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Genome sequencing for early-onset or atypical dementia: high diagnostic yield and frequent observation of multiple contributory alleles

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Abstract We assessed the results of genome sequencing for early-onset dementia. Participants were selected from a memory disorders clinic. Genome sequencing was performed along with C9orf72 repeat expansion testing. All returned sequencing results were Sanger-validated. Prior clinical diagnoses included Alzheimer’s disease, frontotemporal dementia, and unspecified dementia. The mean age of onset was 54 (41–76). Fifty percent of patients had a strong family history, 37.5% had some, and 12.5% had no known family history. Nine of 32 patients (28%) had a variant defined as pathogenic or likely pathogenic (P/LP) by American College of Medical Genetics and Genomics standards, including variants in APP, C9orf72, CSF1R, and MAPT. Nine patients (including three with P/LP variants) harbored established risk alleles with moderate penetrance (odds ratios of ∼2–5) in ABCA7, AKAP9, GBA, PLD3, SORL1, and TREM2. All six patients harboring these moderate penetrance variants but not P/LP variants also had one or two APOE ε4 alleles. One patient had two APOE ε4 alleles with no other established contributors. In total, 16 patients (50%) harbored one or more genetic variants likely to explain symptoms. We identified variants of uncertain significance (VUSs) in ABI3, ADAM10, ARSA, GRID2IP, MME, NOTCH3, PLCD1, PSEN1, TM2D3, TNK1, TTC3, and VPS13C, also often along with other variants. In summary, genome sequencing for early-onset dementia frequently identified multiple established or possible contributory alleles. These observations add support for an oligogenic model for early-onset dementia.

[Supplemental material is available for this article.]
INTRODUCTION

Genomic technologies are increasingly being used in clinical settings, but clinical large-scale sequencing for adult-onset neurological conditions has not been heavily applied. Possible reasons include the use of disease-specific gene panels and uncertain genetic yield, despite promising signals for yield using comprehensive approaches (Blauwendraat et al. 2018). We sought to assess the diagnostic yield and burden of variants implicated in neurodegenerative disease with genome sequencing and C9orf72 expansion testing in cases of early-onset dementia.

Patients were selected from the Memory Disorders Clinic at the University of Alabama at Birmingham (UAB). Inclusion criteria were clinician-diagnosed early-onset dementia. When possible, unaffected parents were included as participants to allow filtering for de novo variants in patients without a family history (a fruitful approach in pediatric genetic disorders [Vissers et al. 2010; Bowling et al. 2017] and amyotrophic lateral sclerosis [ALS] [Chesi et al. 2013; Steinberg et al. 2015]). In addition, unaffected siblings past the age of onset of the patient were enrolled as participants when possible for variant filtering and segregation.

Before starting the analysis, we set criteria for return of results to patients. First, we used the American College of Medical Genetics and Genomics (ACMG) criteria for pathogenicity (Richards et al. 2015) to identify highly penetrant causal variation. For moderately penetrant variants, we set criteria to return (i) APOE ε4 status for early-onset Alzheimer’s disease (EOAD), (ii) any variant with a disease-associated odds ratio >2 in multiple reports as an “established risk variant,” or (iii) one strong report with a disease-associated odds ratio >2 with replication included in the study design as a “likely risk variant.”

RESULTS

Clinical Presentation and Family History

Prior clinical diagnoses for patients included EOAD, frontotemporal dementia (FTD), and other unspecified dementias. Twenty-one patients were female and 11 were male. Twenty-eight self-reported Caucasian, four self-reported African–American, and all reported non-Hispanic ethnicity. The mean age of onset was 54 (range 41–76). Ten patients had ages of onset in their 40s, 17 in their 50s, four in their 60s, and one in his 70s. Two of the patients with onset in their 60s had an age of onset below age 65 (a typically used threshold for early-onset dementia [Lambert et al. 2014]). The three patients with onset after 65 were included based on clinician discretion. The patient with onset in the 70s had uncertainty in the reported onset date and an unusual leukoencephalopathy presentation (in which NOTCH3 variants of unknown significance [VUSs] were identified), and all three patients with ages of onset after 65 had strong family history (modified Goldman score of 1 or 1.5 as defined below).

In addition to enrolling patients, we also enrolled reportedly unaffected family members for variant filtering and segregation analyses. Thirty-one unaffected relatives were enrolled, 29 of whom had genome sequencing (two were only checked for variants by Sanger). Only two families had complete trios (mother, father, and proband) to allow for searching for de novo variants, of which none of interest was identified. In total, 20 unaffected siblings, nine unaffected parents, and two unaffected cousins were enrolled.

A strong family history of dementia was reported for 50% of patients (16/32), whereas 37.5% (12/32) had some family history, and 12.5% (4/32) had no reported family history. Our definition of family history is based on a modification of a four-point scoring system first put forward by Goldman et al. (2005) in which we modified the score as follows: (1) At least
three people in two generations affected with EOAD, FTD, or ALS, with one person being a first-degree relative of the other two; (1.5) same as (1) but with LOAD (late-onset Alzheimer’s disease) instead of EOAD; (2) at least three relatives with dementia or ALS but in whom criteria for autosomal dominant inheritance were not met; (3) a single affected first- or second-degree family member with early-onset dementia or ALS; (3.5) a single affected first- or second-degree family member with late-onset dementia or ALS; or (4) no contributory family history or unknown family history. We considered a score of 1 or 1.5 as strong family history, a score of 2, 3, or 3.5 as some family history, and a score of 4 as no reported family history. All family history information is listed alongside phenotype and variant information in Supplemental Table 1.

To protect patient information, more detailed diagnoses and phenotype information beyond that provided here and listed in Supplemental Table 1 are only provided in the controlled access data set, NIAGADS project NG00082, to qualified researchers approved for access.

Genomic Analyses
Nine of 32 (28%) patients had a highly penetrant variant relevant to their clinical diagnosis (ACMG P/LP [Richards et al. 2015]), whereas seven (22%) had multiple moderately penetrant risk alleles (Fig. 1). Individual cases are discussed next, with variants identified summarized by Table 1 and listed alongside phenotype information in Supplemental Table 1. Note that, in general, the variants identified as either high confidence or possible contributors to disease are rare (median allele frequency in Table 1 is 2.4 per 100,000) and are predicted damaging by Combined Annotation Dependent Depletion (CADD) score (Kircher et al. 2014) (median in Table 1 is a Phred-scaled CADD score of 29.5 or approximately the top 0.1% most predicted damaging variants in the genome).

Pathogenic or Likely Pathogenic Diagnoses
Variants were first evaluated using ACMG criteria for pathogenicity, and all P/LP variants were returned to patients (Richards et al. 2015). We provide a summary below, with detail on the ACMG evidence codes for variants provided in the Supplemental ACMG Pathogenicity Evidence Details.

An APP Pathogenic Variant in Two Siblings. Two siblings with ages of onset in the mid-to-late 40s and a family history of EOAD suggestive of dominant inheritance harbored a pathogenic variant in APP (NM_000484.3:c.2149G > T, p.(Val717Phe)), a well-established...
| Gene    | Chr | HGVS DNA                  | HGVS protein             | Variant type          | Predicted effect | dbSNP ID     | gnomAD alleles per 100,000 | CADD score |
|---------|-----|---------------------------|--------------------------|----------------------|------------------|--------------|---------------------------|------------|
| APP     | 21  | NM_000484.3:c.2149G > T   | p.(Val717Phe)            | SNV                  | Missense         | rs63750264   | 0                         | 35         |
| C9orf72 | 9   | NM_001256054.1:c.-45 + 163_-45 + 168GGGGCC [24_,?] | NA                       | Insertion            | Repeat expansion | rs143561967 | 0                         | NA         |
| ABCA7   | 19  | NM_019112.3:c.5035G > T  | p.(Glu1679∗)             | SNV                  | Stop gained      | rs770510230  | 1.2                       | 37         |
| APOE    | 19  | NM_000041.3:c.388T > C    | p.(Cys130Arg)            | SNV                  | Missense         | rs429358     | 14254                     | 0.007      |
| APOE    | 19  | NM_000041.3:c.526G > T    | p.(Arg176Cys)            | SNV                  | Missense         | rs7412       | 6538                      | 30         |
| PSEN1   | 14  | NM_000201.3:c.103C > T    | p.(Arg35Trp)             | SNV                  | Missense         | rs746691776  | 5.7                       | 26         |
| ABCA7   | 19  | NM_019112.3:c.2126_2132delAGCAGGG | p.(Glu709fs∗86)         | Deletion             | Frameshift       | rs547447016  | 148                       | 35         |
| ARSA    | 22  | NM_000487.5:c.256C > T    | p.(Arg86Trp)             | SNV                  | Missense         | rs199476352  | 0                         | 34         |
| ARSA    | 22  | NM_000487.5:c.585G > T    | p.(Trp195Cys)            | SNV                  | Missense         | rs6151415    | 6538                      | 27         |
| MAPT    | 17  | NM_000910.5:c.1216C > T   | p.(Arg406Trp)            | SNV                  | Missense         | rs63750424   | 1.6                       | 35         |
| APP     | 21  | NM_000484.3:c.1090G > T   | p.(Leu364Phe)            | SNV                  | Missense         | rs749453173  | 1.4                       | 21.7       |
| GRID2IP | 7   | NM_001145118.1:c.429 + 2T > G | NA                       | SNV                  |                  | rs1413118387 | 0                         | 22.4       |
| CSF1R   | 5   | NM_002511.3:c.2699G > A   | p.(Arg900Lys)            | SNV                  | Missense         | rs149976352  | 0                         | 33         |
| PLD3    | 19  | NM_012268.3:c.694G > A    | p.(Val232Met)            | SNV                  | Missense         | rs145999145  | 325                       | 29.9       |
| APP     | 21  | NM_000484.3:c.742G > A    | p.(Asp248Asn)            | SNV                  | Missense         | rs200103591  | 15                        | 24         |
| ABI3    | 17  | NM_016428.2:c.290T > A    | p.(Val97Glu)             | SNV                  | Missense         | rs14151415   | 5323                      | 27         |
| SORL1   | 11  | NM_003105.5:c.314T > C    | p.(Met105Thr)            | SNV                  | Missense         | rs982581946  | 3.2                       | 23.8       |
| TREM2   | 6   | NM_00018965.3:c.140G > A  | p.(Arg47His)             | SNV                  | Missense         | rs75932628   | 248                       | 33         |
| TREM2   | 6   | NM_00018965.3:c.259G > A  | p.(Asp87Asn)             | SNV                  | Missense         | rs142232675  | 115                       | 22.8       |
| AKAP9   | 7   | NM_000751.4:c.7638A > G   | p.(Ile2546Met)           | SNV                  | Missense         | rs144662445  | 82                        | 0.009      |
| GBA     | 1   | NM_000157.3:c.1448T > C   | p.(Leu483Pro)            | SNV                  | Missense         | rs421016     | 131                       | 24.8       |
| VPS13C  | 15  | NM_020821.2:c.10954C > T  | p.(Arg3652∗)             | SNV                  | Stop gained      | rs138846118  | 18                        | 49         |
| VPS13C  | 15  | NM_020821.2:c.1988delC    | p.(Thr663fs∗2)           | Deletion             | Frameshift       | rs101923842  | 0                         | 35         |
| PLCD1   | 3   | NM_006225.3:c.631C > T    | p.(Arg211Trp)            | SNV                  | Missense         | rs752156828  | 0.4                       | 30         |
| NOTCH3  | 10  | NM_000435.2:c.133C > G    | p.(Asp45His)             | SNV                  | Missense         | rs142031490  | 0.8                       | 27.6       |
| NOTCH3  | 10  | NM_000435.2:c.154G > A    | p.(Gly52Arg)             | SNV                  | Missense         | rs148166997  | 1.2                       | 29.5       |
| MAPT    | 17  | NM_000910.5:c.1174A > G   | p.(Ile392Val)            | SNV                  | Missense         | rs991713081  | 0                         | 24.6       |
| ADAM10  | 15  | NM_001110.3:c.359T > C    | p.(Leu364Phe)            | SNV                  | Missense         | rs144890810  | 4.3                       | 14.35      |
| TTC3    | 21  | NM_001320703.1:c.5677G > A| p.(Val1893Met)           | SNV                  | Missense         | rs377550239  | 3.9                       | 34         |
| SORL1   | 11  | NM_003105.5:c.1247G > A   | p.(Arg416Gln)            | SNV                  | Missense         | rs377550239  | 3.9                       | 34         |
| MME     | 3   | NM_000157.3:c.1448T > C   | p.(Leu483Pro)            | SNV                  | Missense         | rs200103591  | 15                        | 24.6       |
| TM2D3   | 15  | NM_001320703.1:c.5677G > A| p.(Val1893Met)           | SNV                  | Missense         | rs377550239  | 3.9                       | 34         |
| TNK1    | 17  | NM_001151902.3:c.393C > G | p.(His131Gln)            | SNV                  | Missense         | rs767381816  | 0                         | 24.5       |
| KCNC1   | 11  | NM_000218.2:c.552C > T    | p.(Arg518∗)              | SNV                  | Stop Gained      | rs17215500   | 11                        | 39         |

Note that many individuals had multiple candidate contributory variants, which is not captured when considering variants individually. For an expanded table that indicates multiple candidate variants, see Supplemental Table 1. All variants were observed in the heterozygous state except for APOE (NM_000041.3:c.388T > C, p.(Cys130Arg)), which was observed in both the heterozygous and homozygous state. APOE (NM_000041.3:c.388T > C, p.(Arg176Cys)) is also noted here, because confirmation of its absence along with APOE (NM_000041.3:c.388T > C, p.(Cys130Arg)) indicates the APOE ε4 allele.

(HGVS) Human Genome Variation Society, (dbSNP) Single Nucleotide Polymorphism Database, (gnomAD) Genome Aggregation Database, (CADD) Combined Annotation Dependent Depletion, (SNV) single-nucleotide variant.
pathogenic variant (see Supplemental ACMG Pathogenicity Evidence Details). This variant is an example of one that would have been identified on commonly used panels for genetic testing for EOAD.

**C9orf72 Expansion Carriers.** Testing for a pathogenic G_{4}C_{2} hexanucleotide expansion at the C9orf72 locus associated with ALS and FTD was ordered for 30 of 32 patients (with two excluded for technical reasons, see Methods). GeneDx conducted a repeat-primed PCR test with 95% sensitivity and 98% specificity (Akimoto et al. 2014) to detect C9orf72 expansions. As a technical aside, C9orf72 expansions were not detectable using ExpansionHunter (Dolzhenko et al. 2017) or STRetch (Dashnow et al. 2018) in genome sequencing libraries prepared with polymerase chain reaction (PCR) amplification assessed here. ExpansionHunter detects C9orf72 expansions in PCR-free genome preparations (Dolzhenko et al. 2017), so PCR-free genome preparations or secondary testing (such as testing conducted by GeneDx here) is necessary for detection of C9orf72 expansions (and would also be necessary for other repeat expansions). Three patients with FTD (one of whom also had ALS) with ages of onset in the 40s and 50s harbored a pathogenic expansion in C9orf72 (see Supplemental ACMG Pathogenicity Evidence Details).

Some studies have suggested that additional contributing alleles could lower age of onset and/or alter clinical presentation for C9orf72 expansion carriers (van Blitterswijk et al. 2012, 2014; Pottier et al. 2015; Giannoccaro et al. 2017; Farhan et al. 2018). Consistent with this, all three C9orf72 expansion carriers harbored other possibly contributory variants.

One carrier had three additional variants that may be contributory: an “established risk” stop gained variant in ABCA7 (NM_019112.3:c.5035G > T, p.(Glu1679∗)), one APOE ε4 allele, and a VUS in PSEN1 (NM_000021.3:c.103C > T, p.(Arg35Trp)) (see Supplemental ACMG Pathogenicity Evidence Details). These variants may have contributed to the patient’s family history of multiple neurodegenerative diseases including ALS and EOAD.

Another carrier had a different “established risk” variant in ABCA7 (NM_019112.3:c.2126_2132delAGCAGGG, p.(Glu709fs∗86)) (see Supplemental ACMG Pathogenicity Evidence Details), along with memory symptoms and a family history of AD, consistent with a possible contributory role of ABCA7.

The third carrier had two VUSs in ARSA, associated with recessive metachromatic leukodystrophy (discussed further in Supplemental ACMG Pathogenicity Evidence Details).

**A MAPT Pathogenic Variant in Three Alzheimer’s Disease Patients.** Three patients with EOAD (one patient also exhibited FTD signs) with ages of onset in the mid-50s to early 60s harbored a pathogenic variant in MAPT (NM_005910.5:c.1216C > T, p.(Arg406Trp)). Although MAPT pathogenic variants are typically associated with FTD (Cruts et al. 2012), this variant has been reported in patients with clinically diagnosed Alzheimer’s disease (AD) in multiple studies (see Supplemental ACMG Pathogenicity Evidence Details). This variant would not have been detected on many AD-specific panels, which often test for only APP, PSEN1, and PSEN2.

All three of these patients exhibited a possible contribution from another allele, just as in C9orf72 expansion carriers. One patient had a loss-of-function “established risk” variant in ABCA7 (NM_019112.3:c.2126_2132delAGCAGGG, p.(Glu709fs∗86)). Another patient had a VUS in APP (NM_000484.3:c.1090C > T, p.(Leu364Phe)). The third patient had a loss-of-function splice variant in GRID2IP (NM_001145118.1:c.429 + 2T > G), which, although not yet firmly associated with EOAD and thus not yet returnable, was implicated in a recent large sequencing study (Raghavan et al. 2018).

The presence of this rare variant in three individuals enrolled at the same clinic suggests they may share a common ancestor. However, none of these individuals is aware of any extended family members participating in the study. Furthermore, the patients are not detectably related by the software used for routine checks of close familial relationships (KING).
A CSF1R Variant in an FTD Patient. A patient presenting with behavioral variant FTD (bvFTD) harbored a likely pathogenic variant in CSF1R (NM_005211.3:c.2699G > A, p.(Arg900Lys)) (see Supplemental ACMG Pathogenicity Evidence Details). Patients with variants in CSF1R can present with bvFTD, but the underlying pathology of pathogenic CSF1R variants is leukencephalopathy (Rademakers et al. 2011; Stabile et al. 2016). Consistent with this, this patient had white matter abnormalities on MRI, with frontal-predominant confluent white matter hyperintensity (Fig. 2A) and global atrophy (Fig. 2B–D). This variant would not have been detected on typical panels testing for FTD.

High-Impact Risk Alleles

One unique aspect of this study is that we returned to patients moderately penetrant risk variants that meet criteria we have described. Intriguingly, rare variants meeting these criteria were observed only in patients who also carried one or two APOE ε4 alleles, the most common moderately penetrant risk allele for AD (see Supplemental ACMG Pathogenicity Evidence Details). In all cases, APOE ε4 alleles were returned as “established risk variants.” The presence of one APOE ε4 allele was returned as likely only a small contributor to symptoms, whereas the presence of two APOE ε4 alleles or one or two APOE ε4 alleles in
combination with a rare moderately penetrant risk variant was returned with language indicating that such a combination of variants is likely to explain a large portion of the genetic contribution to symptoms (but with the caveat that family members should not be presymptomatically tested given incomplete penetrance). We continue with detail on some cases falling into this category.

**A Case with APOE ε4 Homozygosity along with Variants in PLD3, APP, and ABI3.** In a patient with EOAD whose symptoms began in the late 40s with enrolled unaffected parents, we observed an example of how EOAD may occur from a combination of inherited alleles from each parent, consistent with previous observations that EOAD can appear recessive in nature (Wingo et al. 2012). The patient had two APOE ε4 alleles (returned as “established risk,”) a PLD3 variant (NM_012268.3:c.694G > A, p.(Val232Met)) (returned as “likely risk,”), an APP variant (NM_004844.3:c.742G > A, p.(Asp248Asn)) (returned as a VUS), and a private variant in ABI3 (NM_016428.2:c.290T > A, p.(Val97Glu)) (not returned but predicted damaging by PolyPhen-2 [Adzhubei et al. 2010] and SIFT [Ng and Henikoff 2003], with a CADD score of 33) (see Supplemental ACMG Pathogenicity Evidence Details). The ABI3 variant was not returned to the patient because of insufficient evidence to consider the variant as a returnable VUS or risk variant, but is highlighted because a different coding variant in ABI3 (NM_012268.3:c.1124T > C, p.(Ser209Phe)) (Sims et al. 2017) was associated with AD in a rigorous case-control study with an odds ratio of 1.4, yet is not predicted to be as damaging (CADD = 13.5) and is relatively common in population databases (allele frequency of 0.6%). Therefore, we speculate that perhaps the variant we observed could have an effect of similar or greater magnitude given its higher predicted deleteriousness and absence from population databases. One of the APOE ε4 alleles with the variants in PLD3 and APP was inherited from a parent with neurologic symptoms but not EOAD. The other parent harbored an APOE ε4 allele and the ABI3 variant and did not have neurologic symptoms. This case serves as an example of how EOAD may arise with either no family history or limited family history of late-onset disease.

**A Case with APOE ε4 Heterozygosity and a SORL1 Variant.** An individual with EOAD with onset in the mid 50s and a strong family history of AD had one APOE ε4 allele and a variant in SORL1 (NM_003105.5:c.314T > C, p.(Met105Thr)). Although SORL1 variants are not completely penetrant, loss-of-function variants in SORL1 confer one of the highest levels of risk for AD outside of dominant pathogenic variants and APOE. Loss-of-function SORL1 variant carriers in cases from a recent study (Raghavan et al. 2018) are present at an odds ratio of ~4 compared to population databases, a likely underestimate given that some individuals in population databases may develop AD. Indeed, a recent meta-analysis suggests the odds ratio for loss-of-function SORL1 variants could be as high as 12.3 for all AD and 27.5 for EOAD (Campion et al. 2019).

For the SORL1 variant identified here, we checked independent data sets for replication, and observed one M105T carrier in one study (Sassi et al. 2016), three M105T carriers in Alzheimer’s Disease Sequencing Project (ADSP) exomes (Bis et al. 2018), and two M105T carriers in ADSP genomes (one in an AD case and in one a mild cognitive impairment case) with no controls harboring the variant in any of these data sets. No other carriers were identified in cases or controls in four other studies (see Supplemental ACMG Pathogenicity Evidence Details). In addition to these four studies, there is one record in ClinVar from GeneDx (RCV000489328.1), but it lacked a denominator of the number of cases tested and thus was not considered in calculating the replication statistic. Taken together, SORL1 M105T is observed six times out of 13,390 AD cases compared to 11 of 189,196 individuals at a population level for a replication-only odds ratio of 7.7 (P = 0.0005 by Fisher’s exact test). This variant did not completely segregate with disease in four family members of our patient. However, the age-of-onset range for similar variants in SORL1 can be up to 24 yr
(Louwersheimer et al. 2017), which is wider than the age differences between the family members we genotyped, suggesting that this segregation analysis may not be completely informative. Considering all of the evidence, we returned this variant to the patient as a VUS (it could also be considered a “likely risk variant”). Modeling suggests M105T is a highly conserved residue (Fig. 3A) in which change to a threonine may create a PLK1 kinase site that may disrupt function (Fig. 3B) (discussed further in Supplemental ACMG Pathogenicity Evidence Details).

Figure 3. Molecular modeling of the effect of the M105T variant on SORL1. (A) Conservation analysis of the SORL1 gene sequence was performed across open reading frame sequences of 135 species. Scores at each codon were assessed with 100% conservation receiving a score of 1, with addition of a score for codon selection (score of 0 if dN-dS of site is below mean, 0.25 for sites with values above the mean to one standard deviation above the mean, 0.5 for sites greater than one standard deviation but below two standard deviations, 1 for sites greater than two standard deviations). A score of 2 is maximal, suggesting an amino acid that is 100% conserved with codon wobble indicative of a high selection rate at the position. The values were then placed on a 21-codon sliding window (combining values for 10 codons before and after each position) to identify conserved motifs within the gene. (B) Model of SORL1 protein (assessed with YASARA2). Colors are based on 135 species alignments fed into ConSurf such that colors indicate (gray) not conserved, (yellow) conserved hydrophobic, (red) conserved polar acidic, (blue) conserved polar basic, (green) conserved hydrophilic. Note that the M105T variant leads to a predicted gain of a PLK1 kinase target site in SORL1.
APOE ε4 with TREM2, AKAP9, and GBA Risk Variants. In two cases with EOAD beginning in the late 40s, we observed a risk allele in TREM2 and one or two APOE ε4 alleles. The first was TREM2 (NM_018965.3:c.140G > A, p.(Arg47His)) (Guerreiro et al. 2013; Jonsson et al. 2013) with one APOE ε4 allele. This TREM2 variant was returned as an “established risk variant.” Second, we observed TREM2 (NM_018965.3:c.259G > A, p.(Asp87Asn)) (Guerreiro et al. 2013) (see Supplemental ACMG Pathogenicity Evidence Details) with two APOE ε4 alleles. This TREM2 variant was returned as a “likely risk variant.”

In an African–American patient with features of both EOAD and FTD, we observed two APOE ε4 alleles along with a variant in AKAP9 previously reported to increase risk in African–Americans (NM_005751.4:c.7638A > G, p.(Ile2546Met)) (Logue et al. 2014). In this case, despite being observed in only one study with replication, the specificity of this variant disease association to African–American ethnicity and additional functional data (Ikezu et al. 2018) provided enough evidence to return this as an “established risk variant.”

A patient with EOAD with onset in the mid-50s harbored GBA (NM_000157.3:c.1448T > C, p.(Leu483Pro) [previous nomenclature, p.(Leu444Pro)]) and two APOE ε4 alleles, originally associated with Lewy body disorders (Mata et al. 2008), but later also with mixed dementia with Lewy bodies and AD (Tsuang et al. 2012; Nalls et al. 2013). Because of this and a recent association with accelerated cognitive decline (Liu et al. 2016), we returned this as a “likely risk variant.”

VPS13C Predicted Loss of Function with APOE ε4. A patient with mixed symptoms of AD and FTD with onset in the late 60s harbored VPS13C (NM_020821.2:c.10954C > T, p.(Arg3652*)) and two APOE ε4 alleles. A patient with EOAD with onset in the late 40s had VPS13C (NM_020821.2:c.1988delC, p.(Thr663fs*)) and one APOE ε4 allele. Only APOE ε4 was reported back to these patients because of uncertain contribution of the other variants to the phenotype. Homozygous loss of VPS13C is associated with early-onset Parkinson’s (Schormair et al. 2018). We do not know the significance of the observation of one loss-of-function allele here, although unpublished studies have reported an association between heterozygous loss of function in VPS13C and FTD (see Supplemental ACMG Pathogenicity Evidence Details). PLCD1 was proposed as a candidate gene for AD in one study (Shimohama et al. 1998). Observing two loss-of-function variants in VPS13C in this small cohort leads us to speculate that heterozygous loss-of-function variants in VPS13C may contribute to early-onset dementia.

Variants of Uncertain Significance or Research Interest

Five other patients harbored interesting—but speculative—VUSs or combinations of variants of interest for future research. These include (1) a patient with possible CADASIL and a haplotype of uncertain significance with two variants in NOTCH3 (NM_000435.2:c.133G > C, p.(Asp45His)) and NM_000435.2:c.154G > A, p.(Gly52Arg)), (2) a patient with a VUS in MAPT (NM_005910.5:c.1174A > G, p.(Ile392Val)), (3) a patient with an APOE ε4 allele and a variant in both ADAM10 (NM_001110.3:c.359T > C, p.(Ile120 Thr)) and TTC3 (NM_001001894.2:c.5557G > A, p.(Val1893Met)), (4) a patient with an APOE ε4 allele, and a variant in both SORL1 (NM_003105.5:c.1247G > A, p.(Arg416Gln)) and MME (NM_007289.2:c.1241A > G, p.(Tyr414Cys)), and (5) a patient with variants in TM2D3 (NM_078474.2:c.206C > T, p.(Pro69Leu)) and TNK1 (NM_001251902.1:c.393C > G, p.(His131Gln)). Furthermore, one patient harbored a secondary pathogenic variant in KCNQ1 (NM_000218.2:c.1552C > T, p.(Arg518*)). We expand on these cases in the Supplemental ACMG Pathogenicity Evidence Details.

Quantitative Enrichment of Multiple Alleles

Because we observed so many cases harboring multiple established alleles, we asked if this effect was statistically enriched over a control population recruited from the same
geographical area, with controls reporting a family history of dementia excluded. These controls are healthy unaffected parents from a childhood disease study in which de novo mutations are the most common cause of disease (Bowling et al. 2017), making these parents reasonably representative population controls. Genome sequencing data from these controls was produced in the same manner (depth, sequencing technology, processing pipelines, etc.) as the primary data for this study. We set criteria for qualifying variants as follows: (1) TREM2 or GBA missense or loss-of-function variants with CADD > 20 and population frequency <0.5% in both gnomAD (Lek et al. 2016) and TOPMed Bravo (NHLBI 2018), (2) ABCA7, SORL1, Tbk1, or GRN loss-of-function variants with CADD > 20 and population frequency <0.5%, (3) the specific PLD3 and AKAP9 variants observed here because their associations are for single alleles, (4) missense-only variants with CADD > 20 and population frequency <0.5% for SORL1, CSF1R, APP, PSEN1, PSEN2, and MAPT, (5) expansion carriers in C9orf72, and (6) APOE ε4 alleles. We recognize that this may contain bias because these filtering criteria were selected after analysis of cases. However, we attempted to mitigate this by selecting reasonable thresholds that would catch variants not identified in this study but that would still have been considered if they had been identified. For example, we did not observe any variants meeting these criteria in Tbk1 or GRN but included them here because of their important role in disease. We also included C9orf72 carriers without information on if any are present in the control population, but this is a reasonable assumption (see Supplemental ACMG Pathogenicity Evidence Details).

Variants meeting the criteria described are highly enriched in cases, whereas unaffected family members are intermediate between cases and population controls (Fig. 4A). Intriguingly, there is no enrichment of APOE ε4 alleles in the absence of other qualifying alleles in this cohort for cases versus population controls, although the distribution of APOE ε4 alleles is detectably different between population controls and unaffected family members (Fig. 4B). In contrast, the presence of APOE ε4 alleles in combination with another qualifying variant is highly enriched in cases (and also enriched in unaffected family members), regardless of whether Mendelian variants are included in the calculation (Fig. 4C) or excluded (Fig. 4D). The odds ratios for APOE ε4 alleles in combination with another qualifying variant in cases without a Mendelian cause versus population controls suggests that the presence of rare variants increases odds ratios approximately multiplicatively over those typically reported for APOE ε4 alone (typically reported: ~2.5 for one APOE ε4 allele, with a rare variant, 5.5; 10–15 for two APOE ε4 alleles, with a rare variant, 39.1), see Supplemental ACMG Pathogenicity Evidence Details on APOE (Fig. 4D).

Because we observed a clear enrichment of multiple qualifying alleles in cases versus controls, we asked if multiple qualifying alleles were associated with a lower age of onset. Age at onset did not significantly correlate with number of implicated alleles (numbers based on qualifying variants used for Fig. 4), but trends were in the direction of lower age of onset with more implicated alleles (Spearman’s r = −0.2189, P = 0.2288 for all alleles [Supplemental Fig. 1A], Spearman’s r = −0.3664, P = 0.0856 when excluding cases with Mendelian contributors [Supplemental Fig. 1B]). Because the small number of samples in this study may lead to a false-negative observation, we analyzed data from the Alzheimer’s Disease Sequencing Project (2208 cases), and age at enrollment did significantly correlate with implicated alleles based on the same filtering criteria (Spearman’s r = −0.2072, P < 0.0001 [Supplemental Fig. 1C]).

DISCUSSION

One key theme in this study was the frequent observation of multiple possible contributory alleles. We even observed this in multiple cases with clear, highly penetrant, pathogenic
variants despite a small cohort size. The degree to which additional alleles contribute in dominant cases cannot be assessed without larger cohorts to evaluate effects on age of onset or other variables. However, given that other studies have made similar observations in ALS/FTD (van Blitterswijk et al. 2012, 2014; Pottier et al. 2015; Giannoccaro et al. 2017; Farhan et al. 2018), this phenomenon clearly warrants further investigation.

In cases in which a dominant pathogenic variant was not present, there was enrichment for multiple established alleles outside of APOE ε4 homozygosity alone contributing to disease risk. Although the odds ratios for this observation are compelling (5.5 for an established rare risk variant along with one APOE ε4 allele and 39.1 for an established rare risk variant along with two APOE ε4 alleles; Fig. 4D) we recognize that the small sample size in this study limits their interpretability. Future studies with larger sample sizes, and ideally future studies

Figure 4. Multiple variants in neurodegeneration-associated genes are often observed in early-onset dementia, with a critical role for rare variants acting in combination with APOE ε4. Note that for all panels, ε4/ε4 indicates either ε4/ε3 or ε4/ε2 (mostly ε4/ε3). Also for all panels, cases N = 31 (32 probands excluding 1 sibling from an affected sibling pair), controls N = 542, and unaffected family members of cases N = 29. All comparisons are by exact conditional Cochran–Armitage trend test unless otherwise specified. (A) Qualifying candidate alleles associated with neurodegeneration (see text for criteria) are highly enriched in cases (P = 9.2 × 10⁻¹²). Unaffected family members are intermediate between cases and controls (P = 0.001 vs. cases, P = 0.001 vs. controls). (B) Presence of APOE ε4 alone, in the absence of any other qualifying variants, is not enriched in cases (P = 0.57). Unaffected family members show a significantly different APOE ε4 allele distribution from controls (P = 0.026) but not cases (P = 0.97). (C) Presence of APOE ε4 along with at least one qualifying rare variant (including Mendelian variants) is highly enriched in cases (P = 1.0 × 10⁻⁹). Enrichment over controls is also observed in unaffected family members (P = 5.6 × 10⁻⁴), but unaffected family members are not statistically distinguishable from cases (P = 0.055). (D) Presence of APOE ε4 along with at least one qualifying rare variant (excluding Mendelian variants) is highly enriched in cases (P = 1.4 × 10⁻⁶) and also enriched in unaffected family members (P = 5.6 × 10⁻⁴), but unaffected family members are not distinguishable from controls (P = 0.84). The odds ratio for presence of one APOE ε4 allele along with one qualifying rare variant in cases versus controls is 5.5 (P = 0.01 by Fisher’s exact test, 95% CI 1.2–19.3). The odds ratio for presence of two APOE ε4 alleles along with one qualifying rare variant in cases versus controls is 39.1 (P = 9.8 × 10⁻⁵ by Fisher’s exact test, 95% CI 5.3–447.5).
with a prospective design, are required to more precisely determine the effect of presence of multiple established risk alleles on lifetime risk for dementia.

The observation that unaffected family members exhibited either an intermediate number of possibly contributory variants or an enriched number compared to population controls, but not distinguishable from cases, is expected for moderate-penetrance variants and highlights why we strongly emphasize not pursuing testing for unaffected family members when we return risk variant information. Possible explanations for why unaffected family members do not exhibit segregation include known incomplete penetrance of risk alleles, other genetic contributors not currently annotated as conferring risk, environmental influences, and variable age of onset (i.e., some currently unaffected family members may go on to develop disease in the future, as age-of-onset spreads with risk alleles can be as high as 24 yr [Louwersheimer et al. 2017]).

Every case with a moderately penetrant risk variant established by case-control studies identified in this cohort also harbored one or two \(\text{APOE}\varepsilon4\) alleles, emphasizing the importance of \(\text{APOE}\varepsilon4\). In addition, although detectable differences were minimal between cases and unaffected family members, no unaffected family members harbored two \(\text{APOE}\varepsilon4\) alleles along with a qualifying rare variant. That observation, along with the high odds ratio versus population controls (39.1; Fig. 4D), suggests a well-established rare variant contributor along with two \(\text{APOE}\varepsilon4\) alleles confers a high level of risk, and that individuals harboring such a combination of variants should be closely monitored.

Future efforts in the analysis of large cohorts should include analysis of level of risk when rare risk variants are present—for example, by incorporation of signal from rare variation in established risk genes into polygenic risk scores. Several groups have begun developing polygenic risk scores for AD (Escott-Price et al. 2015; Desikan et al. 2017), but these scores are based solely on common variation. This is, of course, a reasonable approach because it maximizes reproducibility, as considering rare variants could lead to an overtrained model. However, although rare variants are rare individually, aggregation approaches may provide replicable and meaningful signals if incorporated for key genes in which rare variants are now established to confer risk for AD, such as \(\text{ABCA7}\), \(\text{SORL1}\), and \(\text{TREM2}\).

This study adds support for an oligogenic model in cases of early-onset dementia, emphasizing that comprehensive genetic approaches are valuable for research studies and could hold value clinically in the future. Mendelian diagnostic yield in this population was 28%, with an additional 22% of patients harboring risk-increasing variants that, in combination with \(\text{APOE}\varepsilon4\), likely account for most of the genetic contribution to their symptoms. Genome sequencing is able to identify relevant variation in conditions with high genetic heterogeneity, nonspecific phenotypes, or established risk factors that do not follow a clear Mendelian pattern, and allowed for the identification of cryptic genotype-phenotype relationships that likely would have been missed by panel testing. However, we note that for future studies, substantially more samples could be evaluated for lower cost using arrays with high coverage of neurodegeneration associated variants and/or targeted sequencing of more comprehensive panels with known genes associated with neurodegenerative diseases (both of which are commercially available) if the goal is not to discover new variants, but to more precisely measure the level of risk when multiple established risk variants are present. This lower cost would be helpful for case-control studies but would be especially important in a prospective study design in which the hit rate for carriers of multiple risk variants outside of \(\text{APOE}\varepsilon4\) homozygosity is expected to be low. For example, only 3.0% of controls in this study harbor multiple contributory alleles meeting the criteria we described for inclusion in
Figure 4D outside of APOE ε4 homozygosity (which contributes an additional 3.3%). In addition to potential prospective studies that would benefit from rare variant information, efforts are currently ongoing to recruit patients for clinical trials based on APOE ε4 status (Langbaum et al. 2019). Incorporation of information about established rare variant risk factor status could be helpful for efforts such as these.

In addition to the research value of this study, it had value for patient care as well—for example, by allowing for referral of families to the Dominantly Inherited Alzheimer’s Network and studies such as the ALLFTD study (a natural history study of FTD) if an actionable variant was identified. Furthermore, although return of risk variants to patients is controversial, in this study we qualitatively observed that patients and their caregivers were generally appreciative of receiving findings even if they were not definitive. We acknowledge that our study conditions were ideal for such an observation: The clinicians involved were deeply knowledgeable about genetic contributions to dementia and the role of risk variants, and the patients were informed at study enrollment and at return of results about limitations of risk variant observations if they were identified. Furthermore, participants had access to genetic counseling services through the study to help clarify the potential significance of results. Future studies to quantitatively evaluate clinician, patient, and caregiver responses to risk variant information are needed. We conclude that application of more comprehensive genetic assessment (including genome sequencing, if appropriate) could aid in interpretation of early-onset dementia cases currently and will continue to grow in utility as future studies designed to both more comprehensively define levels of risk based on the presence of multiple risk alleles and also to study clinician, patient, and caregiver responses to such information are conducted.

METHODS

Genome Sequencing
Genome sequencing was performed at the HudsonAlpha Institute for Biotechnology on Illumina HiSeq X or NovaSeq platforms using paired end 150-base pair reads. Mean depth was 38× with an average of 89.0% of bases covered at 20× (a full sequencing coverage table is available in Supplemental Table 2). Sequencing libraries were prepared by Covaris shearing, end repair, adapter ligation, and PCR using standard protocols. Library concentrations were normalized using KAPA qPCR prior to sequencing. All sequencing variants returned to patients were validated by Sanger in a CAP/CLIA laboratory.

Data Processing and Quality Control
Demuxed FASTQs were aligned with bwa-0.7.12 (Li and Durbin 2009) to hg19. BAMs were sorted and duplicates were marked with Sambamba 0.5.4 (Tarasov et al. 2015). Indels were realigned, bases were recalibrated, and gVCFs were generated with GATK 3.3 (McKenna et al. 2010). gVCFs were batch-called with GATK 3.8. KING 2.1.2 (Manichaikul et al. 2010) was used for sex checks on VCFs, for validation of known familial relationships, and to check for unknown familial relationships (none of which was identified).

C9orf72 Expansion Testing
Samples from 30 of 32 patients were tested for pathogenic C9orf72 repeat expansion alleles by GeneDx. Two patients did not have sufficient material for testing, but both lacked symptoms consistent with a C9orf72 repeat expansion and also had another likely explanation of symptoms: One had a pathogenic APP variant and another harbored both one APOE ε4 allele and a TREM2 established risk allele.
Genomic Data Analysis

The HudsonAlpha-developed Codicem application (http://envisiongenomics.com/codicem-analysis-platform/) was used to analyze and support the interpretation of the variant data (described elsewhere [Holt et al. 2019]). Although this software package was used for analysis, it would not be necessary to use this package to reproduce this work. Simple filtering for population allele frequencies (i.e., gnomAD [Lek et al. 2016] and TOPMed Bravo [NHLBI 2018]), in silico deleteriousness scores (i.e., CADD [Kircher et al. 2014], PolyPhen-2 [Adzhubei et al. 2010], and SIFT [Ng and Henikoff 2003]), and gene lists relevant to the phenotype of interest would recapitulate our findings using any suitable software package or even by a command line interface.

In addition to searching for single-nucleotide variants and small indels, we also searched for large copy-number variations using four callers (DELLY [Rausch et al. 2012], ERDS [Zhu et al. 2012], CNVnator [Abyzov et al. 2011], and BIC-seq2 [Xi et al. 2016]), but did not identify any relevant to patient phenotypes (including absence of APP duplications).

SORL1 Structural Modeling

SORL1 structural modeling and evolutionary conservation analysis was assessed using a previously published sequence-to-structure-to-function workflow (Prokop et al. 2017).

Statistics

The exact conditional Cochran–Armitage trend test was calculated using the CATTexact 0.1.0 package and Fisher’s exact test using fisher.test in R 3.4.1. Spearman correlations were calculated with GraphPad Prism 8.2.1.

Return of Results

Results meeting criteria for return were delivered to patients by clinicians in the UAB Memory Disorders Clinic through letters written by a genetic counselor. Letters included information on the variant, associated disease, recurrence risk, and management recommendations. Patients were given the option to have a genetic counselor present for return of results via phone or videoconference or to follow up with a genetic counselor after delivery of results. Primary results were provided only to probands. Although a secondary result was identified in only one participant who was a patient, we did also offer nonpatient participants (family members) receipt of actionable secondary findings (ACMG 59) if such a result had been identified. Family members of patients that received diagnostic results were provided with information to seek out clinical genetic counseling and targeted testing for familial variants if they desired.

ADDITIONAL INFORMATION

Data Deposition and Access

All data from participants enrolled as a part of this study, including more detailed phenotype data for the cases described here, are available on the National Institute on Aging Genetics of Alzheimer’s Disease Data Storage (NIAGADS) site (https://www.niagads.org/) under project NG00082. Data from control subjects not enrolled as a part of this study are available under dbGaP (https://www.ncbi.nlm.nih.gov/gap/) accession phs001089.v3.p1, which contains data generated by the Clinical Sequencing Exploratory Research (CSER) Consortium established by the National Human Genome Research Institute (NHGRI). Funding support for CSER was provided through cooperative agreements with the NHGRI and the National Cancer Institute (NCI) through grant numbers U01 HG007301 (Genomic Diagnosis in
Children with Developmental Delay). Information about CSER and the investigators and institutions who comprise the CSER consortium can be found at https://cser-consortium.org. ADNI (Alzheimer’s Disease Neuroimaging Initiative, part of the ADSP genomes batch call) and ADSP data are available at NIAGADS under projects NG00066 and NG00067 and on dbGaP under accession phs000572.v7.p4 (see Supplemental Extended Acknowledgements for full list of ADNI and ADSP contributors and funding sources). All variants described here are deposited in ClinVar (http://www.ncbi.nlm.nih.gov/clinvar/) under accession numbers VCV00018089.2, VCV00031151.1, VCV000666796.1, VCV000666796.1, VCV000093125.1, VCV000068126.1, VCV000120224.1, VCV000426729.2, VCV000195350.1, VCV000261064.1, VCV000136339.1, VCV000042883.3, VCV000447782.1, VCV000447788.1, VCV0003131.6, and submission SUB6475528.

Ethics Statement
This study was approved by UAB IRB protocol X161202004, “Evaluation of Genomic Variants in Patients with Neurologic Diseases.” All participants described provided explicit written consent for publication.

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Authors’ Contributions
J.N.C., G.M.C., R.M.M., and E.D.R. designed the study. J.N.C. and R.M.M. secured funding. J.N.C. and E.D.R. wrote the IRB protocol. E.C.M. coordinated all aspects of patient interaction. J.N.C., M.D.A., B.A.M., and B.N.L. analyzed genomes with input from M.C., E.C.M., and E.D.R. M.D.A. coordinated C9orf72 testing. J.N.C., D.E.G., J.M.J.L., J.W.P., E.G.G., J.M.H., and J.S.N. conducted other analyses. M.C. wrote clinical letters and provided genetic counseling. M.L.T provided phenotype information for controls. J.S.Y. accessed ADSP and supervised E.G.G. E.A.W. supervised J.M.H., J.S.N., and the software development team. E.D.R., D.S.G. and M.N.L. recruited participants and returned results. G.M.C. supervised D.E.G., J.M.J.L., and M.L.T. J.N.C. wrote the manuscript, with edits by E.C.M., M.C., M.D.A., B.A.M., B.N.L., J.W.P., E.G.G., J.M.H., E.A.W., G.M.C., and E.D.R. All authors approved the final manuscript.

Competing Interest Statement
The authors have declared no competing interest.

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