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ORIGINAL ARTICLE

Dynamin 2 gene is a novel susceptibility gene for late-onset Alzheimer disease in non-*APOE*-ε4 carriers

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Abstract Alzheimer disease (AD) is characterized by progressive cognitive decline caused by synaptic dysfunction and neurodegeneration in the brain, and late-onset AD (LOAD), genetically classified as a polygenetic disease, is the major form of dementia in the elderly. It has been shown that β amyloid, deposited in the AD brain, interacts with dynamin 1 and that the dynamin 2 (*DNM2*) gene homologous to the dynamin 1 gene is encoded at chromosome 19p13.2 where a susceptibility locus has been detected by linkage analysis. To test the genetic association of LOAD with the *DNM2* gene, we performed a case–control study of 429 patients with LOAD and 438 sex- and age-matched control subjects in a Japanese population. We found a significant association of LOAD with single nucleotide polymorphism markers of the *DNM2* gene, especially in non-carriers of the apolipoprotein E-ε4 allele. Even though subjects with the genotype homozygous for the risk allele at rs892086 showed no mutation in exons of the *DNM2* gene, expression of *DNM2* mRNA in the hippocampus was decreased in the patients compared to non-demented controls. We propose that the *DNM2* gene is a novel susceptibility gene for LOAD.

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Introduction

Alzheimer disease (AD) is the most common form of dementia in the elderly and is characterized by progressive cognitive decline with brain atrophy that is most marked in the temporal lobes. It is thought that β amyloid is a causative molecule in AD by disturbing synaptic function, leading to neuronal death (for review, see Selkoe 2002; Yao 2004). Although both early- and late-onset AD (LOAD) exhibit the same neuropathology in the brain, LOAD is genetically classified as a polygenetic disease and is characterized by more heterogeneous conditions than autosomal dominant early-onset AD. Apolipoprotein E (*APOE*) has been shown to be a major risk factor for LOAD (Corder et al. 1993; Farrer et al. 1997). Genome scans of LOAD detected several susceptibility loci, among which chromosomes 12, 10 and 9 have been the targets of searches for risk genes (Pericak-Vance et al. 1997; Blacker et al. 2003). Multipoint linkage analysis of LOAD families have also demonstrated a susceptibility locus at 19p13.2 between D19S391and D19S914 (Wijsman et al. 2004).

The major role of the dynamin proteins is in the endocytosis of vesicles, and its functions in vesicle budding have been described as being responsible for the constriction of the lipid neck, fission of lipids and regulation of the scission reaction (for review, see Praefcke and McMahon 2004). Expression of the dynamin 2 (*DNM2*) as well as dynamin 1 (*DNM1*) gene is downregulated by β amyloid in hippocampal neurons (Kelly et al. 2005), suggesting that the dynamin proteins are involved in the cascade of neurodegeneration caused by β amyloid. The dynamin-binding protein (*DNMBP*) gene on chromosome 10 has also been shown to be associated with LOAD (Kuwano et al. 2006). We observed that the *DNM2* gene is located at 19p13.2, within the region where a susceptibility locus was noted (Wijsman et al. 2004). Therefore, the *DNM2* gene could be a positional and functional candidate for a genetic risk for LOAD.

To examine whether the *DNM2* gene is genetically associated with LOAD, we performed an age- and sex-matched case–control study in a Japanese population. We propose herein that the *DNM2* gene is a novel genetic factor for LOAD in non-*APOE*-ε4 carriers.

Subjects and methods

Study subjects

Patients with LOAD were diagnosed as having definite or probable AD according to the criteria of the National Institute of Neurological and Communicative Disorders and Stroke–Alzheimer's Disease and Related Disorders Association (NINCDS–ADRDA) (McKhann et al. 1984). Controls consisted of non-demented elderly subjects obtained from the general population. Written informed consent to participate in this study was obtained, and then peripheral blood was drawn and subjected to DNA extraction. For a definite diagnosis of AD, dissections were carried out at the Choju Medical Institute after obtaining the agreement of the patients' guardians for diagnosis and genomic research. In total, 429 (69.9% female) patients participated in the study, of whom 66 had definite AD and 363 had probable AD. The mean age ± SD of the patient population at onset was 72.3 ± 8.1 years (range 60–94 years), and the mean age at blood drawing was 77.4 ± 8.7 years (range 60–98 years). The controls consisted of 438 individuals (63.7% female). The mean age of the controls at assessment was 74.5 ± 5.5 years (range 60–99 years). The age at onset of the patient was matched to the age of controls, and the sex composition was not different between the groups. Hippocampal tissue was also obtained from the postmortem brains of 22 patients with AD (age 82.8 ± 8.5 years, 63.6% female) and 12 controls (age 89.0 ± 7.0 years, age at onset 72.9 ± 7.2 years, 58.0% female). DNA was extracted from peripheral blood using a QIAamp DNA Blood Kit (Qiagen, Tokyo, Japan) and from brain tissue by the phenol–chloroform method (Sambrook et al. 1989). The procedure to obtain the specimens was approved by the Genome Ethical Committee of Osaka University Graduate School of Medicine, Ehime University, and the Choju Medical Institute of Fukushimura Hospital.

Genotyping and sequencing

Single nucleotide polymorphisms (SNPs) in the *DNM2* gene regions used in this study are listed in Table 1. Genotyping was performed by a quantitative genotyping method using the TaqMan SNP Genotyping System (Applied Biosystems, Foster City, CA). The genotype of the *APOE* gene was determined by a PCR-restriction fragment length polymorphism (RFLP) method (Wenham et al. 1991). DNA obtained from six patients and three controls homozygous for the risk allele at rs892086 of the *DNM2* gene was subjected to direct sequencing of its exons using the primers listed in Electronic Supplementary Material.

Quantitative real-time PCR

Total RNA was isolated from frozen hippocampal tissues using the acid guanidine–phenol–chloroform RNA extraction method provided as ISOGEN (Nippon Gene, Toyama, Japan) and purified using an RNeasy Mini kit (Qiagen, Valencia, CA). RNA samples with an A_{260}/A_{280} absorption ratio over 1.9 were subjected to cDNA synthesis using a High-Capacity cDNA Archive kit (Applied Biosystems). Primers and probe sets for the human *DNM2* and *β-actin* genes were purchased from TaqMan Gene Expression Assay products (Applied Biosystems), and quantitative real-time PCR was carried out in an ABI PRISM 7900HT (Applied Biosystems). All quantitative PCR reactions were duplicated, and the ratio of the amount of *DNM2* cDNA to that of the *β-actin* internal control cDNA was determined at the cycle threshold (CT).

Statistical analysis

Linkage disequilibrium (LD) between all pairs of biallelic loci was measured by Lewontin's D′ (|D′|) (Hedrick 1987)

Table 1 Single nucleotide polymorphism (SNP) markers in the *DNM2* gene

NCBI SNP reference ID	Location in NCBI (build 36.1)	Location	SNP sequence (allele ½)	Strand/orientation	Minor allele
rs12974306	10691281	Intron 1	CTCTT[G/T]CCTTT	fwd/B	Allele 2
rs714307	10696405	Intron 1	CGCTA[C/T]TGCTG	fwd/B	Allele 1
rs892086	10698677	Intron 1	GTTAG[A/G]TACCA	rev/T	Allele 1
rs34626880	10701428	Intron 1	AGCTC[C/T]ACCTG	fwd/B	Allele 2
rs10775614	10728219	Intron 1	GGCAC[A/G]TGGCG	fwd/T	Allele 2
rs7246673	10737841	Intron 2	AACCC[G/T]GCTGT	fwd/B	Allele 1
rs3826803	10744126	Intron 2	TTTCT[C/G]ATTTT	fwd/B	Allele 2
rs2043332	10752239	Intron 5	GTGAC[A/C]TCAGG	rev/T	Allele 1
rs873016	10755728	Intron 6	AAATG[A/G]TATTA	rev/T	Allele 1
rs1109376	10775829	Intron 12	AGGAT[A/G]CTTCT	fwd/T	Allele 1
rs3786719	10788100	intron 15	TGGAA[C/G]CTTCC	fwd/T	Allele 2
rs11085748	10788540	intron 15	GTTTT[C/T]CTCAT	fwd/B	Allele 2
rs3760781	10808522	3’UTR	TTGAG[C/T]GCTCA	fwd/B	Allele 2

UTR, Untranslated region; NCBI, National Center for Biotechnology Information

and r^2. Haplotype blocks, defined as segments with strong LD (Gabriel et al 2002), were calculated using Haploview (Barrett et al. 2005). Allele and genotype frequencies were assessed for associations by one-sided chi-squared test for both allele and genotype frequencies in dominant and recessive models, where p values less than 0.05 were tentatively judged to be significant. The effective number of independent marker loci in the *DNM2* gene was calculated to correct for multiple testing, using the software SNPSpD (http://www.genepi.qimr.edu.au/general/daleN/SNPSpD/) based on the spectral decomposition of matrices of pair-wise LD between SNPs (Nyholt 2004). The experiment-wide significance threshold required to keep the type I error rate at 5% was used for judging significance to correct for multiple testing. The values obtained by quantitative PCR, having a normal distribution, were compared by Student's t test, and a p value less than 0.05 was considered to be significant.

Results

We genotyped 13 SNPs located from intron 1 to the 3′-untranslated region (UTR) of the *DNM2* gene (Table 1). In total, 429 cases and 438 sex- and age-matched controls were genotyped, and their genotype distributions of both the cases and controls were in Hardy–Weinberg equilibrium. In these datasets, the *APOE*-ε4 allele was associated with LOAD ($p < 1 \times 10^{-10}$): compared to non-*APOE*-ε4 carriers, the odds ratio for carrying one *APOE*-ε4 allele was 4.3 [95% confidence interval (CI) 3.12−6.16] and that for carrying two *APOE*-ε4 allele was 28.4 (95% CI 6.75−119). Linkage disequilibrium statistics indicated more than three haplotype blocks in the *DNM2* gene region (Fig. 1). No validated SNPs were available between rs873016 and rs1109376 at a distance of approximately 20 kb, and no strong evidence of LD was found between these two SNPs. The case–control study showed that p values of less than 0.05 were found in four SNPs located from intron 6 to the 3′UTR in terms of allele distribution, and in seven SNPs from intron 1 to the 3′UTR in terms of genotype frequencies; their odds ratios were between 1.53 and 1.75 (Table 2). Calculations with SNPSpD indicated that the effective number of independent marker loci was 8.3094 and that the experiment-wide significance threshold was 0.006. Therefore, rs3760781 remained significant after the correction for multiple testing ($p = 0.003$). To examine the interaction between the *DNM2* gene and the *APOE* gene, the cases and controls were divided into *APOE*-ε4 carriers and non-*APOE*-ε4 carriers. In non-*APOE*-ε4 carriers, seven markers showed p values of less than 0.05, and the experiment-wide significance threshold (0.0059) supported a significant association at rs892086 ($p = 0.003$) as well as at rs3760781 ($p = 0.004$) (Table 3). However, no association was found in *APOE*-ε4 carriers (data not shown), indicating that the association of the *DNM2* gene is specific for non-*APOE*-ε4 carriers in our dataset.

To examine whether patients with the risk genotype could harbor any mutations in the *DNM2* gene, we sequenced all exons of the *DNM2* gene in patients and controls homozygous for the risk allele at rs892086, but we did not found any mutations, indicating that no particular mutation resulting in amino acid change is linked to the risk genotype of the *DNM2* gene. To examine the expression of the *DNM2* gene in the AD hippocampal tissue, we measured the amount of *DNM2* cDNA normalized to that of *β-actin* cDNA using quantitative PCR. Analysis of ten LOAD and eight control subjects revealed that there was significantly lower amounts of *DNM2* mRNA in the AD hippocampal tissue than in the controls ($p < 0.01$) (Fig. 2).

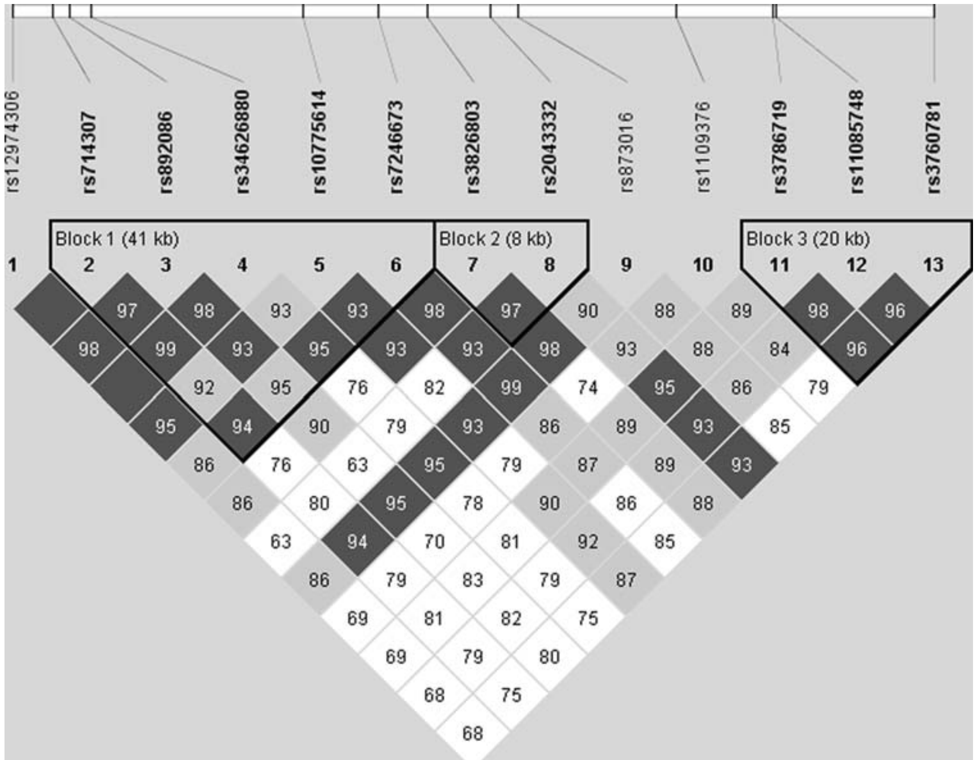

Fig. 1 Linkage disequilibrium coefficients and haplotype blocks in the *DNM2* gene region. Linkage disequilibrium coefficients (|D′|) among *DNM2* single nucleotide polymorphisms (SNPs) and haplotype blocks defined by strong LD are shown

Table 2 Association analysis of late-onset Alzheimer disease in the *DNM2* gene

SNP ID	LOAD				Control				Risk allele	*p* value	Risk genotype	*p* value	O.R (95% CI)
	Genotype number			MAF	Genotype number			MAF					
Genotype	1/1	2/2	½		1/1	2/2	½						
MArs12974306	174	57	196	0.363	204	46	188	0.320	Allele 2	NS	–	NS	
rs714307	16	285	127	0.186	16	304	117	0.170	Allele 1	NS	–	NS	
rs892086	93	134	202	0.452	67	145	226	0.411	Allele 1	NS	1/1	0.015	1.53 (1.08–2.17)
rs34626880	284	16	129	0.188	306	16	116	0.169	Allele 2	NS	–	NS	
rs10775614	306	11	111	0.155	326	14	95	0.141	Allele 2	NS	–	NS	
rs7246673	78	134	215	0.434	55	150	233	0.392	Allele 1	NS	1/1	0.020	1.56 (1.07–2.26)
rs3826803	132	86	209	0.446	145	58	234	0.400	Allele 2	NS	2/2	0.007	1.65 (1.15–2.37)
rs2043332	15	295	118	0.173	11	309	118	0.160	Allele 1	NS	–	NS	
rs873016	80	135	212	0.436	55	153	230	0.388	Allele 1	0.045	1/1	0.012	1.61 (1.11–2.33)
rs1109376	28	256	144	0.234	19	275	144	0.208	Allele 1	NS	–	NS	
rs3786719	145	85	198	0.430	166	57	215	0.376	Allele 2	0.021	2/2	0.007	1.66 (1.15–2.39)
rs11085748	138	81	209	0.433	160	56	222	0.381	Allele 2	0.027	2/2	0.013	1.59 (1.10–2.31)
rs3760781	141	87	199	0.437	157	56	225	0.385	Allele 2	0.028	2/2	0.003*	1.75 (2.21–2.52)

*Significant for experiment-wide significance threshold ($p < 0.006$)

LOAD, Late-onset Alzheimer disease; MAF, Minor Allele Frequency; O.R., odds ratio; 95% CI, 95% confidence interval

Discussion

We found that the *DNM2* gene is genetically associated with LOAD and that this association was specifically significant in non-*APOE*-ε4 carriers. In non-*APOE*-ε4 carriers, two SNPs, not in strong LD, were associated with LOAD. The *DNMBP* gene, which encodes a scaffold protein that binds to DNM1 protein, has been shown to be associated with LOAD in *APOE*-ε3*3 carriers or non-*APOE*-ε4 carriers, but not in *APOE*-ε4 carriers (Kuwano et al. 2006). Therefore, DNM2 protein could interact with proteins encoded in or linked to the *APOE*-ε3 genotype. It is

Table 3 Association analysis of late-onset Alzheimer disease in the *DNM2* gene in non-*APOE*-ε4 carriers

SNP ID	LOAD				Control				Risk allele	*p* value	Risk genotype	*p* value	O.R. (95% CI)
	Genotype number			MAF	Genotype number			MAF					
	1/1	2/2	½		1/1	2/2	½						
rs12974306	87	35	97	0.381	174	37	158	0.314	Allele 2	0.019	2/2	0.033	1.71 (1.04–2.80)
rs714307	6	152	63	0.170	12	259	97	0.164	Allele 1	NS		NS	
rs892086	55	64	102	0.480	56	121	192	0.412	Allele 1	0.023	1/1	0.003*	1.85 (1.22–2.81)
rs34626880	152	6	63	0.170	260	12	97	0.164	Allele 2	NS		NS	
rs10775614	164	5	51	0.139	278	11	77	0.135	Allele 2	NS		NS	
rs7246673	41	62	117	0.452	46	127	196	0.390	Allele 1	0.037	1/1	0.041	1.61 (1.02–2.54)
rs3826803	63	42	115	0.452	121	49	198	0.402	Allele 2	NS		NS	
rs2043332	7	149	64	0.177	7	264	98	0.152	Allele 1	NS		NS	
rs873016	42	63	116	0.452	46	130	193	0.386	Allele 1	0.025	1/1	0.031	1.65 (1.04–2.60)
rs1109376	13	138	69	0.216	15	234	120	0.203	Allele 1	NS		NS	
rs3786719	71	45	104	0.441	141	47	181	0.373	Allele 2	0.021	2/2	0.013	1.76 (1.13–2.76)
rs11085748	68	44	109	0.446	136	46	187	0.378	Allele 2	0.022	2/2	0.015	1.75 (1.11–2.74)
rs3760781	73	47	100	0.441	135	46	188	0.379	Allele 2	0.037	2/2	0.004*	1.91 (1.22–2.98)

*Significant for experiment-wide significance threshold ($p < 0.0059$)

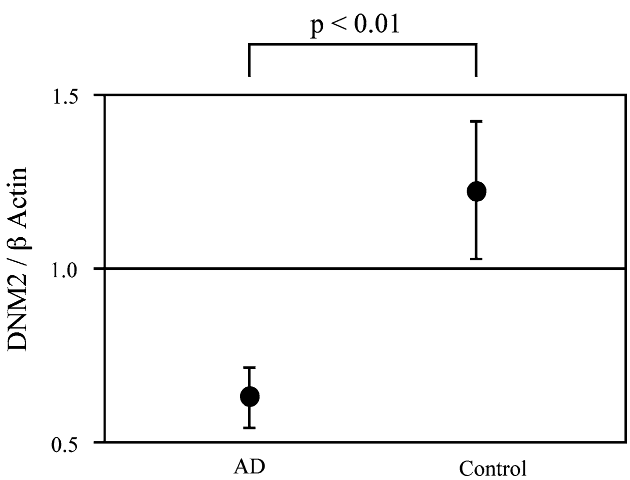

Fig. 2 Expression of *DNM2* mRNA in the hippocampus. The ratio of the amount of *DNM2* cDNA to that of *β-actin* cDNA is shown. *Dots* indicate mean value, *bars* indicate standard error

possible that the causative mechanism of DNM2 for the development of AD could be different from the lipid transfer proteins involved in lipid metabolism, such as the *APOE* (Strittmatter et al. 1993), *LRP* (Kang et al. 1997) and *CYP46* genes encoding cholesterol 24S-hydroxylase (Kolsch et al. 2002). However, the majority of cases genotyped in our study are still living, and the use of still living controls also warrants caution as the incidence of developing dementia increases with age. Therefore, our results could be misrepresented, as the controls may still develop AD, or we may have misdiagnosed AD patients who may actually have another form of dementia.

The *DNM* gene was first identified as the locus for a paralytic phenotype in *Drosophila melanogaster* (Suzuki et al. 1971) and encodes large GTPases that can associate with microtubules in vitro (Shpetner and Vallee 1989; Obar et al. 1990). The dynamin proteins are distinguished from other GTPases by their low GTP-binding affinities and the ability of many members of the dynamin family to interact with lipid membranes (for review, see Praefcke and McMahon 2004). Mutations of the pleckstrin homology domain of the *DNM2* gene, leading to diminished binding of the DNM2 protein to membranes, are responsible for Charcot–Marie-Tooth disease (Zuchner et al. 2005). While Charcot–Marie-Tooth disease is clinically characterized by peripheral neuropathy, the relation between aging and *DNM2* gene expression remains undetermined. Disuse muscle atrophy related to decreased daily activity is commonly found in the elderly, but it is unclear whether exercise is effective for the maintenance of cognitive function.

Kelly et al. (2005) showed that *β* amyloid induces depletion of the DNM1 as well as DNM2 protein in cultured hippocampal neurons and the hippocampus of a Tg2576 mouse model of AD. On the other hand, dominant-negative DNM1, which selectively inhibits receptor-mediated endocytosis, raises the levels of mature amyloid precursor protein (APP) at the cell-surface, which is consistent with retention of APP on the plasma membrane, and endogenous A*β* secretion was significantly increased (Chyung and Selkoe 2003). It has also been shown that the location of *β* amyloid can be changed by decreased activity of the DNM1 protein and that endocytosis affects the precision of PS-dependent epsilon-cleavage in cell culture (Fukumori et al. 2006). Whereas the DNM1 protein is specific for presynaptic terminals in the central nervous system (CNS), the DNM2 protein is ubiquitously expressed and, to our knowledge, does not exist in presynaptic terminals in the CNS. However, DNM2 has a similar structure to DNM1 and might also affect the sequestration and scavenging of β amyloid in relation to its axonal transport in peripheral nervous system.

We found that the expression of hippocampal *DNM2* mRNA was lower in the patients than in the control subjects, but this result should be carefully interpreted. We examined a small number of hippocampal tissue samples and used *β-actin* cDNA as an internal control; however, quantitative PCR revealed that the *β-actin* transcript is differently expressed in brain specimens of AD and control subjects (Gutala and Reddy 2004). Therefore, this decrease should be examined in the other brain areas and also in a larger number of samples using another internal control cDNA, such as *GAPDH* (Gutala and Reddy 2004). Alternatively, *DNM2* gene expression could be depleted in AD due to the widespread devastation of neurons, particularly in the hippocampus, as well as by β amyloid. Therefore, it remains to be determined whether the decrease in *DNM2* expression is the cause or the outcome of AD.

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