

Negative results

No supportive evidence for *TIA1* gene mutations in a European cohort of ALS-FTD spectrum patients

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ABSTRACT

We evaluated the genetic contribution of the T cell–restricted intracellular antigen-1 gene (*TIA1*) in a European cohort of frontotemporal dementia (FTD) and amyotrophic lateral sclerosis (ALS) patients. Exonic resequencing of *TIA1* in 1120 patients (693 FTD, 341 ALS, 86 FTD-ALS) and 1039 controls identified in total 5 rare heterozygous missense variants, affecting the *TIA1* low-complexity domain (LCD). Only 1 missense variant, p.Met290Thr, identified in a familial FTD patient with disease onset at 64 years, was absent from controls yet received a combined annotation-dependent depletion score of 11.42. By contrast, 3 of the 4 variants also detected in unaffected controls, p.Val294Glu, p.Gln318Arg, and p.Ala381Thr, had combined annotation-dependent depletion scores greater than 20. Our findings in a large European patient-control series indicate that variants in *TIA1* are not a common cause of ALS and FTD. The observation of recurring *TIA1* missense variants in unaffected individuals lead us to conclude that the exact genetic contribution of *TIA1* to ALS and FTD pathogenesis remains to be further elucidated.

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1. Introduction

Exome sequencing in an unresolved European amyotrophic lateral sclerosis (ALS)–frontotemporal dementia (FTD) family with transactive response DNA-binding protein-43 (TDP-43) brain pathology identified a co-segregation missense mutation in the low-complexity domain (LCD) of the T cell–restricted intracellular antigen-1 gene (*TIA1*), affecting stress granule dynamics (Mackenzie et al., 2017). Subsequent genetic screening revealed 6 additional rare missense mutations affecting the LCD in 3 unrelated ALS and 2 ALS-FTD patients, all absent from controls, giving an overall mutation frequency of ~2% familial ALS and <0.5% sporadic ALS (Mackenzie et al., 2017). Aiming to replicate the reported genetic association of *TIA1* with ALS and ALS-FTD, we set up a genetic screen of *TIA1* in a European case-control series of ALS-FTD spectrum patients, also including pure FTD patients.

2. Materials and methods

We sequenced the entire *TIA1* coding region (exons 1–13) in a total of 1120 patients and 1039 controls originating from different European countries (detailed methodology description and ethical assurance provided in [Supplementary Material](#)). The patient cohorts were recruited in the framework of the Belgian Neurology (BELNEU)

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Consortium, the European Early-Onset Dementia (EU EOD) Consortium, and the Tübingen FTD Exome series, as described (Blauwendraat et al., 2017; van der Zee et al., 2013; van der Zee et al., 2017). DNA and medical/demographic information was included on all patients, comprising 693 patients diagnosed with FTD, 341 patients with ALS, and 86 patients with concomitant FTD and ALS (FTD-ALS).

3. Results

We identified a total of 5 rare (minor allele frequency [MAF] <1%) heterozygous missense variants, with only 1 variant (p.Met290Thr) absent from the control cohort (Fig. 1, and [Supplementary Material Table S1](#)). All 5 missense variants mapped to the conserved *TIA1* LCD region (exons 11–13).

The p.Met290Thr (rs116707801) was present in an Italian familial FTD patient (age at onset 64 years, age at death 67 years). In ExAC NFE, this variant is counted 3 times in 66,732 alleles and has a combined annotation-dependent depletion (CADD) score of 11.42. The second missense variant identified in patients, p.Val294Glu (rs769199100), was present in an isolated Italian ALS patient (onset age 39 years). It was reported only once in 66,732 alleles of the ExAC NFE data set and received a CADD score of 20.9. However, we also observed the p.Val294Glu variant in one of our 1039 control individuals, also from Italian origin (age at inclusion 58 years). Furthermore, we detected a heterozygous missense variant p.Ala381Thr (rs768554955) in another Italian control individual (age at inclusion 70 years). The p.Ala381Thr variant was observed once in 66,740 alleles in ExAC NFE (MAF 0.001%) with a CADD score of 22.4.

In addition to these rare coding variants, we detected 2 recurring missense variants with ExAC NFE MAFs just below 1%. The p.Gln318Arg (rs115611153) variant was present in 15 patients and 29 controls. Despite its recurrent presence in unaffected individuals, it was scored among the 1% most deleterious variants in the genome, with a CADD score of 23.5. The p.Asn357Ser (rs116621885) variant was present in 14 patient and 18 controls, and had a CADD score of 14.25.

No further low-frequency or common variants were detected.

4. Discussion

We evaluated the genetic contribution of *TIA1* in 693 FTD, 341 ALS, and 86 ALS-FTD patients, including 80 patients with

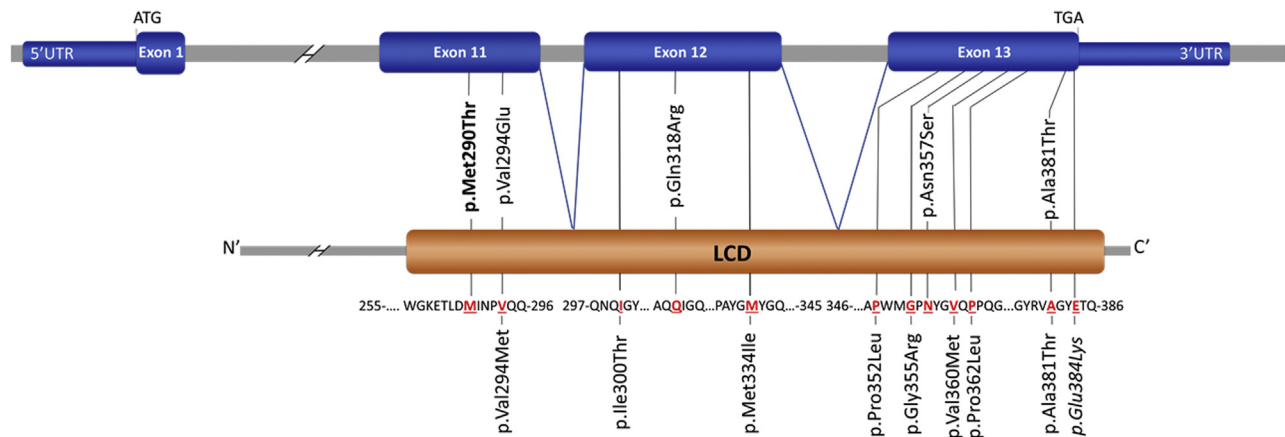


Fig. 1. Schematic representation of *TIA1* gene structure and protein with identified coding variants. Illustrated are the genomic region of *TIA1* exon 11–13 encoding for the low complexity domain (LCD). Variants identified in the present study are listed on top of the LCD structure; bold: patient-specific variant detected in a FTD patient, others: variants also detected in control individuals. Below the LCD structure, amino acid residues encoded by the respective exons and previously reported variants in ALS or ALS-FTD patients (Mackenzie et al., 2017; Yuan et al., 2017), as well as the Glu384Lys mutation identified in Welandar distal myopathy (in *italics*) (Klar et al., 2013).

pathology-confirmed TDP-43 pathology. In line with Mackenzie et al., we did not identify any variants outside the LCD region. Only 1 variant was present in patients only, the other 4 were also observed in unaffected controls.

The patient-specific variant p.Met290Thr was observed in 1 male familial FTD patient of 693 FTDs (0.14%) and absent from a well-characterized control cohort of 1039 individuals. The CADD score however was significantly less than 20, indicating it is less likely to have a deleterious effect on protein function and explain the disease phenotype of the patient. In the absence of supportive co-segregation and functional evidence, we propose to classify this variant as variant of uncertain significance. We identified a female sporadic ALS patient with early disease onset of 34 years with a p.Val294Glu variant classified as deleterious by a CADD score of 20.9. However, we also detected the same variant in 1 male control individual of 58 years old. Of interest is that a different amino acid change at the same codon position (p.Val294Met, CADD score 22.3) was reported in an ALS patient by Mackenzie et al. and proposed it to be pathogenic (Mackenzie et al., 2017). We detected an additional missense variant, suggested to be pathogenic by Mackenzie et al. (p.Ala381Thr, CADD score 22.4), in one of our investigated controls with inclusion age of 70 years. In total, 3 of the 4 missense variants identified in unaffected control subjects had a CADD score >20, including the p.Gln318Arg variant present in 29 of our tested controls (CADD score 23.5).

Despite ours and others' ambiguous genetic observations (Van Der Spek et al., 2017), we acknowledge that *TIA1* is a promising functional candidate gene for TDP-related ALS and FTD.

Similar to other ALS and ALS-FTD genes, it encodes an RNA-binding protein that assembles into stress granules. Mutant *TIA1* was shown to alter these stress granule dynamics and, by this, promote TDP-43 accumulation and aggregation (Mackenzie et al., 2017).

Our findings in a large European patient-control cohort indicate that variants in *TIA1* are not a common cause of ALS and FTD. Furthermore, the observation of recurring *TIA1* LCD missense variants in unaffected individuals, including variants with estimated CADD scores >20, together with the lack of significant co-segregation in informative families, lead us to conclude that it is too early to attribute *TIA1* genetic variation to ALS or FTD risk.

Disclosure statement

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.neurobiolaging.2018.05.005>.

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