

Integrated copy number and gene expression analysis detects a *CREB1* association with Alzheimer's disease

Y Li^{1,10}, CA Shaw^{2,10}, I Sheffer¹, N Sule³, SZ Powell⁴, B Dawson^{2,5}, SNY Zaidi¹, KL Bucasas⁶, JR Lupski^{2,7}, KC Wilhelmsen⁸, R Doody¹ and K Szigeti^{1,9}

Genetic variation, both single-nucleotide variations and copy number variations (CNV), contribute to changes in gene expression. In some cases these variations are meaningfully correlated with disease states. We hypothesized that in a genetically heterogeneous disorder such as sporadic Alzheimer's disease (AD), utilizing gene expression as a quantitative trait and CNVs as a genetic marker map within the same individuals in the context of case-control status may increase the power to detect relevant loci. Using this approach an 8-kb deletion was identified that contains a PAX6-binding site on chr2q33.3 upstream of *CREB1* encoding the cAMP responsive element-binding protein1 transcription factor. The association of the CNV to AD was confirmed by a case-control association study consisting of the Texas Alzheimer Research and Care Consortium and NIA-LOAD Family Study data sets.

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Introduction

Alzheimer's disease (AD) is a devastating neurodegenerative disorder affecting ~5.4 million individuals in the United States and is the most common cause of dementia in North America and Europe.^{1–3} Genetic factors have an important role in the pathogenesis of AD.^{4,5} Rare Mendelian forms of AD have confirmed and elucidated pathways involved in amyloid accumulation, but only account for a small percentage of AD.⁶ GWAS studies have identified 10 susceptibility loci for the more common, late-onset form of AD⁷ using single-nucleotide polymorphisms (SNPs) as a genetic marker map. The non-APOE loci account for 35% of the population attributable fractions, suggesting that there is still missing heritability.⁷ Published copy number variations (CNV) studies in AD^{8–10,11} have focused on large events (>100 kb) to achieve high confidence calls and performed the tests of association on these events.

Genetic variation, both single-nucleotide variations and CNV, contribute to changes in gene expression. In some cases these variations are meaningfully correlated with disease states.¹² As GWAS studies are performed with increasing sample sizes^{7,13–15} it is becoming clear that in disorders with marked genetic heterogeneity where the marker specific risk is low in case-control sets, it is difficult to identify the true positives from the false positives and to replicate the results.^{16,17} In addition, case-control design in AD suffers from additional confounders, such as misclassification bias due to age-dependent penetrance.

The approach of using gene expression data from pathologically ascertained cases and controls eliminates the misclassification bias and gene expression serves as a refined phenotype in a heterogeneous disorder, both increasing the power to detect association signals. We hypothesized that in a genetically heterogeneous disorder such as sporadic AD, utilizing gene expression as a quantitative trait (eQTL) and CNVs as a genetic marker map within the same individuals may increase the power to detect relevant loci, and by incorporating case-control status, these loci will be candidates for case-control association studies.

Materials and methods

Subject cohorts. The discovery cohort consisted of 22 pathological confirmed AD (mean age at death 80, range 61–93) temporal lobes and 15 control temporal lobes (mean age at death 65, range 41–93). Human frozen temporal lobe tissue was obtained from the Alzheimer's Disease and Memory Disorders Center tissue collection and the New York Brain Bank. Neuropathological diagnosis was assigned by board-certified neuropathologists. AD or control neuropathology was confirmed by plaque and tangle assessment and Braak staging. The brain cohort was exempt from IRB approval as the specimens were deidentified.

The case-control association study consisted of the Texas Alzheimer Research and Care Consortium (TARCC) and the

¹Department of Neurology, Alzheimer's Disease and Memory Disorders Center, Baylor College of Medicine, Houston, TX, USA; ²Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA; ³Department of Pathology, Baylor College of Medicine, Houston, TX, USA; ⁴Department of Neuropathology, The Methodist Hospital, Houston, TX, USA; ⁵Howard Hughes Medical Institute, Houston, TX, USA; ⁶Department of Immunology, Baylor College of Medicine, Houston, TX, USA; ⁷Department of Pediatrics, Baylor College of Medicine, Houston, TX, USA; ⁸Department of Neurology, The University of North Carolina at Chapel Hill, Chapel Hill, NC, USA and ⁹Department of Neurology, University at Buffalo, SUNY, Buffalo, NY, USA

Correspondence: Dr CA Shaw, Department of Molecular and Human Genetics, Baylor College of Medicine, 1 Baylor Plaza, Houston, TX, USA.

E-mail: cashaw@bcm.edu or Dr K Szigeti, Department of Neurology, University of Buffalo, SUNY, 100 High Street, Buffalo, NY 14203, USA.

E-mail: szigeti@buffalo.edu

¹⁰These authors contributed equally to this work.

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NIA-LOAD Family Study (LOAD) probands http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000168.v1.p1. The TARCC data set including 381 Caucasian subjects with probable AD and 191 neuropsychologically tested normal controls.¹⁸ Probable AD was assigned by NINCDS-ADRDA criteria after consensus review.¹⁹ Controls were recruited at each participating site by the same inclusion criteria, including age over 55 years, male and female, unrelated to AD subjects, CDR global score 0, normal performance on activities of daily living, and all information was obtained from surrogate historian. After enrollment all control subjects underwent neuropsychological testing including assessment of global cognitive functioning (MMSE and CDR), attention (Digit Span and Trails A), executive function (Trails B and Clock Drawing), memory (WMS Logical Memory I and WMS Logical Memory II), language (Boston Naming and FAS Verbal Fluency), Premorbid IQ (AMNART), Visuospatial Memory (WMS-Visual Reproduction I and II), Psychiatric (Geriatric Depression Scale; Neuropsychiatric Inventory-Questionnaire) and Functional assessment (Lawton-Brody ADL: PSMS, IADL). Control subjects showing impairment were excluded from the control cohort after consensus review.

The Institutional Review Board of BCM and all participating sites approved the study. Informed consent was obtained from all subjects before inclusion. Genomic DNA was isolated from whole blood by the Puregene DNA isolation kit (Qiagen, Germantown, MD, USA) according to the manufacturer's instructions.

Isolation of DNA and RNA from brain tissue, expression profiling and genotyping. DNA was prepared with QIAamp DNA mini kit (Qiagen) according to the manufacturer's instructions. For RNA preparation, brain tissue was homogenized with a tissue homogenizer in Trizol (Invitrogen, Madison, WI, USA) and purified with Rneasy mini kit (Qiagen). DNA and RNA QC criteria for proceeding to array experiments were 260/280 nm 1.6–1.8 for DNA and 1.9–2.0 for RNA, 260/230 nm >2.0 for DNA and >1.5 for RNA by Nanodrop 1000 (Wilmington, DE, USA). RNA quality was further assessed by calculating RIN (RNA integrity number) with Agilent 2100 (Santa Clara, CA, USA) Bioanalyzer (Microarray core facility, Baylor College Medicine). Sample was entered to expression array experiment if RIN >4 (range 4.3–6.9).

Microarray expression profiling was performed on the Illumina Human-6 V3 BeadChip (Illumina, San Diego, CA, USA) (Supplementary information). Genotyping was performed on the Genome-Wide Human SNP Array 6.0 (Affymetrix, Santa Clara, CA, USA) according to the manufacturer's instructions (Supplementary information). Long-range PCR was designed for the deletion genotyping (Supplementary information). APOE genotyping was performed according to manufacturer's instruction with real-time PCR using custom TaqMan probes (Applied Biosystems, Carlsbad, CA, USA) (Supplementary information).

Analysis of array data

Genome-wide CNV inference for the initial analysis. CNV states for each subject were determined by segmentation of the Genome-wide Human SNP Array 6.0 (Affymetrix) data

with the Hidden Markov Model algorithm in the Genotyping Console 3.0 software (Affymetrix, Santa Clara, CA, USA) package using detection threshold of 1 kb.

Expression data. Normalized expression array values were obtained by processing Illumina BeadStudio summary data using the VST transform method as implemented in the lumi R package,^{20,21} which performs variance stabilization on the low level data to achieve normal distribution. We validated the normal distribution for the significant probes by visualizing residual plots. We also required Illumina BeadStudio probewise detection *P*-values <0.05 to be considered in the expression analysis. To ensure cross array comparability after the detection filter quantile normalization was applied to the VST summaries across all subjects.

Definition of CNV expression. The UCSC browser track was utilized for mapping every probe to the human genome Build 36; 500 Kb padding was added on each side of the expression probe (1 Mb total window) and any CNV calls overlapping the 1 Mb window was associated with that probe. The 500 kb was selected based on previously published data²² suggesting that within this distance the likelihood of an effect of a SNP on gene regulation is over 99%. All CNV calls were tabulated as integer values 0 (homozygous loss, extremely rare), 1 (single-copy loss) 2 (diploid) 3 (gain) and 4 (multi-gain) within 500 kb upstream and downstream from each transcript for each person. To avoid distortions for rare multi-copy gains or losses, the encoding of one for both homozygous and hemizygous loss, two for normal CNV state and three for gain CNV state was used.

Statistical analysis of the discovery cohort incorporating expression, disease state and CNV information. The following filters were applied to reduce the data set to meaningful comparisons for the hypothesis: (i) expressed in brain (bead level data detection *P*<0.05), (ii) differentially expressed between cases and controls (*t*-test, *P*<0.05) and (iii) CNV events in at least two individuals that are within 1 Mb of the expression probe (frequency >0.05) to avoid spurious associations caused by single events at the extremes of the expression spectrum.

The null hypothesis is that the difference in expression between cases and controls does not correlate with cis-CNV state. Analysis of covariance (ANCOVA) was performed for each expression probe where a linear effect for CNV together with a shift term for case-control status was estimated by least squares. The fraction of variation (partial *R*²) attributable to CNV state was assessed by taking the ratio between the regression sum of squares for the CNV information to the regression sum of squares for the full model. The *F*-statistic and a corresponding *P*-value were determined by dividing the mean square regression for CNV by the mean square error of the full ANCOVA. This analysis can be performed by selecting corresponding entries from the ANCOVA table from the appropriate statistical software.

Case-control association study. Subsequently to test the hypothesis whether this association could be detected in a larger case-control study we performed a metaanalysis of

the TARCC cohort and the publicly available NCRAD-LOAD (http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000168.v1.p1) Caucasian probands ($N=2166$). The TARCC cohort was genotyped on the Affymetrix 6.0 array. The genotype calls were generated by the GoldenHelix software. The NCRAD-LOAD data were analyzed by the Beadstudio software for log₂ratio calculation and the genotype calls were based on the log₂ratio distributions by inspection of the kernel density estimate of log₂ratios and identification of cutpoints that distinguished the three genotype classes. Fisher's exact test was calculated for the TARCC, LOAD and the metaanalysis. In addition, we developed a factorial model using logistic regression with the logitlink function, which allowed the addition of sex and age as covariates. Odds ratio was calculated for the deletion carrier status in the metaanalysis by collapsing the homozygous and heterozygous deletion carriers.

Results

Thirty-seven expression arrays passed QC criteria and 31 genotyping arrays were adequate for copy number analysis. Consideration was limited to (i) CNVs where at least two

subjects had other than two copies of the region (locus-specific frequency > 0.05), (ii) genes where expression level could be distinguished from background with P -value of < 0.05 and that were within 500 kb upstream and downstream from each CNV. These interval parameters detect 90% of interactions extrapolated from SNP data.²³ Combining the CNV variation and gene expression filters resulted in 2455 probes corresponding to 2063 genes to be considered in our eQTL and CNV integrated analysis. As the aim is to identify genes that have an association with disease state, the analysis was applied to genes (probes) that are differentially expressed between AD cases and controls ($P < 0.05$). Five hundred seventy-four probes corresponding to 531 genes were differentially expressed between cases and controls. These genes were tested for whether expression was correlated with CNV genotype status. Regression results (F-statistic P -values) for the component of variance explained by CNV in the ANCOVA are depicted in the Manhattan plot (Figure 1). Six probes had P -values of < 0.001. These probes also had over 50% of the variance in expression explained by the ANCOVA attributable to CNV. (Table 1) The top hit *ARL17P1* corresponds to CNVR 7114.8 and CNVR 7114.10 (<http://www.sanger.ac.uk/cgi-bin/humgen/cnv/42mio/downloadBigDB.cgi>),²⁴ and the subsequent three probes coding *CREB1* and *FAM119A* correspond to CNVR 1123.1. These latter three probes have similar P -values and identical slopes and thus appear to represent a triplicate experiment. The two additional genes identified on chromosome 1 are *SDF4* and *NBPF10*. *SDF4* does not have a known corresponding CNV and *NBPF10* corresponds to CNVR 93.13 and CNVR 94.3. The distribution of the expression data is represented with box plots for the three probes on chromosome 2 in Figure 2. Multiple testing corrections for this analysis are confounded by the potential of linked probes to have correlated results because they share the associated CNV resulting in overcorrection. An alternative approach is to calculate the probability of a run of 3 in a row in 574 trials where 6/574 are positives, which is 0.0006. The assumption was made that the modest number of linked probes represents replicate experiments examining the association with CNV state instead of independent experiments; any result identified in the eQTL study was anticipated to be confirmed by tests in a larger case-control cohort. Gene expression levels were validated by TaqMan assay for *CREB1* (Supplementary Figure 1). The differential expression of *CREB1* between cases and controls was replicated in the data set by Myers *et al*.²³

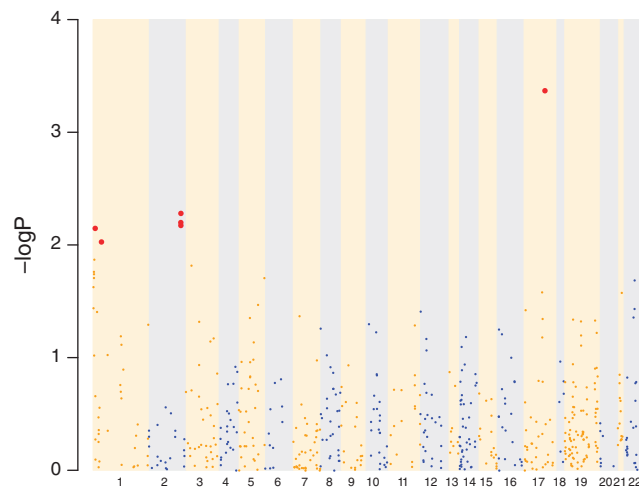


Figure 1 The Manhattan plot depicts the $-\log_{10}P$ for the F-statistic corresponding to the portion of variation of expression explained by copy number variation (CNV) state in the analysis of covariance (ANCOVA) in the reduced data set after the filters ($N=574$). The chromosomes are shaded alternately and each expression probe is represented by a dot. Probes with $P < 0.001$ were considered for a case-control association study (red).

Table 1 Regression results (F-statistic P -values) for the component of case-control variance explained by CNV in the ANCOVA

Probe_Id	ILMN_Gene	Chromosome	Start	Stop	pADCNV	FracColinear	nVariants
ILMN_1698680	<i>ARL17P1</i>	17	41732281	42012404	0.0004	0.90	22
ILMN_2049364	<i>FAM119A</i>	2	208154323	208198218	0.0054	0.77	9
ILMN_2334242	<i>CREB1</i>	2	208102930	208171815	0.0066	0.70	9
ILMN_2334243	<i>CREB1</i>	2	208102930	208171815	0.0070	0.68	9
ILMN_1696065	<i>SDF4</i>	1	1142150	1157310	0.0074	0.64	4
ILMN_2155719	<i>NBPF10</i>	1	16762998	146690991	0.0098	0.53	31

Abbreviations: ANCOVA, analysis of covariance; CNV, copy number variation.

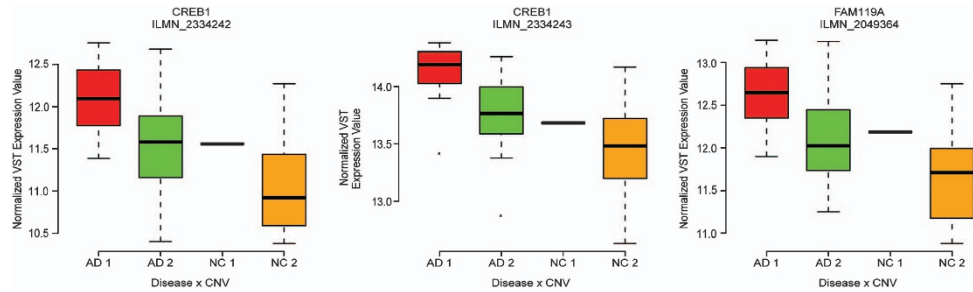


Figure 2 The box plots depict the expression levels in Alzheimer's disease (AD) and controls by copy number state (1 or deletion and 2 or diploid) for the three probes corresponding to the two adjacent genes (*CREB1* and *FAM199A*) on chromosome 2. These probes represent a triplicate experiment as they are associated with the same copy number variation (CNV; CNVR 1123.1) and have similar expression patterns. The association of CNVR 1123.1 with AD was confirmed in the case–control association study.

(#10) (GSE15222); the AD cases had higher expression levels compared with the normal controls (t -test, $P=1.36 \times 10^{-18}$) (Supplementary Figure 2).

The case–control cohort (1230 AD subjects and 936 normal controls) consisted of the TARCC data set (381 cases and 191 controls) and the LOAD Caucasian probands ($N=848$) and Caucasian unrelated controls ($N=745$). First we studied the TARCC data set as it had adequate coverage of the candidate regions to perform segmentation. The cohort characteristics are summarized in Supplementary Table 1. In the chromosome 2 region the contiguous significant P -values of the overlapping sliding windows delineate the position of the deletion (CNVR 1123.1) detected in the discovery cohort. The association between copy number and case–control status for the sliding windows across the 1 Mb regions are depicted in Table 2 for the chromosome 2 region. The genomic locations of the associated CNVRs are depicted by the bolded probe identifiers in each table. The other regions which were not considered significant after correction for multiple comparisons are summarized in Supplementary tables 2–4. As the LOAD genotyping platform offered a limited number of probes (7), the segmentation algorithms had limited utility.

Second, in order to further validate the association of CNVR 1123.1 the association was tested after generating CNV calls (CN 0, 1 and 2 quantitating homozygous deletion, heterozygous deletion and normal diploid state) in both the TARCC and LOAD cohorts. The 8 kb deletion was covered with 23 probes on the Affymetrix array and 7 probes on the Illumina array. Genotype calls were based on the log₂ratio distributions by inspection of the kernel density estimate of log₂ratios and identification of cutpoints that distinguished the three genotype classes. Long-range PCR confirmed the chip based genotyping of CNVR 1123.1 for 277 TARCC samples in which DNA was available for this study. The genotyping accuracy of the Affymetrix array is 96%. Typical genotyping results are depicted in Figure 3. The frequencies of the homozygous and heterozygous deletion samples did not differ between the TARCC and LOAD cohorts genotyped on the Affymetrix and Illumina platforms, respectively (Supplementary Table 5). The PCR validation and similar allele frequencies suggest that the genotyping is accurate. The Fisher's exact test resulted in a P -value of 0.008 in the combined set and the Fisher's exact test was significant in both the TARCC (for both the Affymetrix and the PCR (Supplementary Table 7) based genotype calls) and LOAD cohorts when analyzed separately

(Supplementary Table 6). The odds ratio for the deletion carrier status (collapsed homozygous or heterozygous deletion) was calculated for the metaanalysis (OR 1.23 (1.02–1.49)). Furthermore, we applied a factorial model in the replication set (1230 AD subjects and 936 normal controls) to study the effects of age and gender as covariates. The association remained significant after adding age and gender into the model ($P=0.03$). APOE data was available for the TARCC set; the regression model remained significant for CNV effect (Table 3).

Third, we studied whether this association is expected to be detected in GWAS studies. SNP association with case–control status was explored using the genotypes of 24 SNPs in the region using the TARCC cohort (Supplementary table 8). The strongest linkage disequilibrium with CNVR 1123.1 was for rs2113383 and rs7561038 with r^2 value of 0.39 and 0.22, respectively (Supplementary figure 3). These two SNPs although did not survive multiple testing correction, had the strongest level of association with case–control status (corrected $P=0.26$ and 0.055, respectively). To delineate the potential mechanism for the deletion event the breakpoint of five homozygous deletion samples was sequenced. Interestingly the breakpoint sequences were identical (Figure 3). In the breakpoint sequence an inserted sequence was identified 400 kb downstream from the deletion (Figure 3).

Discussion

Transcribed sequences were identified with evidence of differential expression in the temporal lobe of post mortem patients with and without AD in which a significant portion of the variation in gene expression was attributable to CNV (Figure 1 and Table 1). Five genes were both differentially expressed between cases and controls and had >50% of the variance explained attributable to the cis-CNV state. Three of the six probes are adjacent to CNVR 1123.1 and fall into a linked region in AD on chromosome 2. Two of these probes are replicates of *CREB1* and the third probe is *FAM119A*, a gene adjacent to *CREB1*. The sign and size of the regression coefficients and P -values are similar suggesting that the association is observed in triplicate. *CREB1* has been implicated in memory by multiple lines of evidence.^{25,26} The associated deletion, CNVR 1123.1 has been reported and validated in endeavors to catalog CNVs genome-wide (<http://www.sanger.ac.uk/cgi-bin/humgen/cnv/42mio/>

Table 2 Association results of the probes of the 1 Mb region surrounding *CREB1* and *FAM199A*

Predictor	Chromosome	Position	Trend P	Trend R	Trend Bonferroni P
CN_845075	2	207622072	0.2977	-0.0435	1
SNP_A-1966626	2	207663403	0.5974	0.0221	1
SNP_A-1887677	2	207665482	0.1818	0.0558	1
CN_845090	2	207673903	0.3442	-0.0395	1
SNP_A-8671717	2	207732485	0.2332	-0.0498	1
SNP_A-8465960	2	207733395	0.3069	-0.0427	1
SNP_A-2028696	2	207781838	0.2920	0.0440	1
CN_845130	2	207795277	0.4051	-0.0348	1
SNP_A-2218992	2	207833393	0.3363	-0.0402	1
SNP_A-2136852	2	207858744	0.5511	-0.0249	1
CN_847305	2	207994945	0.5556	0.0246	1
CN_847318	2	208027023	0.7844	-0.0114	1
SNP_A-8299273	2	208048623	0.4719	-0.0301	1
SNP_A-8494281	2	208049459	0.7825	-0.0115	1
SNP_A-8483760	2	208053385	0.6240	-0.0205	1
CN_847334	2	208058167	0.8857	0.0060	1
CN_847330	2	208058424	0.3522	0.0389	1
CN_847331	2	208058480	0.4080	0.0346	1
CN_847332	2	208058495	0.4590	0.0309	1
CN_847333	2	208058552	0.5312	0.0262	1
CN_847335	2	208058859	0.4634	0.0306	1
SNP_A-8302877	2	208058999	0.5217	0.0268	1
CN_847336^a	2	208063145	0.3171	-0.0418	1
CN_847337^a	2	208063188	0.0625	-0.0778	1
CN_847338^a	2	208063411	0.0006	-0.1436	0.0293
CN_847339^a	2	208063571	0.0004	-0.1482	0.0194
CN_847340^a	2	208063929	0.0011	-0.1368	0.0529
CN_847341^a	2	208063951	0.0008	-0.1406	0.0380
CN_847342^a	2	208063985	0.0006	-0.1437	0.0290
CN_847343^a	2	208064228	0.0003	-0.1497	0.0169
CN_847348^a	2	208066987	0.0004	-0.1469	0.0220
CN_847350^a	2	208067258	0.0006	-0.1437	0.0291
CN_847351^a	2	208067382	0.0018	-0.1306	0.0888
CN_847352^a	2	208067569	0.0008	-0.1402	0.0396
CN_847353	2	208067709	0.2648	-0.0466	1
CN_847354	2	208067752	0.3293	-0.0408	1
CN_847355	2	208067793	0.0191	-0.0979	1
CN_847358	2	208068379	0.0853	-0.0719	1
CN_847359	2	208068455	0.1653	-0.0580	1
CN_847360	2	208068501	0.2382	-0.0493	1
CN_847361	2	208069832	0.4702	-0.0302	1
CN_847362	2	208069845	0.3084	0.0425	1
SNP_A-8295329	2	208202479	0.6110	-0.0212	1
CN_849537	2	208223269	0.3599	0.0382	1
SNP_A-1953258	2	208243710	0.3204	0.0415	1
CN_849545	2	208251726	0.4416	-0.0321	1
SNP_A-8545295	2	208263276	0.2956	0.0437	1
CN_849558	2	208293433	0.3533	0.0388	1
SNP_A-4247203	2	208503576	0.2214	-0.0511	1
CN_849623	2	208508184	0.7706	0.0122	1

Abbreviations: CN, copy number; SNP, single-nucleotide polymorphism.

^aThe highlighted probe names mark the genomic location of the CNVR detected in the discovery cohort.

downloadBigDB.cgi). Genotyping was confirmed by long-range PCR.

Subsequently, the associated CNVs were followed-up in a case-control association study. The case-control association study confirmed that harboring the CNVR 1123.1 deletion increases the risk of AD with an odds ratio of 1.23 (1.02–1.49). The TARCC data set was used (i) to perform a SNP association study with SNPs in the same haplotype block with CNVR 1123.1, and (ii) to evaluate linkage disequilibrium between the SNPs and the deletion in the haplotype block. None of the SNPs tag the deletion perfectly (r^2 max 0.39) and while rs2113383 and rs7561038 showed an association with the disease phenotype it was weaker than that of the deletion and did not survive multiple testing correction.

In order to elucidate the mechanism of rearrangement, the breakpoints of five homozygous deletion samples were sequenced. Interestingly the breakpoint sequences were identical. The breakpoint sequence suggests a replication-dependent mechanism²⁷ as the inserted sequence was identified 400 kb downstream from the deletion making recurrent events less likely. The linkage disequilibrium map and the identical breakpoints suggest that the deletion occurred on the ancestral haplotype. As a result the deletion association is a haplotype association where the haplotype is tagged by a single marker (CNVR 1123.1). This haplotype structure likely increased the statistical power and allowed the detection of the association signal. GWAS studies using single SNPs may have not been able to detect this

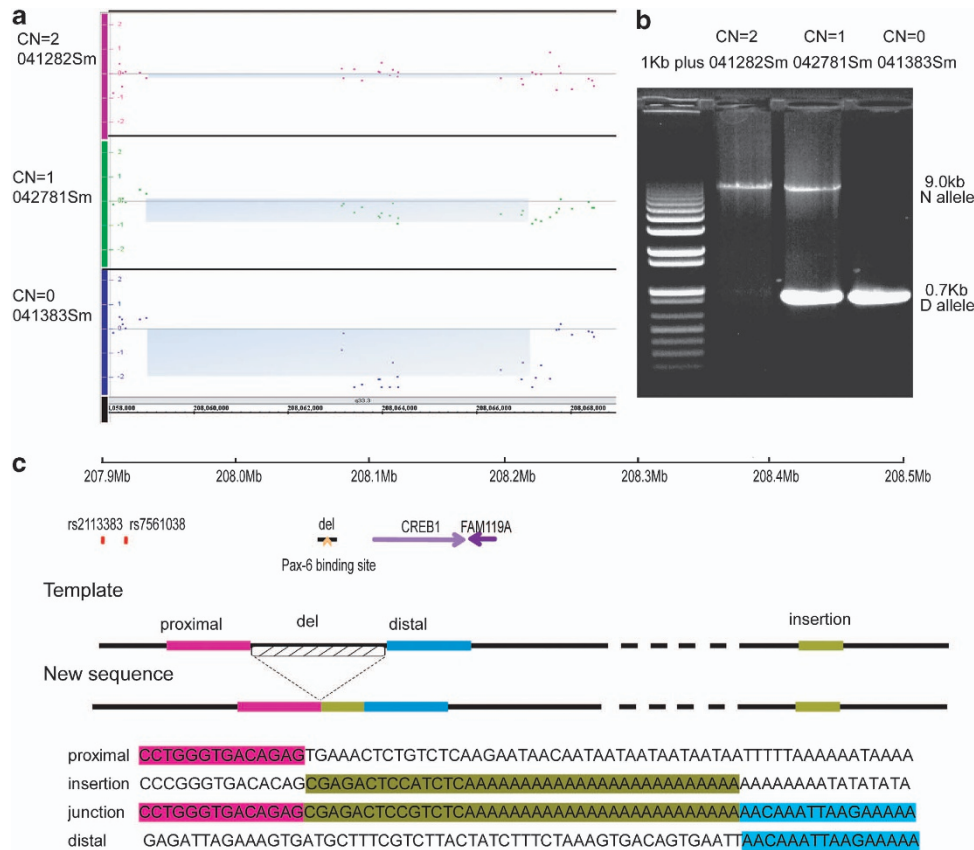


Figure 3 Genotyping, genomic context and breakpoint analysis of CNVR 1123.1. (a) Genome-Wide Human SNP Array 6.0 is presented as plot of normalized probewise log2ratio data in the three panels for diploid, heterozygous and homozygous deletion carriers (CN = 2,1,0). (b) Electrophoresis of long-range PCR products of the same samples. The heterozygous deletion carrier generates two PCR products from the normal and the deletion alleles, respectively. (c) The genomic context of the deletion (black) is outlined in relation to the two genes *CREB1* (light purple) and *FAM119A* (dark purple) in cis. The deletion encompasses a conserved PAX6-binding site (orange arrow). The breakpoint for the deletion was sequenced in five individuals and detected the same inserted sequence at the breakpoint. The inserted sequence is present 400 kb downstream from the deletion suggesting a replicative mechanism for rearrangement.

Table 3 Logistic regression on the dichotomized data (deletion or 1 copy and normal or 2 copies) of CNVR 1123.1, incorporating the number of APOE4 alleles and gender to the model. The genotypes were validated by long-range PCR

Regressor	Coefficient	Standard error	Pr (χ)	Odds ratio	OR lower confidence bound	OR upper confidence bound	Univariate fit
APOE E4_count	1.145	0.1657	6.1102 e-14	3.14	2.27	4.35	2.38e-14
Gender 1 = M, 2 = F	-0.425	0.1972	0.0300	0.65	0.44	0.96	0.0286
CN_847343	0.729	0.2227	0.0008	2.07	1.34	3.21	0.0001

Abbreviations: CN, copy number; OR, odds ratio.

association signal as they did not incorporate the haplotype information.

Variation CNVR 1123.1 400Kb upstream of *CREB1* encompasses a conserved PAX6-binding site,²⁸ which could explain the altered gene expression. PAX6 has been implicated in the development of the eye and nervous system,^{29,30} and effects of *PAX6* mutations were associated with eye developmental anomalies³¹ and developmental anomalies of the brain.³² The effect of loss of this specific PAX6-binding site has not been studied, and the regulation of *CREB1* and *FAM119A* by PAX6 has not yet been described to

our knowledge. Further experimental work will be needed to delineate the relationship between PAX6 and *CREB1* or *FAM119A*. Interestingly, other deletion CNVs in noncoding regions have recently been linked to disease, even common disease.³³ A deletion polymorphism upstream of *IRGM* was found to alter *IRGM* expression and explained the known association signal in Crohn's disease.³⁴

The expression of *FAM119A* adjacent to *CREB1* was also significant in the analysis of CNV-gene expression interaction accounting for the disease state; therefore, its potential role cannot be excluded. *FAM119A* is a predicted

methyltransferase with unknown function. *CREB1* belongs to the CREB family of leucine-zipper transcription factors that have a central role in cell signal transduction. In a molecular triangulation analysis in AD with *APOE*, *APP*, *PSEN1* and *2*, *CREB1* has been predicted as one of the top 10 network nodes.³⁵ Disruption of *CREB1* in a mouse model showed neurodegeneration in the hippocampus.³⁶ Expression of a constitutively active form of *CREB1* in mice interfered with retrieval of spatial information.³⁷ *CREB1* is regulated by alternative splicing and alternative promoters in *Aplysia*.^{38,39}

This study presents an approach to detect a phenotypically relevant association in a genetically heterogeneous disorder using gene expression as an eQTL and genetic markers (CNVs in this case) in the same individuals. One limitation of the study is the use of post mortem human brain tissue in the discovery cohort. Interestingly, three probes corresponding to two genes showed very consistent coefficients and *P*-values; this suggests that degradation was not a major problem at least for these two genes. In addition, the case-control association study used only CNV genotypes derived from blood, with independent methods and statistical approaches, and confirmed the association.

The increased power of the discovery cohort to detect the association is attributable to multiple factors: (i) elimination of misclassification bias by using pathologically confirmed cases and controls, (ii) refined phenotype by using gene expression as eQTL and (iii) deriving genotype and expression data from the same individual allowing for direct correlation. GWAS studies with increasing sample sizes^{7,13–15} suggest that disorders with marked genetic heterogeneity where the marker specific risk is low in case-control sets, may have limitations to detect and replicate association signals.^{16,17} This approach may complement the robust GWAS studies to identify biologically relevant loci in this devastating disease with the ultimate goal to find intervention.

Conflict of interest

Suzanne Z Powell was a speaker at the AAN meeting in Honolulu, and donated her honorarium to the AAN Foundation. She was the ground rounds speaker in July 2011 at the University of Indiana, Department of Pathology and also in March 2012 at the University of Pennsylvania, Department of Pathology and serves on the Editorial Boards of the Archives of Pathology and Laboratory Medicine and Modern Pathology. James R Lupski is a consultant for Athena Diagnostics, holds stock ownership of 23 and Me and Ion Torrent Systems, and is a co-inventor on multiple United States and European patents for DNA diagnostics. The Baylor College of Medicine and Department of Molecular and Human Genetics derive revenue from molecular genetics testing clinical services provided by the Medical Genetics Laboratories; MGL <https://www.bcm.edu/geneticlabs>. Dr Doody provided consultations to AC Immune, Allon, Astellas, Avanir, Biote, Cardeus, Chiesi, Elan, ExonHit, Genzyme, GlaxoSmithKline, Hoffman LaRoche, Medivation, Merck, Nutricia, Otsuka, Pfizer, Prana, QR Pharma, Sanofi-Aventis, Shire, Sonexa, Takeda, Targacept, Transition and Zinfandel regarding experimental approaches to Alzheimer's disease and has stock options in QR Pharma, Sonexa and

Transition. She receives funding from the NIH Alzheimer's Disease Cooperative Study from a contract they have with Lilly. She receives funding from NIH AGO 10483 and AGO 224904, and from the Texas Alzheimer's Research and Care Consortium, and serves as PI on clinical trials funded by Genentech, Janssen with Pfizer, and Pfizer. She serves on the editorial boards of Alzheimer's Research and Therapy and Dementia and Geriatric Cognitive Disorders. Yanchun Li, Chad A Shaw, Irene Sheffer, Norbert Sule, Brian Dawson, Syed NY Zaidi, Kristine L Bucacas, Kirk C Wilhelmsen and Kinga Szigetzi declare no conflict of interest.

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