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Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer’s Disease

Johanna Jakobsdottir1,6*, Sven J. van der Lee5,6*, Joshua C. Bis3,6*, Vincent Chouraki1,6*, David Li-Kroeger1,6,7,8*, Shinya Yamamoto6,7,8*, Megan L. Grove9, Adam Naj10, Maria Vronskaya11, Jose L. Salazar6, Anita L. DeStefano6,12, Jennifer A. Brody3, Albert V. Smith11,13, Najaf Amin7, Rebecca Sims11, Carla A. Ibrahim-Verbaas2,14, Seung-Hoon Cho15,12, Claudia L. Satizabal4,5, Oscar L. Lopez5,15, Alexa Beiser4,5,12, M. Arfan Ikram5,14,16, Melissa E. Garcia17, Caroline Hayward18,19, Tibor V. Varga20, Samuli Ripatti21,22, Paul W. Franke20,23,24, Göran Hallmans25, Olov Rolandsson26, Jan-Håkon Jansson23,27, David J. Porteous19,28, Veikko Salomaa29, Gudny Eiriksdottir1, Kenneth M. Rice30, Hugo J. Beller6,7,8,31, Daniel Levy5,32,4, Andre G. Uitterlinden8,33, Valur Emilsson1,34, Jerome I. Rotter35, Thor Aspelund3,36, Cohorts for Heart and Aging Research in Genomic Epidemiology consortium37, Alzheimer’s Disease Genetic Consortium38, Genetic and Environmental Risk in Alzheimer’s Disease consortium39, Christopher J. O’Donnell5,32, Annette L. Fitzpatrick37,38, Lenore J. Launer17, Albert Hofman2, Li-San Wang39, Julie Williams11, Gerard D. Schellenberg39, Eric Boerwinkle4,5,40, Bruce M. Psaty3,37,41,42,§, Sudha Seshadri4,5,§, Joshua M. Shulman5,7,81*, Vilmundur Gudnason1,31,13*, Cornelia M. van Duijn21,22*

1 Icelandic Heart Association, Kopavogur, Iceland, 2 Department of Epidemiology, Erasmus University Medical Center, Rotterdam, The Netherlands, 3 Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, Washington, United States of America, 4 Boston University School of Medicine, Boston, Massachusetts, United States of America, 5 Framingham Heart Study, Framingham, Massachusetts, United States of America, 6 Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, Texas, United States of America, 7 Jan and Dan Duncan Neurological Research Institute, Texas Children’s Hospital Houston, Texas, United States of America, 8 Program in Developmental Biology, Baylor College of Medicine, Houston, Texas, United States of America, 9 School of Public Health, Human Genetics Center, The University of Texas Health Science Center at Houston, Houston, Texas, United States of America, 10 Department of Biostatistics and Epidemiology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, United States of America, 11 Institute of Psychological Medicine and Clinical Neurosciences, Medical Research Council (MRC) Centre for Neuropsychiatric Genetics & Genomics, Cardiff University, Cardiff, United Kingdom, 12 Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts, United States of America, 13 Faculty of Medicine, University of Iceland, Reykjavik, Iceland, United States of America, 14 Department of Neurology, Erasmus University Medical Center, CA Rotterdam, The Netherlands, 15 Department of Neurology, University of Pittsburgh Medical Center, Pittsburgh, Pennsylvania, United States of America, 16 Departments of Radiology, Erasmus University Medical Center, CA Rotterdam, The Netherlands, 17 Laboratory of Epidemiology and Population Sciences, National Institute on Aging, Bethesda, Maryland, United States of America, 18 MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, United Kingdom, 19 Generation Scotland, Centre for Genomic and Experimental Medicine, University of Edinburgh, Edinburgh, United Kingdom, 20 Department of Clinical Sciences, Genetic and Molecular Epidemiology Unit, Lund University, Malmö, Sweden, 21 Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki, Finland, 22 Department of Public Health, University of Helsinki, Helsinki, Finland, 23 Department of Public Health & Clinical Medicine, Umeå University Hospital, Umeå, Sweden, 24 Department of Nutrition, Harvard T.H. Chan School of Public Health, Boston, Massachusetts, United States of America, 25 Department of Biobank Research, Umeå University, Umeå, Sweden, 26 Department of Public Health & Clinical Medicine, Section for Family Medicine, Umeå University, Umeå, Sweden, 27 Research Unit, Skellefteå Hospital, Skellefteå, Sweden, 28 Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, United Kingdom, 29 National Institute for Health and Welfare, Helsinki, Finland, 30 Department of Biostatistics, University of Washington, Seattle, Washington, United States of America, 31 Howard Hughes Medical Institute, Durham, North Carolina, United States of America, 32 Division of Intramural
Funding: Infrastructure for the CHARGE Consortium is supported in part by the National Heart, Lung, and Blood Institute (NHLBI, http://www.nhlbi.nih.gov) grant HL105756. Funding support for the CHARGE Consortium Exome Chip analyses is provided in part by the NHLBI grant HL120393. Support for centralized calling of the exome chip was provided by Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium exome chip was provided by Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium. The charge consortium is a founding component of the Alzheimer’s Disease Sequencing Project, and receives sequencing and analysis support through the grants from NIH: U01-AG049506, U01-AG049505, and U54-HG003273. AGES study is supported by the National Institute on Aging (NIA, https://www.nia.nih.gov) contracts N01-AG-12100 and HHSN271201200022C with contributions from the National Eye Institute (NEI, https://www.nei.nih.gov), National Institute on Deafness and Other Communication Disorders (NIDCD, https://www.nidcd.nih.gov), NHLBI, the NIA Intramural Research Program, Hjartavérd (the Icelandic Heart Association), and the Atlíthing (the Icelandic Parliament). JMS was supported by grants from the NIH/NIA (R01-AG033193, R01-AG050631, C06-RR029965), the Alzheimer’s Association, the American Federation for Aging Research, National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, Maryland, United states of America, 33 Department of Internal Medicine, Erasmus University Medical Center, CA Rotterdam, The Netherlands, 34 Faculty of Pharmaceutical Sciences, University of Iceland, Reykjavîk, Iceland, 35 Institute for Translational Genomics and Population Sciences, Los Angeles BioMedical Research Institute and Departments of Medicine and Pediatrics, Harbor-UCLA Medical Center, Torrance, California, United States of America, 36 Centre for Public Health, University of Iceland, Reykjavik, Iceland, 37 Department of Epidemiology, University of Washington, Seattle, Washington, United States of America, 38 Collaborative Health Studies Coordinating Center, Seattle, Washington, United States of America, 39 Department of Pathology and Laboratory of Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, United States of America, 40 Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, United States of America, 41 Department of Health Services, University of Washington, Seattle, Washington, United States of America, 42 Group Health Research Institute, Group Health Cooperative, Seattle, Washington, United States of America

These authors contributed equally to this work.
† EB and BMP also contributed equally to this work. SS and JMS also contributed equally to this work. VG and CMvD also contributed equally to this work.
¶ Membership of Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium, Alzheimer’s Disease Genetic Consortium, and Genetic and Environmental Risk in Alzheimer’s Disease Consortium are listed in S1 Text.
* Joshua.Shulman@bcm.edu (JMS); villi@hjarta.is (VG); v.canduijn@erasmusmc.nl (CMvD)

Abstract

We performed an exome-wide association analysis in 1393 late-onset Alzheimer’s disease (LOAD) cases and 8141 controls from the CHARGE consortium. We found that a rare variant (P155L) in TM2D3 was enriched in Icelanders (~0.5% versus <0.05% in other European populations). In 433 LOAD cases and 3903 controls from the Icelandic AGES sub-study, P155L was associated with increased risk and earlier onset of LOAD [odds ratio (95% CI) = 7.5 (3.5–15.9), p = 6.6x10−9]. Mutation in the Drosophila TM2D3 homolog, almondx, causes a phenotype similar to loss of Notch/Presenilin signaling. Human TM2D3 is capable of rescuing these phenotypes, but this activity is abolished by P155L, establishing it as a functionally damaging allele. Our results establish a rare TM2D3 variant in association with LOAD susceptibility, and together with prior work suggests possible links to the β-amyloid cascade.

Author Summary

Alzheimer’s disease (AD) is the most common cause of dementia in the older adult population. There is substantial evidence for an important genetic contribution to AD risk. While prior work has comprehensively evaluated the contribution of common genetic variants in large population-based cohorts, the role of rare variants remains to be defined. Here, we have used a newer genotyping array to characterize less common variants, including those likely to impact the function of encoded proteins, in a combined cohort of 1393 AD cases and 8141 control subjects without AD. Our results implicate a novel, amino acid-changing variant, P155L, in the TM2D3 gene. This variant was discovered to be more common in the Icelandic population, where it was significantly associated with both increased risk and earlier age of onset of AD. Lastly, in order to examine the potential functional impact of the implicated variant, we performed additional studies in the fruit fly. Our results suggest that P155L causes a loss-of-function in TM2D3, in the context of
Notch-Presenilin signal transduction. In sum, we identify a novel, rare TM2D3 variant in association with AD risk and highlight functional connections with AD-relevant biology.

Introduction

Alzheimer’s disease (AD, [MIM: 104300]), the most common form of dementia, affects more than 10% of those 65 years and older, increasing to 30% in those 85 years and older [1–4]. Pathologically, AD is characterized by extensive brain neurodegenerative cell loss in association with extra-cellular β-amyloid plaques and intra-neuronal tangles consisting of hyper-phosphorylated tau protein. Multiple mutations in the amyloid-β precursor protein (APP, [MIM: 104760]) and the presenilin-1 and -2 (PSEN1 [MIM: 104311] and PSEN2 [MIM: 600759]) genes cause familial early-onset (<65 years) AD [5,6]. Genome-wide association studies (GWAS) have also identified numerous common genetic variants of modest effect sizes for late-onset AD (LOAD, [MIM: 104300]) [7–12]. However, Apolipoprotein E (APOE, [MIM: 107741]) still remains the most important known genetic determinant of LOAD susceptibility [13,14]. Recently, rare variants with effect sizes similar to the APOE-ε4 allele have also been identified. While the population-attributable risk of such single rare variants is low, their discoveries may have important implications for understanding disease mechanisms and developing novel treatments [15]. Recent examples include a rare protective allele of APP [16] as well as variants in the novel genes TREM2 [MIM: 605086] [17,18], PLD3 [MIM: 615698] [19], UNC5C [MIM: 603610] [20], and AKAP9 [MIM: 604001] [21]. These findings highlight potentially important, new cellular pathways relevant for disease pathophysiology [15]; for example TREM2 has spurred intense recent interest in the role of microglia in LOAD [22,23]. Importantly, because of population histories and demography, rare variants may be population-specific. The protective APP variant, for example, is found predominantly in Iceland and other Scandinavian populations [16]. The two variants in AKAP9 have only been reported in African-Americans [21], and PLD3 variants appear to vary greatly in frequency between populations [24].

To date, the identification of rare susceptibility variants in LOAD has been hampered by poor representation on genotyping arrays used for large GWAS [25]; moreover, direct sequencing in large numbers of individuals remains costly. Here, using an exome-wide genotyping array (the Illumina HumanExome Beadchip), we report associations with LOAD in four population-based cohorts from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium [26].

Results

Exome-wide association study of LOAD in CHARGE

The discovery phase of our analysis examined single-variant associations with LOAD. Meta-analysis was performed across four CHARGE studies including 1393 LOAD cases and 8141 controls (Table 1), using logistic regression-based scores [27,28] and adjusting for age and sex (see Methods and Supporting methods in S1 Text). Single-variant results were filtered using quality control filters that included minimum minor allele frequency (MAF ≥ 0.5%) or minor allele count (MAC ≥ 5) in cases (see also Methods) resulting in 52026 total variants tested. Given the rarity of many variants captured on the exome array, we additionally performed association analysis, where we considered rare variants from the same gene in aggregate. For this complementary analysis we used the Sequence Kernel Association Test (SKAT) test [29], a
SKAT tests the null hypothesis of no variation of effects and therefore the statistical model of SKAT is applicable to test association of variant sets that may have a combination of variants including both risk and protective alleles or those with no effect. Variants were included in the SKAT analysis based on functional annotation (see Methods) and maximum frequency of 5%. Because the SKAT results were filtered by cumulative set-based MAF and MAC, considering all variants in aggregate, and not by minimum MAF of single SNPs (see Methods), this complementary analysis included many variants that did not meet the criteria for inclusion in the single-variant tests. The results of both the single-variant and SKAT discovery analysis are presented in S1 Table and quantile-quantile plots are in S1 Fig. Below, we discuss each of the top three results, our efforts to replicate the novel loci in independent cohorts, and for TM2D3, subsequent functional validation of the implicated variant in Drosophila.

**APOE**

As expected based on many prior LOAD GWAS [12], three common intronic variants near APOE reached the Bonferroni threshold of exome-wide significance (p < 9.6x10^{-7}) in the single-variant analysis: rs769449 in APOE (p = 5.8x10^{-38}, MAF\textsubscript{case} = 17%, MAF\textsubscript{control} = 10%), rs2075650 in TOMM40 (p = 1.2x10^{-24}, MAF\textsubscript{case} = 18%, MAF\textsubscript{control} = 13%), and rs6859 in PVRL2 (p = 1.5x10^{-9}, MAF\textsubscript{case} = 46%, MAF\textsubscript{control} = 40%). Although APOE is a well-established LOAD risk locus it did not achieve nominal significance in the SKAT analysis, possible because the established common risk variants at this locus exceed our frequency threshold for consideration in the SKAT analysis (MAF<0.05) (S2 Table).

**SKAP2**

rs17154402 in SKAP2 (MIM: 605215) on chromosome 7p15 also showed a significant association with LOAD (p = 2.1x10^{-7}, MAF\textsubscript{case} = 0.22%, MAF\textsubscript{control} = 0%). This SNP is predicted to introduce a non-synonymous amino acid change (S253T in the longer isoform) in the SKAP2 protein. The SKAP2 locus also achieved significant association with LOAD (p = 4.5x10^{-7}) in the SKAT analysis. Although the SKAT analysis included three distinct SKAP2 missense alleles, the SKAT result was fully explained by the variant identified in the single-variant analysis (S2 Table). rs17154402 was not significantly associated with LOAD risk in the ADGC or GERAD cohorts, which are 2 large European-ancestry case-control datasets (13 carriers in 8256 controls [MAF 0.08%] and 9 carriers in 13333 cases [MAF 0.03%], p = 0.05), and compared to the discovery CHARGE cohort, showed an opposite direction of effect in these samples. We noted that rs17154402 has a higher frequency in persons of African compared to European ancestry (MAF~7% in Yorubans and 3% in all African populations combined in the 1000 Genomes...
Project data, and Grove et al [30] reported a ~5% MAF in African populations versus 0.22% in European ancestry subjects. We therefore took advantage of an available African-American subsample of the CHARGE CHS cohort for attempted replication. However, the variant again showed an inconsistent direction of effect and non-significant association (93 [12 carriers] cases, 208 [33 carriers] controls; p = 0.66). Based on the non-replication of SKAP2 in available independent datasets, it was not pursued further.

**TM2D3**

Our discovery analysis also identified rs139709573, a missense variant in TM2D3 (MIM: 610014) on chromosome 15q26. Although the association statistic did not exceed the Bonferroni threshold for exome-wide significance in the CHARGE discovery analysis (single-variant p = 2.0x10^-6, SKAT p = 8.3x10^-6), several important observations led us to consider this variant further. First, we noted that while very rare (0–0.06% MAF in European ancestry populations (S3 Table)) the TM2D3 variant was enriched nearly 10-fold in the Icelandic AGES cohort (0.45% MAF). Second, rs139709573 was significantly associated (p = 5.9x10^-8, Table 2) with LOAD when the analysis was restricted to the AGES-discovery sample (143 cases, 2374 controls). Third, prior experimental studies potentially link TM2D3 to AD-relevant biology. Specifically, TM2D3 shares homology with the β-amyloid peptide binding protein (BBP or TM2D1) [31], and as discussed further below, genetic studies of the conserved Drosophila ortholog amondex (amx) strongly suggest links to γ-secretase function [32].

In the SKAT analysis, the association of TM2D3 with LOAD was fully accounted for by rs139709573; although, 3 other variants were considered in this analysis (S2 Table). In the subsequent analyses and functional follow-up, we therefore restricted our focus on rs139709573. First we evaluated potential inflation in the test statistic of the TM2D3 rs139709573 result in the AGES-discovery cohort (Supporting results in S1 Text) and we further confirmed the genotypes of risk allele carriers by re-genotyping them with a TaqMan assay. We next directly genotyped rs139709573 in an independent Icelandic AGES-followup cohort (290 cases, 1529 controls), consisting of individuals who had not been genotyped previously with the exome array. The rs139709573 association was also detected in this sample (p = 3.1x10^-3, Table 2).

### Table 2. Sample characteristics and association results for P155L (rs139709573) in TM2D3 in the two Icelandic AGES cohorts.

<table>
<thead>
<tr>
<th>Cohort</th>
<th>Group</th>
<th>No(% women)</th>
<th>Age, mean (SD), year</th>
<th>APOE ε4+ No (%)</th>
<th>TM2D3 carriers, No (%)</th>
<th>p (OR, 95% CI)ᵃ</th>
<th>pFisher’s Exactᵇ</th>
<th>pConditionalᶜ</th>
</tr>
</thead>
<tbody>
<tr>
<td>AGES-discovery</td>
<td>Cases</td>
<td>143 (59)</td>
<td>82.5 (4.9)</td>
<td>66 (46)</td>
<td>7 (4.9)</td>
<td>5.9x10^-6 (8.62, 3.43–21.68)</td>
<td>5.6x10^-4</td>
<td>8.4x10^-8</td>
</tr>
<tr>
<td></td>
<td>Controls</td>
<td>2374 (59)</td>
<td>78.9 (5.0)</td>
<td>638 (27)</td>
<td>20 (0.8)</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>AGES-followup</td>
<td>Cases</td>
<td>290 (59)</td>
<td>84.5 (5.1)</td>
<td>127 (44)</td>
<td>6 (2.1)</td>
<td>3.0x10^-3 (5.42, 1.60–18.32)</td>
<td>6.2x10^-3</td>
<td>1.1x10^-2</td>
</tr>
<tr>
<td></td>
<td>Controls</td>
<td>1529 (57)</td>
<td>79.4 (5.3)</td>
<td>396 (26)</td>
<td>6 (0.4)</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>Pooledᵈ</td>
<td>Cases</td>
<td>433 (59)</td>
<td>83.9 (5.2)</td>
<td>193 (45)</td>
<td>13 (3.0)</td>
<td>6.6x10^-5 (7.45, 3.49–15.90)</td>
<td>5.9x10^-5</td>
<td>6.8x10^-8</td>
</tr>
<tr>
<td></td>
<td>Controls</td>
<td>3903 (58)</td>
<td>79.1 (5.1)</td>
<td>1034 (26)</td>
<td>26 (0.7)</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
</tbody>
</table>

All p-values are based on the 2-sided alternative.

ᵃ Score tests adjusted for age and sex based on a logistic regression model. The unconditional MLE of the OR is reported based on fitting the full model including the SNP. Note, that those point estimates of OR could be inflated (Supporting results in S1 Text)

ᵇ P-value from the Fisher’s exact test for carrier status. For the meta-analysis the data were pooled.

ᶜ P-value conditional on APOE ε4 carrier status. Based on a score test after adjusting for age, sex, and APOE ε4.

ᵈ The two cohorts are pooled in a stratified analysis (stratified by cohort).

doi:10.1371/journal.pgen.1006327.t002
expected, an analysis combining all of the AGES data on TM2D3 demonstrated an enhanced association of the TM2D3 variant with LOAD (OR = 7.45; 95% CI 3.49–15.90; p = 6.6x10^{-9}). We also observed an association with age-at-onset in the AGES cohorts (hazard ratio = 5.3; 95% CI 2.7–10.5; p = 1.1x10^{-6}, see also non-parametric Kaplan–Meier curves in Fig 1). Using the PHASE program [33–35] we estimated that rs139709573 resides on a single haplotype in the Icelandic population (Supporting results in S1 Text), and we further excluded potential confounding due to cryptic relatedness (Supporting results in S1 Text). Similarly, the association between rs139709573 and LOAD was robust to adjustment for APOE genotype (Table 2).

Given the low frequency of rs139709573 in individuals of European ancestry, there were limited numbers of carriers in GERAD and ADGC (11 carriers in 13333 cases [0.041% MAF]; 4 carriers in 8256 controls [0.024% MAF]). While, the association was not statistically significant (p = 0.4), the direction of effect was consistent with that observed in AGES (OR = 1.7, 95% CI 0.5–7.3).

Analysis of TM2D3 transcripts and expression

The TM2D3 gene has several alternatively spliced transcripts, including six protein-coding transcripts [36]. rs139709573 falls within an exon common to all six isoforms (S2 Fig) and causes a Proline to Leucine amino acid change (P155L in the longest isoform). Gene and transcript expression estimates were extracted from publically available Genotype-Tissue Expression consortium (GTEx) data [37], estimated as “transcripts per million” (TPM), using the Toil workflow [38] in the UCSC Xena browser (http://xena.ucsc.edu/). TM2D3 is expressed in all GTEx tissues, including from many brain regions (S3 Fig). The GTEx expression data further
show that the alternative TM2D3 transcripts are similarly expressed across diverse human tissues (S4 Fig).

Structure of TM2D3 protein

TM2D3 encodes a predicted double-pass transmembrane protein with evidence of evolutionary conservation (Fig 2A). The variant falls within the overall well-conserved C-Type Lectin domain and is adjacent to other invariant residues in the first predicted extracellular domain [32] (Fig 2B). While P155L is not predicted to be strongly damaging by PolyPhen [39], SIFT [40], or CADD (C-Score = 7.3) [41] and cross-species alignments show that the Proline residue is not conserved (Fig 2A), the two amino-acids do have important property differences, consistent with a potentially non-conservative substitution. Proline, the only cyclic amino-acid, frequently resides on the surface of folded proteins, and can underlie structural “kinks” or bends. Proline is unique in its inability to form hydrogen bonds that stabilize alpha-helices and beta-sheets. By contrast with Proline, Leucine favors alpha-helical secondary structure, and is more commonly buried in the interior of folded protein structures [42].

Functional validation of TM2D3 (P155L) in Drosophila

In order to investigate the potential functional consequences of P155L and its possible link to AD, we turned to the fruit fly, Drosophila melanogaster. Human TM2D3 and the homologous fly gene, amx, are 51% identical and 64% similar (Fig 2A). Mutations in amx cause a strong maternal effect neurogenic phenotype, characteristic of defective Notch signaling, and lead to embryonic lethality (Fig 3A and 3B) [43,44]. Similar to the cleavage of APP to generate the pathogenic β-amyloid peptide, Notch receptor signaling requires homologous cleavage by γ-secretase for receptor activation. In Drosophila, loss of Notch or its regulators (e.g. presenilin) cause similar neurogenic phenotypes, due to impaired lateral inhibition and the inappropriate differentiation of ectodermal tissue toward a neural fate [45–47]. Moreover, prior genetic epistasis experiments suggest that amx may function at the γ-secretase cleavage step [32].

To determine whether TM2D3 and amx have conserved molecular functions, we “humanized” the Drosophila amx gene by replacing its coding sequence with that of human TM2D3 in the context of a genomic rescue construct (Fig 3C). Following establishment of stable transgenic lines, this construct was crossed into an amx mutant genetic background (amx/1/Df(1) Exel9049). Consistent with prior reports [43,44], when crossed to amx mutant males, all embryos laid by amx mutant females exhibited a strong neurogenic phenotype, failing to hatch from their eggs (Fig 3B and 3D). This embryonic defect and the resulting female sterility can be fully rescued by a genomic rescue construct with the wild-type (+) fly amx gene (Fig 3D and 3E). Due to the lethality of Df(1)Exel9049/Y hemizygous male progeny, complete rescue of the amx phenotype is predicted to lead to a maximum of ~75% egg hatching based on Mendelian expectations (Fig 3D, S5 Fig). Introduction of wild-type human TM2D3, under control of endogenous amx regulatory sequences, demonstrated significant rescue activity compared to amx mutant females (34.2% vs. 0% egg hatching p<0.001). Overall, based on the egg hatching assay (Fig 3D), the activity of the human TM2D3 construct was estimated to be roughly half that observed for fly amx. Consistent with this, we observed a range in the severity of the neurogenic phenotype severity (S6 Fig), including embryos exhibiting a complete rescue (Fig 3G) and producing viable progeny that can develop into adult flies with no obvious morphological phenotypes. By contrast, an otherwise identical TM2D3P155L genomic construct, but harboring the AD-associated P155L variant, was unable to rescue the neurogenic phenotype (Fig 3H) or the associated female sterility (Fig 3D). No animals hatched out of more than 900 eggs laid from TM2D3P155L female flies. Consistent results were also seen in complementary assessments
of rescue activity for the amx peripheral nervous system neurogenic phenotype (S6 Fig). In sum, our results demonstrate that human TM2D3 can functionally substitute for fly amx in the context of embryonic Notch signaling, and that the P155L variant causes a loss-of-function in this context.

Discussion

We identified a novel LOAD-associated gene, TM2D3, harboring a rare missense mutation (P155L) that is associated with increased risk and earlier onset of LOAD diagnosis in an Icelandic population. Our experiments in Drosophila further suggest that this LOAD-associated P155L variant leads to a loss-of-function of TM2D3 in the context of Notch signaling during embryogenesis. While we could neither confirm nor negate the TM2D3 finding in available European ancestry populations—possibly because of the low P155L allele frequency, a consistent association was demonstrated in an Icelandic cohort. Although the TM2D3 variant failed to achieve the Bonferroni significance threshold in our CHARGE-wide meta-analysis our observation of increased frequency and enhanced association within the Icelandic AGES-discovery cohort highlighted the TM2D3 variant for further consideration. Significant association in the AGES-followup sample coupled with variant functional validation in Drosophila suggests a role for TM2D3 in AD susceptibility. Our investigation thus exemplifies the importance not only for statistical rigor and transparency, but also flexibility in study design, when performing rare variant genetic association studies, in particular when statistical results are accompanied by relevant functional experiments.

TM2D3 has not previously been directly linked to AD. The encoded protein is predicted to contain two transmembrane regions, and additional domains with homology to C-Type lectins and G-protein coupled receptors (DRF motif) (Fig 2B). Since the P155L variant resides within the well-conserved C-Type lectin domain, the variant could plausibly disrupt the interaction of TM2D3 with a putative glycosylated binding partner. Alternatively, as suggested above, distinct structural properties of Leucine versus Proline may disrupt protein folding [42]. Interestingly, TM2D3 shares homology with the β-amyloid peptide binding protein (BBP or TM2D1), which avidly binds to and sensitizes cells to toxicity caused by the β-amyloid peptide [31]. However, overexpression of TM2D3 (referred to as BLP2 in Kajkowski et al. [31]) was not associated with similar toxicity in cell culture. In mammals, TM2D3 it is highly expressed in the brain, including in the hippocampus, hypothalamus, and amygdala, potentially consistent with a role in AD pathogenesis (http://biogps.org/goto/geneReport&id=80213 and S3 Fig) [31,48,49]. Additionally, micro-array analysis suggests that the expression of TM2D3 is down-regulated in the hippocampus of AD cases compared to controls [50].

While incompletely studied in mammals, loss-of-function mutants in the well-conserved Drosophila homolog of TM2D3, amx, cause embryonic phenotypes associated with disruptions in Notch signaling [51]. Further, genetic epistasis experiments support a potential role for amx in Notch receptor intramembranous proteolysis [32], a process that is mediated by the presenilin/γ-secretase complex. One speculative hypothesis is that TM2D3/Amx participates either directly or indirectly in the intramembranous cleavage of Notch as well as in the homologous proteolytic processing of APP by γ-secretase. In this model, the P155L variant might potentially influence the generation of toxic β-amyloid peptides, similar to well-established disease susceptibility variants in APP, PSEN1, and PSEN2 [52].
Taking advantage of the potential functional conservation, we found that human TM2D3 expressed under the control of endogenous Drosophila amx regulatory elements is capable of rescuing the embryonic neurogenic phenotype, indicating that Amx and TM2D3 are orthologs and have conserved molecular functions in vivo. Importantly, we found that introduction of the LOAD-associated P155L variant into anotherwise identical TM2D3 genomic rescue construct abolishes the rescue activity. This result is consistent with either a partial or complete loss-of-function mechanism of the P155L variant, albeit within the heterologous context of Notch signaling in the Drosophila embryo. It is notable that the P155L variant was neither well-conserved nor predicted by bioinformatics as damaging; nevertheless, our cross-species approach convincingly demonstrates its functional impact. Our overall strategy of first rescuing the loss-of-function phenotype of the predicted homologous gene in flies, followed by examining the potential consequences of an implicated variant can be a powerful approach for the follow-up of many similar findings emerging from human genomic studies, including others using exome genotyping arrays or next generation sequencing approaches [53,54].

In summary, we have identified a missense mutation in the TM2D3 gene with a strong impact on LOAD risk. The TM2D3 variant is enriched ~10-fold and associated with both risk and age-at-onset of LOAD in the Icelandic population. We further show that P155L is associated with a loss-of-function in the heterologous but potentially relevant context of Notch signaling in Drosophila embryos. We therefore speculate that TM2D3 may participate in the proteolytic processing of both Notch and APP, linking it to the amyloid cascade like other well-established AD susceptibility variants. Although we have demonstrated an association of the TM2D3 variant only in the Icelandic population, our findings may thus have broader implications for understanding LOAD.

**Methods**

**Studies and participants**

Four studies from the CHARGE consortium genotyped a total of 1393 AD cases and 8141 cognitively intact controls for an ExomeChip (EC) genotyping array. All participants in the discovery phase of the analysis were of European or European American descent (Table 1). In the follow-up analysis we included Icelandic individuals from the AGES-followup cohort, African-American participants of the Cardiovascular Health Study (CHS), and European or European American individuals from the Alzheimer’s Disease Genetics Consortium (ADGC) and
Genetic and Environmental Risk in Alzheimer’s Disease consortium (GERAD). Further details on phenotyping and other cohort characteristics are in the Supporting methods in S1 Text.

Ethics statement
All participants provided informed consent and all studies were approved by their respective ethics committees.

Genotyping
All four CHARGE cohorts were genotyped for the HumanExome BeadChip v1.0 from Illumina (San Diego, CA, USA). Genotype calling and quality control was performed centrally as described previously [30]. Each study also performed quality control locally (Supporting methods in S1 Text). Post-analysis quality control on the top results included visual inspection of cluster plots (S1 Fig) and re-genotyping of TM2D3 carriers using a TaqMan assay (genotype calls were 100% validated). TM2D3 variant was genotyped in the AGES-followup cohort using the TaqMan assay. In ADGC and GERAD consortia the SKAP2 and TM2D3 variants were genotyped on the Illumina HumanExome BeadChip v1.0 or v1.1 from Illumina (Supporting methods in S1 Text).

Statistical analysis

Statistical methods of the discovery phase. In the discovery phase of our analysis we used score tests [27] for the single-variant analysis and the Sequence Kernel Association Test (SKAT [29]) to test for the aggregate effect of multiple low-frequency variants within a gene on LOAD. Each study adjusted for age, sex, and for those principal components associated with LOAD (see Supporting methods in S1 Text). The discovery analysis was not adjusted for APOE genotypes; however this important LOAD risk factor was considered in secondary analyses of top findings. Both tests were performed in R with the seqMeta package (http://cran.r-project.org/web/packages/seqMeta/) to meta-analyze study-specific scores and respective variances and covariances (see details in Supporting methods in S1 Text) [28]. In the single-variant analysis we included variants present in at least two studies, variants with a minor allele frequency (MAF) ≥ 0.5% or assuming that rare damaging alleles could be prevalent predominantly in cases we also included variants with minor allele count (MAC) ≥ 5 in cases. This resulted in 52,026 single-variant tests. In the SKAT analysis we grouped the variants by genes using the start and stop positions as annotated by dbNSFP v2.0 [55] to define gene boundaries. We included only variants of MAF < 5% in the combined sample, and further annotated as missense, stop-gain, stop-loss, or splice-site variants. Then we required that genes have at least two such variants as well as at least two studies having a polymorphic variant. This resulted in 11,303 SKAT tests. After filtering, the Bonferroni correction thresholds that accounted for multiple testing were 9.6x10^{-7} for single-variant tests and 4.4x10^{-6} for SKAT. Two analysts independently performed the meta-analysis, leading to identical results.

Statistical methods in follow-up analysis of TM2D3 in AGES. We used a score test and Fisher's exact test for the follow-up analysis based on an independent Icelandic AGES sample (AGES-followup). We report (Table 2) estimates of the ORs based on fitting the full model (AD ~ age + sex + TM2D3) instead of the one-step approximation used in seqMeta (see Supporting Methods in S1 Text for details). For the AGES-discovery cohort we similarly update and report estimates of the ORs (Table 2) based on fitting the full model (S1A Table, S2 Table). In the AGES study, we also used a mixed-model to account for potential confounding effect relatedness might have on the association of P155L in TM2D3 with LOAD (Supporting results in S1 Text). Cox regression was used to test for association of P155L with age-at-onset
in the AGES data after adjusting for sex and APOE genotype. Individuals with LOAD diagnosis at the baseline visit were excluded so only at-risk individuals were included in the analysis. As detailed in the Supporting methods in S1 Text, the survival analysis accounted for left-truncation (i.e. follow-up begins after 65 years) and right-censoring (i.e. censoring that happens if a participant is lost to follow-up before having an event).

Drosophila

Detailed methods for our Drosophila experiments can be found in the Supporting methods in S1 Text. Briefly, the rescue activity of amx, TM2D3, or TM2D3P155L genomic constructs was examined in female flies of the genotype amx1/Df(1)Exel9049; (Rescue Transgene)/+ or amx1/Df(1)Exel9049; (Rescue Transgene) when crossed to amx1 males (with or without the (Rescue Transgene))[43]. To visualize the developing nervous system, resulting embryos were stained with anti-Hrp (1:1000) [56], a neuronal membrane marker and anti-ELAV (1:100) [57], a neuronal nuclear marker. For egg hatching, adults were allowed to lay eggs for 5 hours on grape juice agar plates, and larvae were counted 24 hours later.

Supporting Information

S1 Text. Supporting results and methods. Four supporting results sections and seven supporting methods sections, and sections with collaborators, and detailed funding information. (PDF)

S1 Fig. Quantile-quantile and cluster plots. Top row Quantile-quantile plots for the exome-wide discovery meta-analysis. Known genes are in orange. The genomic control coefficient ($\lambda_{GC}$) is reported. Middle panel: Variants near APOE excluded Bottom row Cluster plots for SNPs in SKAP2 and TM2D3 demonstrate appropriate calling of the rare variant genotypes. (PDF)

S2 Fig. Schematic of TM2D3 transcripts. A schematic of TM2D3 transcripts. Ensembl identifiers (amino acid change due to rs13970957 in parenthesis) are marked by the schematic of each protein-coding transcripts. Bold text highlights transcripts that are also in RefSeq. The exon that contains rs13970957 is marked with an arrow. The schematic was retrieved 27 May 2016 from the Ensembl browser. (PDF)

S3 Fig. Expression of TM2D3 in GTEx samples. Overall gene expression in various tissues, brain tissues are in yellow. TPM (“transcripts per million”) estimated using RSEM [58] on the GTEx data [37] (retrieved 26 May 2016 from UCSC Xena browser). (PDF)

S4 Fig. Expression of TM2D3 protein-coding transcripts in GTEx tissues. Expression of protein-coding transcripts in all tissues (excluding blood), all brain tissues, and hippocampus only. TPM (“transcripts per million”) estimated using kallisto [59] on the GTEx data [37] (retrieved 26 May 2016 from UCSC Xena browser). Transcript ENST00000559107 was not included in the plots because it is very lowly expressed and visualization was better without it. (PDF)

S5 Fig. Experimental crossing scheme for rescue experiments. The general crossing scheme is shown for the egg hatching rescue, quantified in Fig 2D. Due to the lethality of Df(1)Exel9049/Y hemizygous male progeny, complete rescue of the amx neurogenic phenotype is expected to lead to a maximum of ~75% egg hatching. (TIFF)
S6 Fig. Neurogenic phenotypes in developing flies. TM2D3[+] but not TM2D3[P155L] can suppress the neurogenic phenotype in the developing fly embryonic peripheral nervous system (PNS). (A–B) Maternal effect neurogenic defects in amx mutants can also be seen in the PNS. Compared to control embryos (A), maternal amx mutant embryos (B) show increased number of Sensory Organ Precursor cells (SOPs), labeled by Senseless (Sen, red), due to defective lateral inhibition. Embryos are counterstained with DAPI (blue). (C–F) PNS phenotypes in embryos laid by amx mutant females with or without amx[+], TM2D3[+], and TM2D3[P155L] genomic rescue constructs. Thoracic segments (T1, T2, T3) of stage 11 embryos are shown. TM2D3[+] can rescue the lateral inhibition defects in SOPs in some (Compare C, D and E) but not all embryos (E’). In contrast, all embryos from amx mutant females with TM2D3[P155L] exhibit neurogenic PNS phenotypes (F, F’). Scale bars = 100 μm for A–B, = 50 μm for C–F.

S1 Table. Results of exome-wide discovery analysis. Top results of exome-wide single variant (A) and SKAT (B) discovery analysis. Complete results are available in dbGAP (accession phs000930). A: Direction = AGES-CHS-FHS-RS, Alleles = non-coding/coding, AF displayed as percentage (%). B: cumAF = cumulative allele frequency displayed as percentage (%), N_SNPs = number of SNPs in test.

S2 Table. Variant- and study-specific break-down of TM2D3, SKAP2, and APOE results.

S3 Table. Allele frequency of P155L in populations of European ancestry.

Author Contributions
Conceptualization: CMvD VG JMS SY SS LJL EB.
Methodology: JJ SjvdL TA JCB VC JAB KMR CMvD VG SS LJL JMS SY DLK.
Software: JJ SjvdL JCB VC ALD JAB KMR.
Validation: JJ SjvdL MLG SY DLK JLS.
Formal analysis: JJ SjvdL NA JCB JAB VC AN MV RS ALD AVS CAIV SHC CLS TVV CH SR MAI KMR TA LSW.
Investigation: SY DLK JLS HJB JMS MLG JIR BMP EB ALF VG SS CMvD JJ SjvdL LJL VC JCB.
Resources: CMvD SS LJL VG LSW OLL AB MAI MEG GE DJP PWF GH OR JHJ VS DL AGU JIR ALF AH JW GDS BMP SY CJO EB HJB JMS.
Writing original draft: JJ CMvD SjvdL JMS SS LJL VG.
Writing review & editing: JJ SjvdL JCB VC DLK SY MLG AN MV JLS ALD JAB AVS NA RS CAIV SHC CLS OLL AB MAI MEG CH TVV SR PWF GH OR JHJ DJP VS GE KMR HJB DL AGU VE JIR TA CJ O ALF LJL AH LSW JW GDS EB BMP SS JMS VG CMvD.
Visualization: JJ SjvdL SY DLK JLS MLG.
Supervision: CMvD VG JMS SS LJL BMP.
Project administration: CMvD VG JMS SS LJL ALF EB JIR BMP.
Funding acquisition: VG LJJ CML VM MAH AGU JMS SY HJB SS CJ OLL ALF EB JIR WF OR JH DJP VS LSW GDS JW.

References


