The role of variation at APP, PSEN1, PSEN2, and MAPT in late onset Alzheimer’s disease

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The Role of Variation at $\alpha\beta$PP, PSEN1, PSEN2, and MAPT in Late Onset Alzheimer’s Disease

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INTRODUCTION

The neuropathological hallmarks of late-onset Alzheimer’s disease (LOAD) are assumed to provide major clues to pathogenesis. These include extracellular plaques, which are predominantly made up of insoluble amyloid-β protein, and neurofibrillary tangles (NFTs), intracellular accumulations of paired helical filaments, which are comprised mainly of hyperphosphorylated forms of the microtubule associated protein, tau [1]. Genes involved in the amyloid pathway and the tau gene, MAPT, have therefore long been considered as putative candidates for involvement in LOAD susceptibility.

Amyloid-β is formed from the cleavage of amyloid-β protein precursor (AβPP) by β- and γ-secretases. Mutations within AβPP, plus presenilin 1 (PSEN1) and presenilin 2 (PSEN2), which encode part of the γ-secretase complex, can cause the autosomal dominant, predominantly early-onset forms of Alzheimer’s disease (EOAD) (Alzheimer Disease & Frontotemporal Dementia Mutation Database; http://www.molgen.ua.ac.be/admutations). These mutations increase cleavage of AβPP by β-secretase [4]. In addition, 185 PSEN1 and 13 PSEN2 pathogenic mutations have been observed in EOAD patients which increase γ-secretase cleavage of AβPP [4].

Genetic variation at the MAPT locus has been convincingly associated with an increased risk of the sporadic tauopathies progressive supranuclear palsy (PSP) and corticobasal degeneration (CBD) [5]. The associations reported include several polymorphisms that span the MAPT locus and which are in high linkage disequilibrium (LD). These variants form two extended haplotypes H1 and H2, which have been shown to capture the common haplotypic variation across the gene. H1, the more common haplotype, consists of multiple sub-haplotypes. One of these, H1c has been found to capture the observed association between H1 and both PSP and CBD more effectively [6]. H2 is a less common, single, un-recombining haplotype.

In addition a recent genome-wide association study (GWAS) identified association between MAPT and Parkinson’s disease (PD) [7], where three single nucleotide polymorphisms (SNPs) at the locus surpassed genome-wide significance. Simón-Sánchez and colleagues observed that the risk alleles at each SNP are in LD with the H1 haplotype, thus the findings are consistent with those from other neurodegenerative disorders.

While AβPP, PSEN1, and PSEN2 are established contributors to rare forms of AD, as is MAPT to other neurodegenerative disorders including PD, PSP, and CBD, the question remains whether these genes are implicated in the common form of AD which occurs later in life (>65 years). Relatively recent studies testing these genes for association with LOAD have produced both positive [8–17] and negative results [18–24]. This includes analyses of the MAPT H1 and H1c haplotypes [8, 16, 17, 19, 21, 24]. However, these studies have been underpowered to detect common risk alleles of the effect sizes typically seen in common disorders. We therefore tested variants at the AβPP, PSEN1, PSEN2, and MAPT loci for association with LOAD in an extended version of the Genetic and Environmental Risk in AD Consortium 1 (GERAD1).
case-control dataset, previously published by Harold and colleagues [25], consisting of 3,940 AD cases and 13,373 controls.

MATERIALS AND METHODS

SNPs within 20 kb of AβPP, PSEN1, PSEN2, and MAPT were analyzed for single-marker and gene-wide association to LOAD within the GERAD1 GWAS dataset (directly genotyped and imputed). Meta-analysis between GERAD1 and two publically available datasets was also performed for markers selected from the GERAD1 single-marker analysis. The details of all analyses are given below.

GERAD1 samples

The total sample analyzed in this study was comprised of 4,957 AD cases and 9,682 controls previously described in Harold and colleagues [25] plus an additional 5,529 controls. The sample included 4,113 cases and 1,602 elderly screened controls recruited by the Medical Research Council (MRC) Genetic Resource for AD (Cardiff University; Institute of Psychiatry, London; Cambridge University; Trinity College Dublin); the Alzheimer’s Research UK (ARUK) Collaboration (University of Nottingham; University of Manchester; University of Southampton; University of Bristol; Queen’s University Belfast; the Oxford Project to Investigate Memory and Ageing (OPTIMA), Oxford University; Washington University; St Louis, United States; MRC PRION Unit, University College London; London and the South East Region AD project (LASER-AD), University College London; Competence Network of Dementia (CND) and Department of Psychiatry, University of Bonn, Germany and the National Institute of Mental Health (NIMH) AD Genetics Initiative. In addition, 844 AD cases and 1,255 elderly screened controls were ascertained by the Mayo Clinic, Jacksonville, Florida; Mayo Clinic, Rochester, Minnesota; and the Mayo Brain Bank. All AD cases met criteria for either probable (NINCDS-ADRDA [26], DSM-IV) or definite (CERAD [27]) AD.

The GWAS was performed as described by Harold and colleagues [25]. 5,715 samples were genotyped using the Illumina 610-quad chip; genotypes for the remaining subjects (n = 14,453) were made available either from population control datasets or through collaboration and were genotyped on the Illumina HumanHap 1.2M, 610, 550 or 300 BeadChips. Prior to association analysis, all samples and genotypes underwent stringent quality control (QC), which resulted in the elimination of 58,841 autosomal SNPs and 2,855 subjects. Thus, in Stage 1, we tested 528,747 autosomal SNPs for association in up to 17,313 subjects (3,940 AD cases and 13,373 controls, of whom 3,534 were elderly controls who were screened for cognitive decline or neuropathological signs of AD). The genomic control inflation factor $\lambda$ [33] was 1.060 ($\lambda_{1000} = 1.010$), suggesting little evidence for residual stratification. SNPs were tested for association with AD using logistic regression, assuming an additive model. Specific details of the logistic regression analysis and the covariates included are given elsewhere [25]. Genome-wide significance was defined as $p < 5 \times 10^{-8}$ as suggested by Pe’er and colleagues [34].

GERAD1 imputation analysis

AD summary statistics were based on 3,940 cases and 13,373 controls from UK, USA, and Germany typed with the Illumina Chips 1.2M, 610, 550, and 300. Genotypes at the 201,228 SNPs common to each of the 4 chips were used as input for imputation. The imputation was performed using IMPUTE2 software [35] with two phased reference panels, the Heinz Nixdorf Recall Study [29, 30], and amyotrophic lateral sclerosis controls [31]. Additional controls, not previously analyzed, included 1,456 elderly screened controls from the Lothian birth cohort, University of Edinburgh (http://www.lothianbirthcohort.ed.ac.uk/), plus 4,069 population controls from either the 1958BC (n = 1,596) or the National Blood Service [32] (n = 2,477). Additional genotypes were also made available for 1,068 1958BC controls previously included in the Harold and colleagues publication [25]. All individuals included in the analysis have provided informed consent to take part in genetic association studies and we obtained approval to perform a GWAS including 19,000 participants (MREC 04/06/030, Amendment 2 and 4; approved 27 July 2007).

Genome-wide analysis

The GWAS was performed as described by Harold and colleagues [25]. 5,715 samples were genotyped using the Illumina 610-quadr chip; genotypes for the remaining subjects (n = 14,453) were made available either from population control datasets or through collaboration and were genotyped on the Illumina HumanHap 1.2M, 610, 550 or 300 BeadChips. Prior to association analysis, all samples and genotypes underwent stringent quality control (QC), which resulted in the elimination of 58,841 autosomal SNPs and 2,855 subjects. Thus, in Stage 1, we tested 528,747 autosomal SNPs for association in up to 17,313 subjects (3,940 AD cases and 13,373 controls, of whom 3,534 were elderly controls who were screened for cognitive decline or neuropathological signs of AD). The genomic control inflation factor $\lambda$ [33] was 1.060 ($\lambda_{1000} = 1.010$), suggesting little evidence for residual stratification. SNPs were tested for association with AD using logistic regression, assuming an additive model. Specific details of the logistic regression analysis and the covariates included are given elsewhere [25]. Genome-wide significance was defined as $p < 5 \times 10^{-8}$ as suggested by Pe’er and colleagues [34].
Gene-wide analysis

All SNPs located within 

PP, PSEN1, PSEN2, and MAPT that were either directly genotyped within the GERAD1 sample or imputed were identified. SNPs were assigned to a gene if they were located within ±20 kb of any transcript corresponding to that gene. P-values were calculated under an additive disease model and adjusted for genomic control (geno-
typed \( \lambda = 1.06 \), imputed \( \lambda = 1.11 \)).

Gene-wide analysis was performed based on the Simes \([37]\) method for conducting multiple tests of significance. The Simes method is less conservative than the Bonferroni method when the tests are not inde-
dependent, and is thus better suited for analyzing multiple SNPs from the same gene (where the individual asso-
ciation tests are likely to be correlated due to linkage disequilibrium). If the p-values for the individual tests are ordered such that \( p(1) \leq p(2) \leq \ldots \leq p(n) \) then the null hypothesis of no association in the gene is rejected at significance level \( \alpha \) if \( p(j) \leq \alpha/n \) for any \( j = 1, \ldots, n \).

The corrected p-value for the joint significance test of all SNPs in a gene using this method (denoted “Simes p-value”) is given by the minimum of \( p(j) \times (n/j) \).

Meta-analysis with additional datasets

Meta-analysis was performed on GERAD1 and two publically available GWAS datasets from the Trans-
lational Genomics (TGEN) Research Institute and the Alzheimer’s Disease Neuroimaging Initiative (ADNI).

The TGEN sample, previously reported by Reiman and colleagues \([23]\), is comprised of 861 cases and 550 controls. Imputation of this dataset was performed using MACH software \([38]\) with the August 2010 1000 genomes reference panel. SNPs were tested for asso-
ciation using logistic regression assuming an additive model. Sample population (USA or Netherlands) was included as a covariate.

Meta-analysis was performed by inverse variance weights (IVW) meta-analysis using summary data (i.e., odds ratios [OR] and standard errors). The standard error statistic included in the inverse variance weights meta-analysis accounts for variation in sample size between studies. The Cochran’s Q-test and the I^2 hetero-
genesis index were used to assess heterogeneity between studies. Significant evidence of heterogene-
ity was determined by a Cochran’s Q-statistic p < 0.1 or I^2 > 50. In these instances a random effects meta-
analysis was performed; alternatively, meta-analysis with a fixed effect model was used.

RESULTS

Analysis of PP, PSEN1, PSEN2, and MAPT

A summary of the results is given in Table 1. The most significant SNP at the PSEN1 locus is a 1000 genomes marker at chr4:72745579 (NCBI36, imputed \( p = 1.9 \times 10^{-4} \)) which is located within intron 8 of PSEN1 isoform 1 (NM_016835). The most significant SNP at the PSEN1 locus is a 1000 genomes marker at chr4:72745579 (NCBI36, imputed \( p = 1.9 \times 10^{-4} \)) which is located within intron 8 of PSEN1 isoform 1 (NM_016835) and lies within a 4555 bp of a deletion which has been identified in two AD families. This deletion spans exon 9 of PSEN1 which results in an in-frame skipping of exon 9 and an amino acid change at the splice junction of exon 8 and 9 [40, 41]. At the PP locus, rs381743 shows the greatest evidence for association with AD (imputed \( p = 8.8 \times 10^{-8} \)). rs11656151 is located within intron 8 of MAPT isoform I-467 (NM_016835). The most significant SNP at the PSEN1 locus is a 1000 genomes marker at chr14:72745579 (NCBI36, imputed \( p = 1.9 \times 10^{-4} \)) which is located within intron 8 of PSEN1 isoform 1 (NM_016835) and lies within a 4555 bp of a deletion which has been identified in two AD families. This deletion spans exon 9 of PSEN1 which results in an in-frame skipping of exon 9 and an amino acid change at the splice junction of exon 8 and 9 [40, 41]. The most significant SNP at the PSEN1 locus is a 1000 genomes marker at chr14:72745579 (NCBI36, imputed \( p = 1.9 \times 10^{-4} \)) which is located within intron 8 of PSEN1 isoform 1 (NM_016835) and lies within a 4555 bp of a deletion which has been identified in two AD families. This deletion spans exon 9 of PSEN1 which results in an in-frame skipping of exon 9 and an amino acid change at the splice junction of exon 8 and 9 [40, 41].
Table 1
Analysis of AβPP, PSEN1, PSEN2, and MAPT in the GERAD1 dataset

<table>
<thead>
<tr>
<th>Gene</th>
<th>Gene position ±20 KB (NCBI36)</th>
<th>SNP ID</th>
<th>Info</th>
<th>OR</th>
<th>p value</th>
<th>Simes p value</th>
<th>SNP ID</th>
<th>Info</th>
<th>OR</th>
<th>p value</th>
<th>Simes p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>AβPP</td>
<td>chr21:26,154,752-26,485,003</td>
<td>rs2830088</td>
<td>0.91</td>
<td>0.010</td>
<td>0.962</td>
<td>rs381743</td>
<td>0.87</td>
<td>0.91</td>
<td>0.010</td>
<td>0.962</td>
<td>0.87</td>
</tr>
<tr>
<td>PSEN1</td>
<td>chr14:72,652,932-72,776,862</td>
<td>rs362350</td>
<td>0.90</td>
<td>0.020</td>
<td>0.240</td>
<td>chr14:72,745,579</td>
<td>0.80</td>
<td>1.37</td>
<td>1.9×10⁻⁴</td>
<td>0.077</td>
<td>0.80</td>
</tr>
<tr>
<td>PSEN2</td>
<td>chr1:225,104,896-225,170,427</td>
<td>rs2073489</td>
<td>0.96</td>
<td>0.136</td>
<td>0.611</td>
<td>rs12405469</td>
<td>0.81</td>
<td>0.94</td>
<td>0.041</td>
<td>0.784</td>
<td>0.81</td>
</tr>
<tr>
<td>MAPT</td>
<td>chr17:41,307,544-41,481,546</td>
<td>rs1079415</td>
<td>1.00</td>
<td>0.003</td>
<td>0.034</td>
<td>rs14651551</td>
<td>0.84</td>
<td>1.13</td>
<td>8.8×10⁻⁵</td>
<td>0.009</td>
<td>0.84</td>
</tr>
</tbody>
</table>

The most significant results are shown for SNPs directly genotyped and those imputed in the dataset. Odds Ratios (OR) are based on the minor allele. Gene-wide analysis of AβPP, PSEN1, PSEN2, and MAPT in the GERAD1 dataset using the Simes method is also given.

Table 2
Single-marker and meta-analysis results for the most significant SNPs within AβPP, PSEN1, PSEN2, and MAPT, plus the H1 haplotype tag SNP rs9468, within three independent LOAD GWAS samples (GERAD1, TGEN, and ADNI)

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP ID</th>
<th>GERAD1</th>
<th>TGEN</th>
<th>ADNI</th>
<th>Meta-analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td>AβPP</td>
<td>rs381743</td>
<td>0.87</td>
<td>0.91</td>
<td>0.002</td>
<td>0.96</td>
</tr>
<tr>
<td>PSEN1</td>
<td>chr14:72,745,579</td>
<td>0.80</td>
<td>1.56</td>
<td>1.9×10⁻⁴</td>
<td>0.71</td>
</tr>
<tr>
<td>PSEN2</td>
<td>rs12405469</td>
<td>0.81</td>
<td>0.94</td>
<td>0.041</td>
<td>0.99</td>
</tr>
<tr>
<td>MAPT</td>
<td>rs14651551</td>
<td>0.84</td>
<td>1.13</td>
<td>8.8×10⁻⁵</td>
<td>0.89</td>
</tr>
<tr>
<td>MAPT</td>
<td>rs9468</td>
<td>0.87</td>
<td>0.89</td>
<td>7.8×10⁻⁴</td>
<td>0.95</td>
</tr>
</tbody>
</table>

Inverse variance weights (IVW) meta p-values were calculated from summary statistics. Odds ratios (OR) refer to the minor allele. Meta p-values given are based on a fixed effect model unless Q statistic p<0.1 or I² > 50. In these instances a random effects model was used. N/A = Not available.
MAPT in an imputed GWAS dataset of 3,940 cases to LOAD, we analyzed effects on neurodegenerative disorders. In order to indicated by AD pathology and been shown to have genetic this variant (rs11656151) provided evidence of consistency between samples. However, the TGEN and ADNI datasets are relatively small and replication in much larger samples is needed.

In conclusion, it is unlikely that common variation at AβPP, PSEN1, PSEN2, and MAPT does not provide a strong contribution to AD risk, it is possible that these loci contain as yet undetected rare variants of larger effect. Genome-wide association studies are underpowered to detect these variants and sequencing of several thousand cases and controls would be required to detect rare variants at these loci.

In conclusion, it is unlikely that common variation at AβPP, PSEN1, PSEN2, and MAPT does not provide a strong contribution to disease risk. Replication of this result is necessary although it is likely that large sample
sizes will be required to achieve the power necessary to show a true effect.

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