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Multiple candidate gene analysis identifies α-*synuclein* as a susceptibility gene for sporadic Parkinson's disease

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Parkinson's disease (PD), one of the most common human neurodegenerative diseases, is characterized by the loss of dopaminergic neurons in the substantia nigra of the midbrain. PD is a complex disorder with multiple genetic and environmental factors influencing disease risk. To identify susceptible genes for sporadic PD, we performed case–control association studies of 268 single nucleotide polymorphisms (SNPs) in 121 candidate genes. In two independent case–control populations, we found that a SNP in α-*synuclein* (*SNCA*), rs7684318, showed the strongest association with PD ($P = 5.0 \times 10^{-10}$). Linkage disequilibrium (LD) analysis using 29 SNPs in a region around rs7684318 revealed that the entire *SNCA* gene lies within a single LD block ($D' > 0.9$) spanning ∼120 kb. A tight LD group ($r^2 > 0.85$) of six SNPs, including rs7684318, associated most strongly with PD ($P = 2.0 \times 10^{-9}$–1.7×10^{-11}). Haplotype association analysis did not show lower *P*-values than any single SNP within this group. SNCA is a major component of Lewy bodies, the pathological hallmark of PD. Aggregation of SNCA is thought to play a crucial role in PD. *SNCA* expression levels tended to be positively correlated with the number of the associated allele in autopsied frontal cortices. These findings establish *SNCA* as a definite susceptibility gene for sporadic PD.

INTRODUCTION

Sporadic Parkinson's disease (PD) (OMIM no. 168600) is the second most common neurodegenerative disease following Alzheimer's disease. PD is late onset and progressive, affecting 1–2% of persons older than 65 years. Clinical features of PD include resting tremor, bradykinesia, rigidity and postural instability. The disease is pathologically characterized by the loss of dopaminergic neurons in the substantia nigra and the presence of intracellular inclusions known as Lewy bodies. Various medical managements are available for PD, including drugs (l-dopa, dopamine agonists, anti-cholinergic drugs, etc.) and surgery (thalamotomy, pallidotomy, deep brain stimulation, etc.) (1). These treatments improve PD symptoms, but do little to deter disease progression. Identifying risk factors for PD can be helpful in delaying disease onset and slowing its progression.

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PD is a complex common disease, caused by multiple genetic and environmental factors (2). The contribution of genetic factors to sporadic PD is indicated by several findings. First, ~10% of patients with PD have a positive family history (3). Secondly, a recent large-scale survey in Iceland showed that the risk ratio for PD was increased in related individuals (6.7 for siblings, 3.2 for offspring and 2.7 for nephews and nieces of patients with PD) (4). Thirdly, a twin study using [^{18}F]dopa PET showed that the concordance rate for PD, including subclinical cases, is approximately three times higher in monozygotic twins (55%) than in dizygotic twins (18%) (5).

Causal genes for Mendelian-inherited PD have been reported, including *α-synuclein* [4q21, autosomal dominant (AD)] (6), *parkin* [6q25.2–27, autosomal recessive (AR)] (7), *UCH-L1* (4p14, AD) (8), *PINK1* (1p36, AR) (9), *DJ-1* (1p36, AR) (10), *LRRK2/dardarin* (12q12, AD) (11,12) and *NR4A2/Nurr1* (2q22–23, AD) (13).

Many case–control association studies using single nucleotide polymorphisms (SNPs) in candidate genes have been reported, but few consistent findings have been obtained (2). This is due, in part, to limited numbers of available samples, target genes and/or genetic markers. Since 2001, genome-wide, non-parametric linkage analysis of PD families has revealed significant linkage in multiple chromosomal regions (14–17), leading to the identification of *tau* (18) and *FGF20* (19) as susceptibility genes.

To date, polymorphisms that influence PD as strongly as *APOE-ε4* influences Alzheimer's disease have not been identified. Through extensive candidate gene association studies, we have established *α-synuclein* (*SNCA*) as a definite susceptibility gene for sporadic PD.

RESULTS

Screening of SNPs in candidate genes for PD

We selected candidate genes from the literature describing genetic, pathological and biochemical findings in PD, as well as genes that participate in the proposed mechanisms for PD. Finally, we picked up 121 genes relevant to familial PD, Lewy bodies, dopaminergic neurons, cytokines and trophic factors, mitochondrial functions, oxidative stress, proteasome function, autophagy, endoplasmic reticulum-associated degradation (ERAD) and toxins. One to seven SNPs per gene (268 SNPs total) were selected from the dbSNP, JSNP and Celera Discovery System databases.

In the initial screen, we genotyped 190 patients and 190 controls (Supplementary Material, Table S1). To avoid false negatives, we set the α-value at 0.05 in the first screen. From 268 SNPs, 22 SNPs in 16 genes showed association with PD ($P < 0.05$) in genotype frequency, allele frequency, dominant model or recessive model. We genotyped the 22 qualifying SNPs in a replication panel of 692 patients and 748 controls and tested again for association. This independent test revealed that SNP0070 (rs7684318 C/T) was prominently associated with PD ($P = 5.0 \times 10^{-10}$ for allele frequency) (Table 1). We corrected the α-value to 0.00019 after Bonferroni's correction (tests for 268 SNPs). The remaining 21 SNPs did not show *P*-values lower than 0.00019 (data not shown). SNP0070 is located in intron 4 of the *α-synuclein* (*SNCA*) gene on chromosome 4q21. SNCA is a primary component of intracellular inclusions called Lewy bodies, which are considered to be the pathological hallmark of PD (20). Aggregation of SNCA is thought to play a crucial role in the pathogenesis of PD (21). The allele C frequency of SNP0070 was higher in PD (0.67) than in controls (0.57) (Table 1). The association of SNP0070 was significant in genotype frequency, allele frequency, dominant model and recessive model. Of the two disease models, allele C of SNP0070 was more significantly associated in the recessive model than in the dominant model (Table 1).

Linkage disequilibrium (LD) mapping and search for susceptibility SNPs

We performed LD mapping in a 430 kb region around SNP0070. This region contains two genes: *SNCA* and *MMRN1*. Using SNP0070 and 28 additional SNPs in this region, we genotyped 134 control subjects and constructed an LD map based on pairwise D' and r^2 (Fig. 1) (Supplementary Material, Table S2). Three LD blocks were observed on the basis of D' ($D' > 0.9$). The entire *SNCA* gene was included in a block containing SNP0070 (block 2). The *MMRN1* gene was in another LD block, indicating that *MMRN1* does not correlate with the SNP0070 association (Fig. 2).

To search for the most strongly associated SNP(s) in the region, we next performed association studies with these 29 SNPs (Fig. 2; Table 2). We found significant associations for SNPs in block 2, but not in blocks 1 and 3. Block 2, thought to be a susceptibility block for PD, was further analyzed on the basis of r^2-values. Of the 19 SNPs in block 2, 16 belonged to three groups with high pairwise r^2 (>0.85) and the remaining three did not belong to any group (Fig. 1; Table 2) (Supplementary Material, Table S2). Six SNPs in group 1, including originally screened SNP0070 and five additional SNPs (0203, 0204, 0205, 0207 and 0209), showed prominent association with PD ($P = 2.0 \times 10^{-9}$–1.7×10^{-11}, allele 1 versus allele 2) (Fig. 2; Table 2). Population attributable risk (PAR) (22) of SNP0070 was 42.5% in the dominant model and 18.5% in the recessive model.

We next performed haplotype analysis using six representative SNPs in block 2 (Table 3). Six common haplotypes (>1% of PD and controls) covered >90% of the population haplotypes in both PD and controls. The major haplotypes 1 and 2 showed significant associations; however, their *P*-values were not lower than that of any single SNP in group 1. Therefore, the presence of hidden SNP(s) with a lower *P*-value than group 1 seemed unlikely, as was the possibility that the haplotype(s) is implicated in PD susceptibility. These findings establish the six SNPs in group 1 as the strongest susceptibility SNPs. All showed stronger associations in the recessive model than in the dominant model, similar to the originally screened SNP0070 (Table 4).

Taken together, our genetic analyses indicate that *SNCA* is a definite susceptibility gene for sporadic PD and that multiple SNPs in group 1 are susceptibility SNPs, likely in a recessive model.

Table 1. Association of SNP0070 in *SNCA* between cases and controls

	Genotype				Allele			*P*-value (χ^2-test)			
	CC	CT	TT	Total	C	T	Total	Genotype	Allele	Dominant[a] model	Recessive[b] model
First screen											
Case	87 (0.46)	87 (0.46)	14 (0.07)	188	261 (0.69)	115 (0.31)	376	3.4×10^{-4}	1.8×10^{-4}	1.8×10^{-4}	1.1×10^{-2}
Control	62 (0.33)	85 (0.46)	39 (0.21)	186	209 (0.56)	163 (0.44)	372				
Replication											
Case	298 (0.44)	307 (0.45)	75 (0.11)	680	903 (0.66)	457 (0.34)	1360	1.3×10^{-6}	4.2×10^{-7}	1.5×10^{-3}	9.0×10^{-7}
Control	233 (0.31)	387 (0.52)	126 (0.17)	746	853 (0.57)	639 (0.43)	1492				
Total											
Case	385 (0.44)	394 (0.45)	89 (0.10)	868	1164 (0.67)	572 (0.33)	1736	2.7×10^{-9}	5.0×10^{-10}	5.7×10^{-6}	2.8×10^{-8}
Control	295 (0.32)	472 (0.51)	165 (0.18)	932	1062 (0.57)	802 (0.43)	1864				

Frequencies of genotypes and alleles are in parentheses.
[a]Genotype CC+CT versus TT.
[b]Genotype CC versus CT+TT.

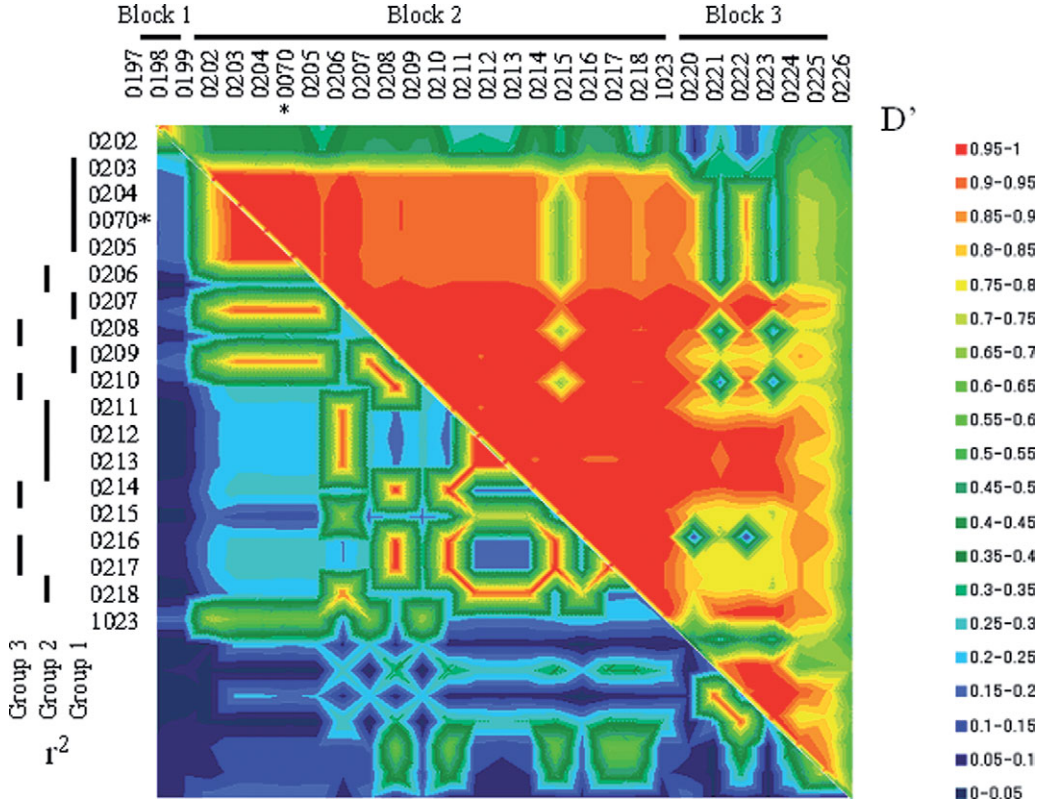

Figure 1. LD structure of the susceptibility region for sporadic PD. Pairwise LD between SNPs, as measured by D' in 134 controls, is graphically indicated. The region spanning 430 kb around the originally screened SNP0070(*) was divided into three LD blocks ($D' > 0.9$) (upper right). On the basis of r^2, SNPs in block 2, including SNP0070, were further divided into three groups ($r^2 > 0.85$) and three solitary SNPs (lower left). The scale is nominal.

SNCA gene expression in relation to susceptibility genotypes

To examine whether the strongest associated SNPs (group 1) affect *SNCA* gene expression, we further quantified *SNCA* mRNA in autopsied frontal cortices and compared the values among the genotypes. SNP0070, in which allele C is associated with PD, was used as a representative of group 1.

The relative values of *SNCA* mRNA for all cases ($n = 21$) and all controls ($n = 18$) were 1.07 ± 0.10 and 0.95 ± 0.13, respectively, showing almost the same level ($P = 0.46$, Student's *t*-test). When compared among the genotypes in cases, the mean tended to decrease in the order of CC, CT and TT (Fig. 3), although the differences did not reach the significant levels ($P = 0.71$ for CC versus CT, $P = 0.16$ for CT versus TT and $P = 0.32$ for CC versus TT). Similar tendency

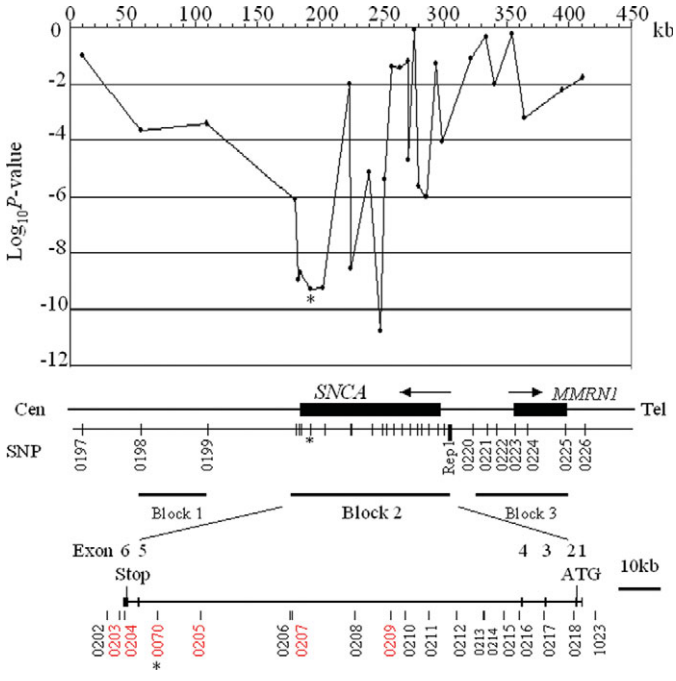

Figure 2. Genomic structure and SNPs of the susceptibility region for sporadic PD and case–control association studies (882 cases and 938 controls). Log *P*-values (allele 1 versus allele 2) are plotted against the physical location of the SNPs. The region includes two genes: *SNCA* and *MMRN1*; transcription orientation is indicated by horizontal arrows. Physical locations of SNPs are shown as axial bars with our experimental ID number. The originally screened SNP0070 is indicated by an asterisk. The location of Rep1, a well-known repeat polymorphism in the *SNCA* promoter region, is indicated by a thick bar. SNPs in block 2 are nominated in an expanded map with the exon–intron structure of *SNCA*. SNPs in group 1 are shown in red. Note that *P*-values are prominently low at the group 1 SNPs located in the 3′ region of *SNCA*. *P*-values in the region around Rep1 are far from significant when compared with those in group 1.

was observed in controls. The mean tended to decrease in the order of CC, CT and TT (Fig. 3) ($P = 0.33$ for CC versus CT, $P = 0.59$ for CT versus TT and $P = 0.54$ for CC versus TT).

These results indicate the possibility that expression of *SNCA* mRNA in the brain tends to be positively correlated with the number of PD-associated allele.

DISCUSSION

To identify susceptibility genes for PD, we performed an extensive candidate gene approach by screening 268 SNPs in 121 genes and identified a prominent association with SNP0070 (rs7684318) in the *SNCA* gene (Table 1). LD mapping localized the entire *SNCA* gene within a single LD block (Figs 1 and 2). Within this block, six SNPs including SNP0070 were in a tight LD group and most strongly associated with PD (Fig. 2; Table 2). The major allele of each SNP in group 1 was positively associated with PD, more strongly in the recessive model than in the dominant model (Table 4). Our genetic analyses establish *SNCA* as a definite susceptibility gene for PD and identify multiple SNPs in group 1 as susceptibility SNPs. Recently, Mueller *et al.* (23) reported that multiple regions of *SNCA* are associated with PD in the German population. Associated SNPs identified by Mueller *et al.* included rs356165 ($P = 1.5 \times 10^{-4}$), which corresponds to SNP0204 in our study, indicating that this SNP has a similar association in Caucasians. Pals *et al.* (24) previously reported no association of the haplotype containing rs356165 with PD in Belgian samples. This contradictory finding may be, at least in part, due to a small sample size (175 cases and 186 controls), as mentioned by the authors.

SNCA/α-synuclein was originally identified in the electric organ of the Pacific electric ray (25). SNCA is a presynaptic protein that is highly and broadly expressed in the brain, but its normal function remains unknown (21). It is a major component of Lewy bodies, the pathological hallmark of PD (20), and the aggregation of SNCA protein is thought to play a crucial role in the loss of dopaminergic neurons (21,26).

SNCA was also the first gene identified as a causative gene in familial PD. Three missense mutations in *SNCA* were reported in families with AD inheritance (6,27,28). These mutations are thought to increase the aggregation of SNCA protein. Point mutations in *SNCA* have not been identified in sporadic PD (27,29), and no SNPs have been found in the coding region, suggesting that disease-related amino acid changes in SNCA are unlikely in sporadic PD.

Genes' overdosage is a potential mechanism for the influence of *SNCA* in PD. Triplication of the *SNCA* locus has been seen in an AD PD family (30), and doubling of *SNCA* gene dosage by triplication has been shown to result in the doubling of mRNA and protein expression in blood and brain (31). Duplication of *SNCA* has also been identified as a cause of familial PD (32,33). Clinical features of patients with *SNCA* duplication resemble those of sporadic cases and are much milder than those with triplication. Taken together, these observations indicate a correlation between increased SNCA protein levels and disease risk. Identification of one or more polymorphisms related to *SNCA* expression level might reveal strong susceptibility indicators for sporadic PD. Many studies have focussed on a mixed repeat microsatellite polymorphism called Rep1 (34), because of its location in the *SNCA* promoter region. However, their significance is uncertain, possibly because of the small number of samples (35–37). Our study demonstrates that the *P*-values of SNPs around Rep1 (0218, 1023 and 0220) are less significant than that of the SNPs in group 1 (Fig. 2). In addition, we genotyped our samples for Rep1. Pairwise *D*′-values showed that Rep1 was not in block 2, but on the boundary (Supplementary Material, Table S2). *P*-value of Rep1 was 7.5×10^{-7} (Supplementary Material, Table S3), which might be explained by its intermediate correlation with the strongest susceptibility SNPs (group 1, $P = 2.0 \times 10^{-9}$–1.7×10^{-11}). Our findings suggest that *P*-value of Rep1 depends on its LD strength with SNPs in group 1. LD strength may be modified by the unstableness of microsatellite markers (38) and may vary among races (39). Taken together, these findings may also partly explain the contradictory findings of previous Rep1 association studies.

To investigate the relationship between the SNPs in group 1 and the *SNCA* expression levels, we analyzed *SNCA* mRNA expression in autopsied frontal cortices (Fig. 3). *SNCA* expression levels tended to be positively correlated with the number of the PD-associated allele, supporting the popular hypothesis that increased SNCA leads to the disease.

Table 2. Association analysis in *SNCA* and surrounding region

SNPs			LD block	Genotype							
ID (rs ID)	Alleles 12	Location	(group)	Case 11/12/22	(Total)	Control 11/12/22	(Total)	MAF Case/control	Allele 1 versus allele 2 *P*-value	OR (95% CI)	HWE Case/control
0197 (rs3733450)	TC		1	38/286/549	(873)	33/280/619	(932)	0.21/0.19	0.10	1.15 (0.97–1.36)	1.00/0.93
0198 (rs1390280)	AG		1	366/384/118	(868)	316/454/162	(932)	0.36/0.42	2.1×10^{-4}	1.29 (1.13–1.46)	0.32/1.00
0199 (rs3733449)	CT		1	117/375/374	(866)	154/451/322	(927)	0.35/0.41	3.7×10^{-4}	1.28 (1.11–1.48)	0.16/0.91
0202 (rs356221)	TA	3′-flanking	2	73/369/431	(873)	123/449/360	(932)	0.30/0.37	7.2×10^{-7}	1.42 (1.25–1.63)	0.69/0.40
0203 (rs3857053)	TC	3′-flanking	2 (1)	380/406/87	(873)	293/476/164	(933)	0.33/0.43	1.1×10^{-9}	1.53 (1.33–1.73)	0.18/0.24
0204 (rs356165)	GA	3′-UTR	2 (1)	379/399/89	(867)	289/482/159	(930)	0.33/0.43	2.0×10^{-9}	1.52 (1.33–1.74)	0.32/0.09
0070[a] (rs7684318)	CT	Intron 4	2 (1)	385/394/89	(868)	295/472/165	(932)	0.33/0.43	5.0×10^{-10}	1.54 (1.35–1.75)	0.47/0.35
0205 (rs3775424)	CT	Intron 4	2 (1)	87/406/376	(869)	166/477/288	(931)	0.33/0.43	5.4×10^{-10}	1.52 (1.34–1.75)	0.16/0.22
0206 (rs3775426)	CT	Intron 4	2 (2)	56/350/456	(862)	53/324/555	(932)	0.27/0.23	0.0098	1.22 (1.05–1.41)	0.35/0.59
0207 (rs3796661)	CT	Intron 4	2 (1)	91/367/382	(840)	154/482/296	(932)	0.33/0.42	2.7×10^{-9}	1.52 (1.31–1.76)	0.90/0.08
0208 (rs3775435)	GA	Intron 4	2 (3)	157/434/272	(863)	115/439/375	(929)	0.43/0.36	7.3×10^{-6}	1.36 (1.18–1.56)	0.53/0.48
0209 (rs2737029)	TC	Intron 4	2 (1)	84/377/402	(863)	156/480/297	(933)	0.32/0.42	1.7×10^{-11}	1.60 (1.40–1.83)	0.81/0.12
0210 (rs3775442)	TC	Intron 4	2 (3)	158/438/274	(870)	114/440/378	(932)	0.43/0.36	4.2×10^{-6}	1.37 (1.19–1.58)	0.50/0.46
0211 (rs3756055)	GA	Intron 4	2 (2)	50/339/481	(870)	49/319/565	(933)	0.25/0.22	0.042	1.17 (1.00–1.37)	0.38/0.72
0212 (rs3775446)	TG	Intron 4	2 (2)	50/340/480	(870)	49/317/565	(931)	0.25/0.22	0.034	1.19 (1.01–1.38)	0.36/0.67
0213 (rs3756056)	CT	Intron 4	2 (2)	50/340/482	(872)	48/323/557	(928)	0.25/0.23	0.062	1.16 (0.99–1.34)	0.37/0.97
0214 (rs894278)	GT	Intron 4	2 (3)	156/438/275	(869)	117/441/375	(933)	0.43/0.36	1.9×10^{-5}	1.34 (1.18–1.52)	0.46/0.52
0215 (rs1812923)	CA	Intron 4	2	74/383/413	(870)	92/392/447	(931)	0.31/0.31	0.79	1.01 (0.89–1.16)	0.30/0.71
0216 (rs2298728)	AG	Intron 4	2 (3)	163/432/274	(869)	117/435/380	(932)	0.44/0.36	2.2×10^{-6}	1.38 (1.22–1.56)	0.80/0.72
0217 (rs3796667)	AT	Intron 3	2 (3)	159/430/271	(860)	114/428/383	(925)	0.44/0.36	9.2×10^{-7}	1.41 (1.23–1.61)	0.66/0.80
0218 (rs2035268)	TG	Intron 2	2 (2)	475/339/54	(868)	556/326/51	(933)	0.26/0.23	0.049	1.16 (0.99–1.37)	0.59/0.79
1023 (rs1023777)	CT	5′-flanking	2	66/318/464	(848)	86/433/411	(930)	0.27/0.33	9.3×10^{-5}	1.33 (1.15–1.55)	0.31/0.08
0220 (rs2736994)	GA		3	542/263/22	(827)	529/292/33	(854)	0.19/0.21	0.081	1.16 (0.98–1.38)	0.17/0.41
0221 (rs11097239)	CA		3	245/437/182	(864)	272/431/226	(929)	0.46/0.48	0.48	1.05 (0.92–1.19)	0.67/0.04
0222 (rs1899389)	AG		3	592/245/29	(866)	586/297/46	(929)	0.18/0.21	0.009	1.25 (1.05–1.46)	0.64/0.34
0223 (rs2289515)	AT		3	180/436/238	(854)	221/423/267	(911)	0.47/0.48	0.6	1.03 (0.90–1.18)	0.49/0.04
0224 (rs3775464)	GA		3	109/414/346	(869)	95/385/449	(929)	0.36/0.31	5.9×10^{-4}	1.28 (1.11–1.46)	0.43/0.40
0225 (rs1246270)	GA		3	372/394/84	(850)	474/372/81	(927)	0.33/0.29	0.0061	1.21 (1.05–1.40)	0.19/0.56
0226 (rs3822098)	CT		3	50/300/514	(864)	59/376/494	(929)	0.23/0.27	0.017	1.21 (1.04–1.40)	0.54/0.30

MAF, minor allele frequency. When the odds ratio (OR) is less than 1, an inverted score is indicated.
[a]Originally screened SNP.

Table 3. Haplotype association analysis using representative SNPs in block 2

Haplotypes	Representative SNP (group)						Haplotype frequency		*P*-value
	202	0070 (1)	0206 (2)	0214 (3)	0215	1023	Case	Control	
1	A	C	T	G	A	T	0.39	0.33	4.4×10^{-5}
2	T	T	T	T	A	C	0.24	0.3	5.0×10^{-6}
3	A	C	C	T	C	T	0.24	0.21	0.071
4	A	T	T	T	C	T	0.03	0.06	3.3×10^{-4}
5	T	T	T	T	C	T	0.02	0.03	0.083
6	T	T	T	G	A	T	0.01	0.02	0.62

Table 4. Association of the SNPs in group 1 of block 2

SNP	Allele	Genotype						Dominant model (MM + Mm versus mm)		Recessive model (MM versus Mm + mm)	
		Case			Control						
	M/m	MM	Mm	mm	MM	Mm	mm	*P*-value	Odds ratio (95% CI)	*P*-value	Odds ratio (95%CI)
0203	T/C	380	406	87	293	476	164	3.0×10^{-6}	1.95 (1.45–2.52)	1.0×10^{-7}	1.68 (1.41–2.07)
0204	G/A	379	399	89	289	482	159	2.7×10^{-5}	1.81 (1.36–2.38)	3.0×10^{-8}	1.72 (1.43–2.13)
0070[a]	C/T	385	394	89	295	472	165	5.7×10^{-6}	1.90 (1.44–2.53)	2.8×10^{-8}	1.71 (1.42–2.06)
0205	T/C	376	406	87	288	477	166	1.8×10^{-6}	1.98 (1.45–2.61)	6.0×10^{-8}	1.69 (1.40–2.05)
0207	T/C	382	367	91	296	482	154	5.3×10^{-4}	1.66 (1.25–2.16)	3.0×10^{-9}	1.78 (1.47–2.16)
0209	C/T	402	377	84	297	480	156	1.4×10^{-5}	1.89 (1.41–2.51)	1.5×10^{-10}	1.86 (1.55–2.27)

M and m are major allele and minor allele, respectively. CI, confidence interval.
[a]Originally screened SNP.

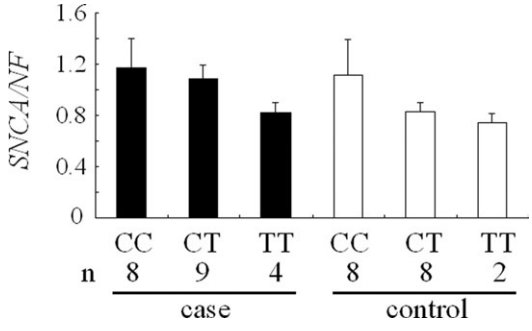

Figure 3. *In vivo* expression of *SNCA* mRNA in relation to susceptibility genotypes. SNP0070 (C/T) is used as a representative of group 1. *SNCA* expression levels in autopsied frontal cortices of cases (solid bar; 8 CC, 9 CT and 4 TT) and controls (open bar; 8 CC, 8 CT and 2 TT). Relative *SNCA* mRNA levels (normalized to *neurofilament L, NF*) are indicated. In cases, mean ± SEM of CC, CT and TT were 1.17 ± 0.23, 1.08 ± 0.11 and 0.82 ± 0.08, respectively. In controls, mean ± SEM of CC, CT and TT were 1.11 ± 0.28, 0.83 ± 0.07 and 0.75 ± 0.07, respectively.

The PD-associated alleles may positively correlate with the basal transcription level of *SNCA* and/or the induction of *SNCA* expression by certain stimulators, for example, oxidative stress.

Other possible functional effects of associated SNPs include alternative splicing, which may result in a protein isoform that aggregates more readily. The C-terminal region of SNCA is rich in acidic amino acid residues, and its truncation promotes aggregation *in vitro* (40,41). The known splice variant *SNCA112* lacks exon 5, which encodes 28 amino acids (10 of which are acidic) in frame. Thus, SNCA112 may also promote aggregation. We investigated *SNCA112* mRNA expression in frontal cortices using splice variant-specific primers, but observed little difference among the three genotypes (data not shown).

In summary, our study establishes *SNCA* as a susceptibility gene for sporadic PD. Focussed investigations of SNCA function will further enhance our understanding of how genetic factors contribute to the complex etiology of PD.

MATERIALS AND METHODS

Subjects

We recruited 882 unrelated sporadic PD patients (age, 64.9 ± 9.8; male/female ratio, 0.79) and 938 unrelated controls (age, 45.3 ± 16.3; male/female ratio, 1.10). The diagnosis of idiopathic PD was based on the presence of two or more of the cardinal features of PD (tremor, rigidity, bradykinesia and postural instability), according to the criteria for sporadic PD (42). Patients were evaluated by the certified neurologists specializing in PD. The average age of onset was 57.4 ± 10.9 years. Forty-two patients showed early onset of PD (<40 years) and 51 patients had a positive family history of PD. Patients who carried *parkin* mutations were excluded. All patients and controls were of Japanese ancestry. Informed consent was obtained from each individual, and approval for the study was obtained from the University Ethical Committees.

SNP genotyping

Genomic DNA was extracted from whole blood using FlexGene (Qiagen). SNP information was obtained from the dbSNP (http://www/ncbi.nlm.nih.gov/SNP/), JSNP (http://snp.ims.u-tokyo.ac.jp/) (43) and Celera Discovery System

(http://myscience.appliedbiosystems.com/) databases. We genotyped SNPs using the Invader assay (Third Wave Technologies), TaqMan (Applied Biosystems) or direct sequencing using an ABI3730 capillary sequencer (Applied Biosystems). Rep1 genotyping and allele designations followed those described previously (35). The Rep1 region was amplified using FAM5′-CCTGGCATATTTGATTGCAA-3′ and 5′-GACTGGCCCAAGATTAACCA-3′ as primers and analyzed using ABI3730 capillary sequencer.

Statistical analysis

SNPAlyze software (DYNACOM, Japan) was used for the case–control study (χ^2-test), calculation of odds ratio and its 95% CI (Bootstrap method), haplotype analysis (Expectation–Maximization algorithm) and pairwise LD analysis (Lewontin's coefficient D' and standardized coefficient r).

Real-time RT–PCR

Autopsied frontal cortices were obtained from the Brain Bank for Aging Research (Tokyo Metropolitan Geriatric Hospital/Tokyo Metropolitan Institute of Gerontology) and from the Department of Neurology, Juntendo University School of Medicine. The samples contained 21 cases [age, 82.6 ± 7.1 (SD) years; 11 males and 10 females] with Lewy body pathology defined by the third Consensus Guideline for Dementia with Lewy Bodies (44), comprising PD with and without dementia and dementia with Lewy bodies, and 18 control subjects (age, 81.2 ± 5.2; 12 males and six females) without parkinsonism or dementia and without neurodegenerative pathological changes. Total RNA was extracted from tissues using RNeasy (Qiagen), and cDNA was prepared using Superscript reverse transcriptase (Invitrogen). Real-time RT–PCR was carried out on ABI PRISM 7900 sequence detection system (Applied Biosystems) using SYBR Premix Ex Taq (TAKARA, Japan). First-strand cDNA was amplified using primers specific for *SNCA* (forward: 5′-GCAGAAGCA GCAGGAAAGAC-3′; reverse: 5′-CTGGGCTACTGCTGTC ACAC-3′; product size: 159 bp) and *NF* (*neurofilament L*, forward: 5′-AGAACGCTGAGGAATGGTTC-3′; reverse: 5′-CTGGTGAAACTGAGTCGGGT-3′; product size: 391 bp). A single band of the expected size was amplified from cDNA samples, but not from RNA samples. For quantification, we used a relative standard curve method. Standard curves of *SNCA* and *NF* were generated from the amplification of diluted series of cDNA from cortices. *SNCA* expression levels were normalized to those of *NF*. One of the experimental samples was used as the calibrator. Each of the normalized *SNCA* values was divided by the calibrator normalized *SNCA* value to generate the relative expression levels. The values were determined in triplicate. Reproducibility of the results was confirmed by repeating cDNA synthesis and real-time PCR twice for seven samples, and similar results were obtained.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG Online.

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Conflict of Interest statement. None declared.

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