**SORL1** mutations in early- and late-onset Alzheimer disease

**ABSTRACT**

**Objective:** To characterize the clinical and molecular effect of mutations in the sortilin-related receptor (**SORL1**) gene.

**Methods:** We performed whole-exome sequencing in early-onset Alzheimer disease (EOAD) and late-onset Alzheimer disease (LOAD) families followed by functional studies of select variants. The phenotypic consequences associated with **SORL1** mutations were characterized based on clinical reviews of medical records. Functional studies were completed to evaluate β-amyloid (**Aβ**) production and amyloid precursor protein (**APP**) trafficking associated with **SORL1** mutations.

**Results:** **SORL1** alterations were present in 2 EOAD families. In one, a **SORL1** T588I change was identified in 4 individuals with AD, 2 of whom had parkinsonian features. In the second, an **SORL1** T2134 alteration was found in 3 of 4 AD cases, one of whom had postmortem Lewy bodies. Among LOAD cases, 4 individuals with either **SORL1** A528T or T947M alterations had parkinsonian features. Functionally, the variants weaken the interaction of the **SORL1** protein with full-length **APP**, altering levels of **Aβ** and interfering with **APP** trafficking.

**Conclusions:** The findings from this study support an important role for **SORL1** mutations in AD pathogenesis by way of altering **Aβ** levels and interfering with **APP** trafficking. In addition, the presence of parkinsonian features among select individuals with AD and **SORL1** mutations merits further investigation. *Neural Genet* 2016;2:e116; doi: 10.1212/NXG.0000000000000116

**GLOSSARY**

- **AAO** = age at onset; **Aβ** = β-amyloid; **AD** = Alzheimer disease; **APP** = amyloid precursor protein; **APPβ** = APP soluble β-secretase; **APPβs** = Swedish APP mutant; **EOAD** = early-onset Alzheimer disease; **ER** = endoplasmic reticulum; **FL-APP** = full-length APP; **HIHG** = John P. Hussman Institute for Human Genomics; **LOAD** = late-onset Alzheimer disease; **PD** = Parkinson disease; **SORL1** = sortilin-related receptor; **WES** = whole-exome sequencing.

Alzheimer disease (AD) is the leading cause of dementia in the elderly. Multiple genes have been implicated in risk for both late-onset Alzheimer disease (LOAD; onset >65 years of age) and early-onset Alzheimer disease (EOAD; onset <65 years of age) including the sortilin-related receptor (**SORL1**) gene. Located on chromosome 11q23.2-q24.2, **SORL1** influences the differential sorting of the amyloid precursor protein (**APP**) and regulation of β-amyloid (**Aβ**) production, making it biologically plausible for AD risk. Compelling evidence for the involvement of **SORL1** in AD comes from a large meta-analysis of >30,000 individuals, which confirmed that variants in **SORL1** are associated with AD risk. 

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Furthermore, whole-exome sequencing (WES) has identified potentially damaging SORL1 mutations in patients with both EOAD and LOAD.\(^{11,12}\) Of note, a WES study of a large EOAD cohort found a greater frequency of predicted damaging missense SORL1 variants in cases vs controls, with this effect enriched among cases with a positive family history.\(^{13}\) Clearly, rare coding variants in SORL1 are tied to risk for EOAD and LOAD. Finally, while SORL1 mutations have been reported in multiple patients with AD, there has been little investigation of clinical phenotypes beyond dementia and age at onset (AAO) among these individuals.

For this study, we examined well-characterized EOAD families using WES to discover AD risk genes. Our efforts focused on clinical characterization of individuals with SORL1 alterations and investigation of the functional effect of the identified SORL1 alterations in a series of gene overexpression experiments.

**METHODS** Standard protocol approvals, registrations, and patient consents. All participants ascertained for this study gave written informed consent prior to their inclusion. If an individual was not competent to give consent, the immediate next of kin or a legal representative provided written consent on their behalf. All participants were ascertained using a protocol that was approved by the appropriate Institutional Review Board. Oversight of this study falls under the University of Miami Institutional Review Board #20070307.

Sources of participants. EOAD families were ascertained as part of a larger study on AD genetics whose participants were enrolled under protocols previously described.\(^{4,15}\) Individuals were ascertained for this study after they provided informed consent at the John P. Hussman Institute for Human Genomics (HIHG) at the University of Miami Miller School of Medicine (Miami, FL). The majority of these families were self-reported non-Hispanic whites (N = 47); the remaining families were self-reported African Americans (N = 3). Clinical data from cognitively impaired individuals, including any that changed affection status, were evaluated by the HIHG AD clinical staff which includes a psychiatrist, neurologist, and neuropsychologist. Familial EOAD cases were defined as AAO <65 years of age. As reported in previous studies, AAO was defined as the age at which an individual or family historian reported onset of significant cognitive problems that interfered with normal activity, or the AAO of problems as documented in the medical record.\(^{15}\) All affected individuals met the internationally recognized standard NINCDS-ADRDA criteria.\(^{16,17}\) The cognitive status of participants was measured using either the Mini-Mental State Examination\(^{18}\) or the Modified Mini-Mental State.\(^{19}\)

Patients with LOAD (N = 151) were part of a study investigating coding mutations in SORL1 in AD.\(^{11}\) These patients were drawn from a larger study of AD genetics restricted to Caribbean Hispanics. All affected individuals were of Caribbean Hispanic ancestry. All participants were assessed using standard clinical examinations and cognitive testing as described elsewhere.\(^{20}\) For this study, we reviewed the clinical records of participants who had SORL1 mutations to assess for possible features of Parkinson disease (PD) or more broadly, parkinsonism.

**WES and variant calling.** All samples were prepared using DNA extracted from the blood. Genomic DNA was then sheared and processed using the SureSelect Human All Exon 50 Mb v4 capture kit (Agilent Technologies, Santa Clara, CA) according to the manufacturer’s protocol at the HIHG Center for Genome Technology. After capture, the DNA was tested for uniform enrichment of targets via quantitative PCR. Sequencing was then performed on the Illumina HiSeq2000 at 2× 150 bp paired-end cycles at 40–50× on target depth. Exomes were sequenced to sufficient depth to achieve a minimum threshold of 80% of coding sequence covered with at least 15 reads, based on UCSC hg19 “known gene” transcripts. The mean depth of coverage across SORL1 was 68.

Sequencing data from the Illumina HiSeq2000 were processed using an established semiautomated pipeline. Initial image files were processed using the Firecrest module (Illumina, San Diego, CA) to determine cluster intensities and noise. After initial quality control, BWA-ELAND and CASAVA v1.9 were used for realignment to the human genome version hg19. Results from BWA and CASAVA are then fed into additional software packages (CLC Genomics Workbench and GenomeStudio) for secondary analysis, visualization of the called variants, and browsing of consensus reads.\(^{21,22}\) Genotype calling was performed with GATK Unified Genotyper. Variants were then normalized using BCFTools.\(^{23}\) Single nucleotide polymorphisms with read depth <6, variant quality score log odds ratio <0, and Phred-scaled likelihood score <100 were removed from further analysis. Variants were filtered to identify alterations that were likely to be damaging (missense, splicing, stop-gain, stop-loss, and insertion/deletions) in Gencode v19, NCBI RefSeq, or Ensembl gene annotations.\(^{24,25}\) Variants were screened to determine whether they occurred in a known or suspected EOAD gene (APP, GRN, MAPT, PSEN1, PSEN2, SORL1, and TREM2). Minor allele frequencies were obtained from the Exome Aggregation Consortium.\(^{26}\)

**Cloning of SORL1 variants.** Site-directed mutagenesis was used to generate the SORL1 T588I and SORL1 T2134I mutation constructs using human SORL1-MYC pcDNA3.1 as a backbone according to the manufacturer’s instructions as previously published.\(^{3,11,27–30}\) Sequencing was used to verify mutant constructs. Cell culture and transfection followed previously described standard protocols.\(^{3,11,27–30}\)

**Aβ, Western blot, and co-immunoprecipitation assays.** Aβ assays were measured by sandwich ELISA assay in culture medium from stably transfected HEK293 cells expressing the Swedish APP mutant (APPsw) and either wild-type SORL1 or mutant SORL1 as previously described.\(^{3,11,27–30}\) Cell surface biotinylation was performed using 1 mg/mL Sulfo-NHS-LC-Biotin (Sigma-Aldrich, St. Louis, MO) for 20 minutes at 4°C to prevent internalization. Cells were then washed and lysed, and biotynlated proteins were precipitated with NeutrAvidin beads (Thermo Fisher Scientific, Waltham, MA). Western blot band intensities were measured with ImageJ software and samples normalized to the wild-type control. Co-immunoprecipitation was performed after cell lysis in 1% CHAPSO buffer,\(^{3}\) using G Plus beads with 2 μg mouse monoclonal anti-c-MYC antibody for the immunoprecipitation of SORL1-myc, immunoblotted with anti-C-terminal APP antibody (Ab365), and anti-C-terminal SORL1 (S9200). Western blot band intensities were
measured with ImageJ software. Full-length (FL) APP coprecipitated with c-MYC antibody was quantified and normalized to the amount of immunoprecipitated SORL1 as previously described.3,11,27–30

**Statistical analyses.** Statistical analyses were performed using Graphpad statistical software (graphpad.com/guides/prism/5/user-guide/prism5help.html; using_tour_overview.htm; GraphPad Prism 5). Analysis of variance and t tests were used to analyze statistical difference, followed by Bonferroni correction (*p < 0.05; **p < 0.01; and ***p < 0.001).

**RESULTS SORL1 variants in EOAD families.** WES identified 10 individuals with SORL1 mutations in 2 unrelated EOAD families (table 1, figure 1). Neuropathology results were available for 1 affected individual. The first family, number 191, has 6 individuals with the predicted damaging SORL1 T588I mutation (rs752726649; C>T); all 4 affected individuals for whom DNA was available were found to carry this variant. These 4 affected individuals had AAOs that ranged from 59 to 82 years. While the progressive cognitive decline of each individual was consistent with dementia, individuals 104 and 111 had also parkinsonian features. Individual 104 began to show cognitive impairment at age 82. On examination, he demonstrated tremor at rest, hypophonia, micrographia, masked facial expression, smaller steps on gait, and overall bradykinesia. Chart review indicated that these symptoms were levodopa/carbidopa responsive. Imaging revealed white matter changes and moderate cerebral atrophy, and EEG was remarkable for a loss of alpha waves. Individual 111 had the earliest AAO in the family at age 59, with diminished memory function in all domains, clinically judged to most likely represent EOAD. When seen by research staff at age 70, the individual was noted to exhibit parkinsonian features. This presentation was confounded by several years of treatment with haloperidol, a typical antipsychotic agent that can cause parkinsonian side effects. Two unaffected individuals in family 191 also carried the SORL1 T588I mutation. These individuals were last examined at ages 81 and 84, respectively. Individuals 116 and 9004 demonstrated a normal cognitive and physical examination.

The second family, number 1240 (table 1 and figure 1), contains 3 affected individuals with the SORL1 T2134M mutation (rs142884576; C>T). These 3 affected individuals had AAOs that ranged from 55 to 84 years. While the clinical examinations revealed no motor abnormalities, there was autopsy evidence for Lewy bodies in individual 1, with the earliest AAO in the family at 55 years. Neuropathologic diagnosis of individual 1 was indicative of Braak & Braak stage IV tangles and limbic Lewy bodies. In addition, 1 individual (119) demonstrated progressive cognitive decline consistent with AD without the T2134M SORL1 mutation. This individual had an AAO of 76 years. Finally, there was 1 unaffected individual (113) with this T2134M SORL1 mutation who was last examined at 79 years of age.

**Parkinsonian features in patients with LOAD with SORL1 variants.** Given the clinical results from these 2 EOAD families, we examined in greater depth the clinical status of previously reported patients with SORL1 changes.11 Review of clinical history and physical examination data identified 4 additional AD individuals, all with LOAD (no neuropathology results were available), and who had evidence of

<table>
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<th>Family-individual</th>
<th>Sex</th>
<th>Affection status</th>
<th>Additional features</th>
<th>AAO/AAE</th>
<th>Base pair position (hg38 assembly)</th>
<th>Nucleotide</th>
<th>Amino acid</th>
<th>dbSNP number*</th>
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<td>—</td>
<td>—</td>
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<td>3/3</td>
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<tr>
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<td>C&gt;T</td>
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<td>3/3</td>
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<tr>
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<td>—</td>
<td>80</td>
<td>121627591</td>
<td>C&gt;T</td>
<td>T2134M</td>
<td>rs142884576</td>
<td>3/3</td>
</tr>
<tr>
<td>1240-111</td>
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<td>Dementia AD</td>
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<td>121627591</td>
<td>C&gt;T</td>
<td>T2134M</td>
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<td>3/3</td>
</tr>
<tr>
<td>1240-113</td>
<td>M</td>
<td>—</td>
<td>—</td>
<td>79</td>
<td>121627591</td>
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<td>76</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>3/4</td>
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</tbody>
</table>

Abbreviations: AAE = age at examination; AAO = age at onset; AD = Alzheimer disease; DLB = dementia with Lewy bodies; PD = Parkinson disease; SNP = single nucleotide polymorphism.

*Minor allele frequencies (MAF): rs752726649 global MAF = 8.2 × 10<sup>−6</sup>; rs142884576 global MAF = 2.2 × 10<sup>−4</sup>. 
parkinsonian features (Table 2). The SORL1 mutations in these 4 individuals were distinct from those identified in the first 2 families. Specifically, 3 individuals which we previously reported carry a common variant at A528T (rs2298813A>G). Clinically, these individuals were diagnosed with both AD and PD and had ages of AD onset ranging from 78 to 84 years. The fourth individual had a different previously reported missense T947M variant (rs143571823, C>T). This individual had a clinical diagnosis of AD and parkinsonism with an age of AD onset at 90 years.

SORL1 variants alter Aβ levels and APP trafficking. Next, we examined the functional consequences of the SORL1 T588I and T2134M alterations identified in the EOAD families; the variants identified in the LOAD individuals (A528T and T947M) were previously assessed and reported.11 To determine the effects on Aβ production by these SORL1 variants, Aβ42 and Aβ40 levels were measured in conditioned media collected from cultured HEK293 cells expressing equivalent levels of wild-type SORL1 protein, SORL1 T588I, or SORL1 T2134M. Both mutants increased Aβ42 secretion compared with the control (T588I: 113% ± 1.6% and T2134M: 117% ± 5.1%, p < 0.05, figure 2A). Overexpression of SORL1 T2134M also increased Aβ40 secretion (167% ± 9.9%, p < 0.001, figure 2B). While the

Table 2: Clinical features in late-onset AD individuals with SORL1 variants

<table>
<thead>
<tr>
<th>Family-individual</th>
<th>Sex</th>
<th>Affection status</th>
<th>Additional features</th>
<th>AAO</th>
<th>Base pair position (hg38 assembly)</th>
<th>Nucleotide</th>
<th>Amino acid</th>
<th>dbsNP number*</th>
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<td>3/4</td>
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<td>Parkinsonian</td>
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<td>A&gt;G</td>
<td>A528T</td>
<td>rs2298813</td>
<td>3/3</td>
</tr>
</tbody>
</table>

Abbreviations: AAO = age at onset; AD = Alzheimer disease; SNP = single nucleotide polymorphism.
*Minor allele frequencies (MAF): rs2298813 MAF = 0.072; rs143571823 MAF = 0.0013.
SORL1 T588I alteration trended toward an increase of Aβ40 secretion in cells, it did not reach statistical significance (131% ± 17.6%, figure 2B).

SORL1 has been proposed to modulate the post-translational biology of APP at several intracellular sites including during transport out of the Golgi and during re-entry and recycling from the cell surface. To examine further the effect of these SORL1 mutants on APP trafficking, we measured APP soluble β-secretase (APPsβ) secretion in a conditioned medium. Both mutations caused an increase in APPsβ secretion compared with the wild-type SORL1 (T588I: 132% ± 6.3%, p < 0.05; T2134M: 140% ± 9.4%, p < 0.05, figure 2C). Both mutations also increased production of the soluble α-secretase cleavage product compared with control cells (T588I: 207% ± 15.8%, p < 0.01; T2134M: 223% ± 29.6%, p < 0.05, figure 2D). These observations suggest that in the presence of these SORL1 mutants, APP is neither retained efficiently in the Golgi nor effectively retrieved from the cell surface into recycling pathways. This could result in additional APP lingering at the cell surface. This hypothesis was supported by surface biotinylation experiments which revealed that both SORL1 mutants increased the amount of surface APP compared with the control (T588I: 143% ± 13.1%, p < 0.05; T2134M: 138% ± 7.5%, p < 0.05, figure e-1 at Neurology.org/ng).

SORL1 variants decrease APP binding. To understand the mechanism by which these SORL1 mutants might alter APP trafficking at the cell surface, we next measured levels of SORL1 protein at the cell surface. The T588I variant showed essentially normal levels of SORL1 both at the cell surface and in total cell lysates (∼87% ± 13.1% of control value, figure e-1). However, while the T2134M mutant showed normal levels of total cellular SORL, there were decreased amounts of surface SORL1 (∼25%, p < 0.05, figure e-1B).
Previous work by us and others have demonstrated that SORL1 directly binds APP and regulates its sorting into secretory, endocytic, or recycling pathways. To assess whether the SORL1 T588I and T2134M mutations might alter the binding affinity of SORL1 to APP, we immunoprecipitated SORL1 from whole cell lysates using an anti-myc antibody directed to the myc epitope on the exogenous SORL1 protein. This strategy circumvents possible risk that the SORL1 mutants might alter binding affinity of anti-SORL1 antibodies, or that endogenous SORL1 might be pulled down in addition to overexpressed SORL1 in the mutant APPsw cell lines. We then measured the amount of FL-APP that co-immunoprecipitated with the myc-tagged SORL1 proteins and expressed the binding as a normalized ratio of the abundance of coprecipitated FL-APP relative to the abundance of immunoprecipitated SORL1. Both mutations caused reductions in APP binding (T588I: ~77.1% ± 5.8%, p < 0.05; T2134M: ~61.5% ± 8.3%, p < 0.05, figure 3).

**DISCUSSION**

In this study, we identified SORL1 alterations in EOAD families thus confirming previously reported studies showing a role for SORL1 in risk for EOAD. Furthermore, we presented functional evidence that these SORL1 alterations are pathogenic.

Evidence for functional consequences of SORL1 mutations is scant. However, the evidence shown here suggests that the variants identified in the EOAD families, SORL1 T588I and T2134, weaken the interaction of SORL1 with FL-APP. This can culminate in excessive APP accumulating at the cell surface either due to failure of the mutant SORL1 to slow trafficking of APP to the cell surface or failure of mutant SORL1 to retrieve FL-APP into the retromer-recycling endosome pathway. Our result agrees with prior work which suggests that some SORL1 mutants cause reduced trafficking of the mutant SORL1 protein from the endoplasmic reticulum (ER)/Golgi network to the cell surface. The resulting misdirection of more APP into the late endosome pathway exposes the APP to β-secretase and γ-secretase cleavage, with the consequent increase in Aβ production, especially Aβ42. Intriguingly, but consistent with prior work, our data suggest that the molecular mechanisms underlying this common overall effect differ between the 2 variants. Thus, the T2134M mutant, which is located close to the transmembrane domain (figure 1), appears to disrupt trafficking of SORL1 to the cell surface, presumably due to its removal from the ER-Golgi secretory pathway by the ER quality control systems which remove misfolded proteins. In contrast, the T588I mutant survives the ER quality control mechanisms, but appears to be less efficient than wild-type SORL1 in binding to APP. The molecular mechanism for the reduced binding of T588I is unclear, but may relate to subtle changes in the fold of the extracellular domain of SORL1 such that putative APP-binding sites in VPS10 and/or in complement type repeat domains. Crucially, while they may have different underlying molecular mechanisms, the net effect of both mutations is the same.

A secondary finding in our study was the observation of additional clinical features beyond AD among select individuals with SORL1 alterations. These clinical findings, based on extensive clinical reviews, included clinical Parkinson-related features and neuropathology-proven Lewy bodies without clinical parkinsonism. While these findings point to
a potential association between SORL1 alterations and a broader spectrum of neurodegenerative disorders, it is important to note that these clinical features were not present in all individuals with SORL1 alterations and may simply represent features of coincidental sporadic PD.

The results from this study demonstrate that select SORL1 variants present in EOAD and LOAD alter Aβ levels and interfere with APP trafficking. In addition, we observed parkinsonian features among some EOAD/LOAD individuals with SORL1 alterations. These clinical findings should be viewed cautiously but suggest the need for exploration of the additional phenotype consequences of SORL1 alterations beyond dementia.

**AUTHOR CONTRIBUTIONS**

M.L.C., R.M.C., B.W.K., and M.A.P.-V. conceived and designed the experiments. M.L.C., R.M.C., R.M., and M.A.P.-V. acquired and assessed participants. P.L.W. and H.N.C. performed custom capture sequencing and exome sequencing. B.W.K., H.N.C., and M.A.P.-V. analyzed the sequencing data. B.W.K. and M.A.P.-V. performed the statistical analysis. Y.Z., C.B., and P.S.G.-H. cloned the SORL1 variants, performed all assays, and analyzed all resulting data. M.L.C. and R.M.C. drafted the manuscript. M.L.C., R.M.C., Y.Z., C.B., B.W.K., H.N.C., P.S.G.-H., and M.A.P.-V. edited the manuscript. The authors jointly discussed the experimental results over the course of the study. All authors read and approved the final manuscript.

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