquisition of data; and study concept or design</td>
</tr>
<tr>
<td>Karla Figueroa, MS</td>
<td>Department of Neurology, University of Utah, Salt Lake City, UT</td>
<td>Drafting/revision of the manuscript for content, including medical writing for content</td>
</tr>
<tr>
<td>Mark Bromberg, MD, PhD</td>
<td>Department of Neurology, University of Utah, Salt Lake City, UT</td>
<td>Drafting/revision of the manuscript for content, including medical writing for content; major role in the acquisition of data; and study concept or design</td>
</tr>
<tr>
<td>Stefan Pulst, MD, DDr med</td>
<td>Department of Neurology, University of Utah, Salt Lake City, UT</td>
<td>Drafting/revision of the manuscript for content, including medical writing for content; major role in the acquisition of data; and study concept or design</td>
</tr>
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**References**


Expanding Clinical Spectrum of \textit{C9ORF72}-Related Disorders and Promising Therapeutic Strategies: A Review
Sarah Breevoort, Summer Gibson, Karla Figueroa, et al.

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This information is current as of April 29, 2022
In the Review “Expanding Clinical Spectrum of C9ORF72-Related Disorders and Promising Therapeutic Strategies: A Review” by Breevoort et al.,¹ the third and fourth authors should be listed in the byline as Karla P. Figueroa and Stefan M. Pulst. The publisher regrets the error.

Reference