

schizophrenia in Japanese subjects (4.8% in patients vs. 2.3% in control subjects). We observed a similar tendency for the T allele frequency (3.7% in patients vs. 2.2% in control subjects), although the difference was not statistically significant ($p = 0.090$).

In contrast, other previous studies failed to find such an association in Finnish (Anttila et al., 2005), European (Galderisi et al., 2005) and Polish (Szczepankiewicz et al., 2005) populations. These conflicting results may be due to an ethnic heterogeneity in the C132T polymorphism. The control subjects in Anttila et al. (2005), Galderisi et al. (2005) and Szczepankiewicz et al. (2005) showed higher frequencies of the T allele (7.1%, 9.9% and 4.6%, respectively) than those in Szekeres et al. (2003), Nanko et al. (2003) and the present study (2.8%, 2.3% and 2.2%, respectively). Our sample size ($n = 792$) is similar to that in Szczepankiewicz et al. ($n = 777$) and larger than those of Szekeres et al. ($n = 169$), Nanko et al. ($n = 510$), Anttila et al. ($n = 192$) and Galderisi et al. ($n = 217$). However, we could not exclude the possibility of a type II error due to an insufficient statistical power, since our sample size only had a power of 0.25 to detect a significant association between the T allele and schizophrenia using the Genetic Power Calculation (Purcell et al., 2003). Thus, further studies with larger samples in

several ethnic populations will be required to draw any definitive conclusions. When we pooled our sample with that of Nanko et al. (2003), the C/T genotype and T allele were associated with schizophrenia ($p = 0.008$, OR = 1.9, 95% CI = 1.2-3.0 for the C/T genotype; $p = 0.009$, OR = 1.9, 95% CI = 1.3-2.6 for the T allele). However, even if there is a significant association, the majority of Japanese schizophrenia patients are not related to this polymorphism, since the risk allele is very rare.

The (GT)_n dinucleotide repeat was one of the most extensively investigated polymorphisms in the *BDNF* gene for associations in schizophrenia, although we did not examine this repeat as described above. Muglia et al. (2003) showed biased transmission of (GT)_n alleles from parents to schizophrenia probands, whereas other studies failed to find this association (Sasaki et al., 1997; Hawi et al., 1998; Wassink et al., 1999; Krebs et al., 2000; Virgos et al., 2001; Fanous et al., 2004; Neves-Pereira et al., 2005). Recently, Koizumi et al. (2005) reported that this repeat consists of three different and continuous dinucleotide repeats, rather than a simple (GT)_n repeat. Accordingly, this polymorphism should be reanalyzed to confirm an association between the (GT)_n repeats and schizophrenia.

In conclusion, the results of the present study suggest that three *BDNF* gene polymorphisms (rs988748, C132T and rs6265) do not play major roles in conferring susceptibility to schizophrenia in a Japanese population, although the possibility that the C132T polymorphism is associated with schizophrenia still remains to be elucidated. Further studies with larger samples for the *BDNF* gene polymorphisms, including the C132T polymorphism and (GT)_n repeats, should be performed in several other ethnic populations.

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Electronic Database Information

The URLs for the data presented herein are as follows:

Genetic Power Calculator, <http://wbiomed.curtin.edu.au/genepop/>

National Center for Biotechnology Information, Single Nucleotide Polymorphism Database, <http://www.ncbi.nlm.nih.gov/SNP/> (for SNP reference identification numbers)

Table 1Genotype and allele frequencies of three *BDNF* gene polymorphisms in the schizophrenia patients and control subjects.

SNP	Genotype			<i>p</i>	Allele		<i>p</i>
	C/C	C/G	G/G		C	G	
rs988748				0.891			0.959
Patients	122 (35.0%)	162 (46.4%)	65 (18.6%)		406 (58.2%)	292 (41.8%)	
Controls	143 (33.8%)	204 (48.2%)	76 (18.0%)		490 (57.9%)	356 (42.1%)	
C132T				0.090			0.095
Patients	323 (92.6%)	26 (7.4%)	0 (0.0%)		672 (96.3%)	26 (3.7%)	
Controls	404 (95.5%)	19 (4.5%)	0 (0.0%)		827 (97.8%)	19 (2.2%)	
rs6265				0.828			0.918
Patients	122 (35.0%)	163 (46.7%)	64 (18.3%)		407 (58.3%)	291 (41.7%)	
Controls	142 (33.6%)	207 (48.9%)	74 (17.5%)		491 (58.0%)	355 (42.0%)	

Table 2Linkage disequilibrium (LD) indices (D' and r^2 ; above and below the diagonal line, respectively) in the control subjects.

SNP	rs988748	C132T	rs6265
rs988748	-	<u>0.5828</u>	<u>0.9804</u>
C132T	<u>0.0057</u>	-	<u>0.7248</u>
rs6265	<u>0.9566</u>	<u>0.0087</u>	-

Significant ($p < 0.05$) LD indices are underlined.**Table 3**

Estimated haplotype frequencies in the schizophrenia patients and control subjects.

Haplotype	rs988748	C132T	rs6265	Patients	Controls	Permutation <i>p</i>
1	C	C	G	0.551	0.565	0.553
2	G	C	A	0.414	0.417	0.890
3	C	T	G	0.035	0.018	0.044

The global permutation *p* value of haplotypes 1-3 is 0.113.

**No association between the *tumor necrosis factor- α* gene promoter polymorphisms
and schizophrenia in a Japanese population**

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Abstract

Tumor necrosis factor- α (TNF- α) is a pleiotropic cytokine and exerts neuroprotective and neurodegenerative effects in brain. Several studies have indicated that TNF- α is likely related to the pathogenesis of schizophrenia. Recent genetic researches have revealed that a *TNF- α* gene promoter polymorphism (-G308A) is associated with schizophrenia, although contradictory negative findings have also been reported. To assess whether the *TNF- α* gene promoter variants including -G308A could be implicated in vulnerability to schizophrenia, we conducted a case-control association analysis (265 cases and 424 controls) and the transmission disequilibrium test (TDT) analysis (83 trios) for four polymorphisms (-G238A, -G308A, -C857T, and -T1031C) in Japanese subjects. In a case-control analysis, there was no significant association between the promoter polymorphisms or haplotypes in the *TNF- α* gene and schizophrenia. In the TDT analysis, we also did not observe transmission distortion. Our results suggest that the above four polymorphisms in the promoter region of the *TNF- α* gene might not confer increased susceptibility for schizophrenia in a Japanese population.