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Association study of *interleukin 2 (IL2)* and *IL4* with schizophrenia in a Japanese population

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■ **Abstract** Interleukin 2 (IL-2) and IL-4 are pleiotropic cytokines regulating Th1/Th2 balance and have a regulatory activity in brain function. Thus these cytokines have been implicated in the pathophysiology of schizophrenia. The latest studies provided controversial results regarding the genetic associations of these cytokines. The functional polymorphisms, IL2-330T/G and IL4-590C/T, were associated with schizophrenia in a German population, although contradictory findings were also reported in a Korean population. To ascertain whether IL2 and IL4 contribute to vulnerability to schizophrenia, we conducted a moderate-scale case-control (536 patients and 510 controls) association study for seven polymorphisms in Japanese subjects. There were no significant associations of these genes with schizophrenia using either single marker or haplotype analyses. The present study suggests that IL2 and IL4 do not contribute to vulnerability to schizophrenia in the Japanese population.

■ **Key words** case-control study · interleukin 2 · interleukin 4 · schizophrenia · single nucleotide polymorphism

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Introduction

Cytokines are implicated in the etiology or pathology of schizophrenia [33, 34]. T helper (Th) lymphocytes are classified into Th1 and Th2 according to their cytokine profile [31]. Schizophrenia has been associated with an imbalance in Th1/Th2 cytokines, with a shift toward the Th2 system [32]. Interleukin 2 (IL-2) and IL-4 are cytokines produced by Th1 and Th2, respectively. In brain, these cytokines also play important roles in inflammatory reactions, synaptic plasticity and glial differentiation [45]. For example, IL-2 prevents the induction of long-term potentiation in rat hippocampus [46], and IL-4 antagonizes inhibitory effects of amyloid- β on long-term potentiation, and modulates microglial cell activation [26, 27].

A decrease in IL-2 production is one of the most frequently confirmed immunological phenomena in schizophrenia [1, 5, 12, 13, 18, 22, 28, 42, 43, 48, 49], although contradictory findings have also been reported [6-8, 36, 51]. A recent meta-analysis including 20 studies with 1,149 subjects obtained evidence for a decrease in secretion of IL-2 by peripheral blood leukocytes from patients with schizophrenia (effect size = -0.420, 95% CI = -0.058to -0.781) [37]. Also, several studies demonstrated increased blood and cerebrospinal fluid concentrations of IL-2 in patients with schizophrenia [17, 21, 22, 25, 29, 53-55]. However, these observations remain controversial [3, 14, 40, 47, 52]. Interestingly, administration of IL-2 has been associated with the development of clinically significant neuropsychiatric changes including delusions and hallucinations [10]. Similar to the findings on IL-2, some studies have shown abnormal blood and cerebrospinal fluid concentrations of IL-4 and impaired in vitro production of this cytokine in patients with schizophrenia [2, 23, 30], whereas other studies failed to replicate these changes [6, 7, 39, 51]. Antipsychotics have effects on

human plasma levels and in vitro production of IL-4 [6, 23, 24]. Taken together, these findings suggest that disturbances in IL-2 and IL-4 may be related to the pathophysiology of schizophrenia.

John et al. [19] identified a T to G substitution at position -330 relative to the transcription start site of IL2. This single nucleotide polymorphism (SNP) in the promoter is associated with IL-2 protein production in anti-CD3/CD28-stimulated peripheral blood lymphocytes, suggesting that the IL2 -330T/G polymorphism might be functional [16]. Rosenwasser et al. [41] described a C to T substitution at position -590 upstream from the open reading frame of IL4. The −590T allele was associated with increased gene expression of IL4 [41]. These two functional polymorphisms, IL2 –330T/ G and IL4 -590C/T, have been tested for their associations with schizophrenia. Jun et al. [20] found no significant association between the IL4 -590C/T polymorphism and schizophrenia. Recently, Schwartz et al. [44] reported that both the *IL2* –330T/G polymorphism and the IL4 -590C/T polymorphism were associated with schizophrenia. These studies examined a limited number of markers with relatively small sample sizes.

Replication at only the significant SNP from the previous studies runs a high risk of false-negative results [35]. To clarify the controversy, therefore, detailed studies, in which all common variations within a candidate gene are considered jointly, are required. Here, we tried to increase the power by testing more markers, taking into account linkage disequilibrium (LD) structure and increasing sample size. We conducted a moderate-scale case-control association study in Japanese subjects on *IL2* and *IL4*. We discuss differences in their genetic associations with schizophrenia across populations.

Methods

The present study was approved by the Ethics Committee on Genetics of the Niigata University School of Medicine, and written informed consent was obtained from all participants. All participants were unrelated Japanese subjects living in the Niigata Prefecture or Fukushima Prefecture.

Fig. 1 Genomic structure and linkage disequilibrium (LD) of *IL2*. **a** Genomic structure of *IL2* and the locations of the single nucleotide polymorphisms (SNPs) analyzed in the present study. *IL2* has four exons (*rectangles*) and spans approximately 5 kb. *Horizontal arrow* and *vertical arrows* indicate the transcriptional orientation and locations of SNPs, respectively. **b** LD between markers of *IL2*. A block is defined in accordance with Gabriel's criteria using Haploview v4.0. Each *box* represents the D' value and *r*² value (in parentheses) corresponding to each pair-wise SNP

Subjects

The study population consisted of 536 patients with schizophrenia (281 men and 255 women; mean age, 40.1 [SD 14.2] years) and 510 control subjects (275 men and 235 women: mean age, 37.4 [SD 10.2] years). No significant difference in the sex ratio was observed between the two groups ($\chi^2 = 0.235$, df = 1, P = 0.628). Although the mean age of the patients was significantly higher than that of the control subjects (P = 0.025, Mann-Whitney U test), the difference in mean age between the groups was relatively small (2.7 years). Patients meeting the diagnostic and statistical manual of mental disorders fourth edition (DSM-IV) criteria for schizophrenia were recruited from 14 hospitals. The diagnosis of schizophrenia had been assigned on the basis of all available sources of information, including unstructured interviews, clinical observations and medical records. The control subjects were mainly recruited from the staff of the participating hospitals. Although these subjects were not assessed by a structured psychiatric interview, they all showed good social and occupational skills and reported that they had no history of psychiatric disorders.

Genotyping

Genomic DNA was extracted from peripheral blood using standard phenol/chloroform methods. We examined three SNPs in IL2 and four SNPs in IL4. Their order and physical locations are shown in Figs. 1a and 2a. We included the IL2 -330T/G polymorphism (rs2069762) and the *IL4* –590C/T polymorphism (rs2243250), which have been reported to be associated with schizophrenia [44]. Next, we consulted the HapMap database (release#22, population: Japanese in Tokyo [JPT], minor allele frequency [MAF]: more than 0.05). For IL2, only one SNP (rs2069772) was listed in the HapMap database. For IL4, three 'tagging SNPs' (rs2227282, rs2243267 and rs2243283), which covered the IL4 gene region but not the 5' and 3' flanking regions, were selected with the criterion of an r^2 threshold greater than 0.8 in 'aggressive tagging: use 2- and 3-marker haplotype' mode using the 'Tagger' program [9], an implement of Haploview v4.0 [4]. We also investigated one SNP in IL2, JST063967 (rs2069763), which was listed in the JSNP database [15]. All SNPs were genotyped using the TaqMan 5'-exonuclease assay, as described previously [50].

Statistical analysis

Deviation from the Hardy-Weinberg equilibrium (HWE) was tested by using the χ^2 test for goodness-of-fit. LD blocks defined in accordance with Gabriel's criteria [11] and haplotype frequencies were determined using Haploview v4.0 [4]. The allele, genotype and

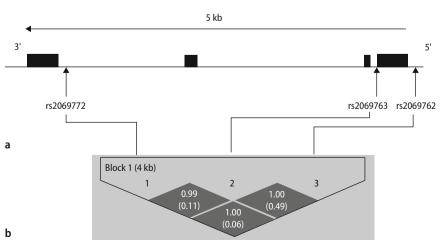


Fig. 2 Genomic structure and linkage disequilibrium (LD) of *IL4*. (A) Genomic structure of *IL4* and the locations of the single nucleotide polymorphisms (SNPs) analyzed in the present study. *IL4* has three exons (rectangles) and spans approximately 9 kb. Horizontal arrow and vertical arrows indicate the transcriptional orientation and locations of SNPs, respectively. (B) LD between markers of *IL4*. A block is defined in accordance with Gabriel's criteria using Haploview v4.0. Each box represents the *D'* value and *r*² value (in parentheses) corresponding to each pair-wise SNP

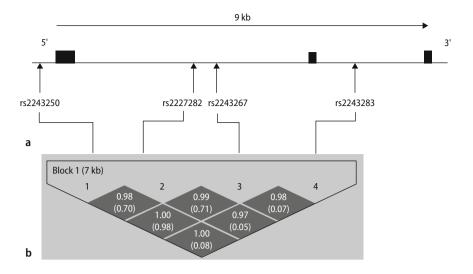


Table 1 Genotype and allele frequencies of IL2 and IL4 polymorphisms in patients with schizophrenia and control subjects

Gene symbol	SNP	Allelea	Patients					Controls						Р		
			n	HWE	1/1 ^b	1/2 ^b	2/2 ^b	MAF	n	HWE	1/1 ^b	1/2 ^b	2/2 ^b	MAF	Genotype	Allele
IL2	rs2069772	T/C	536	0.029	432	93	11	0.107	510	0.684	415	91	4	0.097	0.225	0.441
	Rs2069763	G/T	536	0.869	140	266	130	0.491	510	0.425	125	264	121	0.496	0.766	0.805
	rs2069762	T/G	536	0.210	232	251	53	0.333	510	0.947	225	228	57	0.335	0.701	0.912
IL4	rs2243250	T/C	536	0.116	254	241	41	0.301	509	0.437	237	215	57	0.323	0.136	0.281
	rs2227282	G/C	536	0.270	299	209	28	0.247	510	0.182	294	179	37	0.248	0.227	0.965
	rs2243267	C/G	536	0.116	254	241	41	0.301	510	0.463	235	217	58	0.327	0.118	0.215
	rs2243283	G/C	534	0.747	398	125	11	0.138	510	0.910	369	130	11	0.149	0.725	0.458

SNP single nucleotide polymorphism, HWE Hardy–Weinberg equilibrium, MAF minor allele frequency

haplotype frequencies of the patients and control subjects were compared using the χ^2 test. A probability level of P < 0.05 was considered to be statistically significant.

Power calculation was performed using Genetic Power Calculator [38]. Power was estimated with an α of 0.05, assuming a disease prevalence of 0.01 and the risk allele frequencies to be the values observed in control samples.

Results

Table 1 shows the genotype and allele frequencies of three SNPs in IL2 and four SNPs in IL4 in the patients and control subjects. None of the genotype distributions of the SNPs examined deviated significantly from HWE in either group (P > 0.05), with the exception of rs2069772 in the patients (P = 0.029). None of the genotype or allele frequencies of the SNPs examined differed significantly between patients and control subjects (P > 0.05). We observed that either IL2 or IL4 were present in a single LD block (Figs. 1b and 2b, respectively). There were no associations between the common haplotypes of these LD blocks and schizophrenia (P > 0.05, Table 2).

 $\begin{tabular}{ll} \textbf{Table 2} & \begin{tabular}{ll} Haplotype analyses of $\mathit{IL2}$ and $\mathit{IL4}$ polymorphisms in patients with schizophrenia and control subjects \\ \end{tabular}$

Gene symbol	Haplotype	Patients (frequency)	Controls (frequency)	Р
IL2 IL4	TTT TGG TGT CTT TGCG CCGG TGCC CGGG	0.383 0.333 0.176 0.107 0.558 0.244 0.138 0.057	0.401 0.335 0.168 0.096 0.529 0.243 0.146 0.078	0.421 0.937 0.629 0.414 0.175 0.966 0.589 0.056

Global P values of haplotypes of IL2 and IL4 were 0.755 and 0.211, respectively

Discussion

In the present study, we failed to find significant associations of three *IL2* polymorphisms and four *IL4* polymorphisms with schizophrenia in our Japanese subjects, using both single-marker and haplotype analyses. Schwartz et al. [44] found an association of the T/T genotype of the *IL2* –330T/G polymorphism (rs2069762) with schizophrenia in a German popula-

^aMajor/minor alleles

^bGenotypes, major and minor alleles are denoted by 1 and 2, respectively

tion. Interestingly, peripheral blood lymphocytes from individuals with the G/G genotype produce significantly more IL-2 than those from individuals with T/T and T/G genotypes [16]. Therefore, an association of the T/T genotype with schizophrenia could partly explain a reduced IL-2 production in schizophrenia, which is one of the most frequently confirmed immunological phenomena in schizophrenia [1, 5, 12, 13, 18, 22, 28, 37, 42, 43, 48, 49]. By contrast, we failed to replicate the previous finding for an association between the T/T genotype and schizophrenia (P > 0.05). In addition, there was no significant association between the G/G genotype and schizophrenia (P > 0.05). The genotype frequencies of the IL2 -330T/G polymorphism did not differ significantly between patients and control subjects (P > 0.05). When we assessed HWE in control subjects of Schwartz et al. [44], the genotype distributions of the IL2 -330T/G polymorphism significantly deviated from HWE ($\chi^2 = 4.890$, df = 1, P = 0.027), whereas they described that their control subjects followed HWE ($\chi^2 = 2.705$, df = 2, P = 0.259). The deviation from HWE can be caused by multiple factors such as typing error and population stratification, and can inflate the chance of a false-positive association. Thus, an association of the T/T genotype with schizophrenia reported by Schwartz et al. [44] should be interpreted with caution, although the deviation from HWE may not necessarily invalidate the results of an association study. In the present study, rs2069772 showed significant deviation from HWE only in the patient group. This kind of departure from HWE might be due to the fact that the case group is a nonrandom mating population, and not a result of typing errors.

Two previous association studies of schizophrenia and IL4 focused on only the -590C/T polymorphism (rs2243250) [20, 44]. We conducted a moderate-scale case-control association study using four markers including -590C/T and three 'tagging SNPs'. However, we failed to find significant associations of these IL4 polymorphisms with schizophrenia in our Japanese subjects, using either single-marker or haplotype analyses. Our results are in line with previous negative findings for a Korean population [20]. By contrast, Schwartz et al. [44] showed evidence for an association between the -590C allele and schizophrenia in a German population. Thus, there is the possibility that the IL4 -590C/T polymorphism could be implicated in vulnerability to schizophrenia in Caucasian but not in Asian populations. Our failure to replicate the previous positive finding for a German population may be due to ethnic differences. Indeed, there are differences in the allele frequencies of this polymorphism across populations. The frequencies of the -590C allele in Korean and Japanese control subjects (18.8 and 32.3%, respectively) are lower than that in German control subjects (83.3%).

We recognize several limitations of the study. No standardized structured interview was applied to verify the clinical diagnoses of included patients, but the diagnosis of schizophrenia had been assigned on the basis of all available sources of information. The control samples were not well characterized. We could not exclude the possibility that our control samples might contain some younger individuals who will be suffered with schizophrenia after getting on in years. To the best of our knowledge, however, there were no control subjects who were likely to develop schizophrenia at their stage of life. Thus, it is unlikely that our failure to find a significant association is attributable to misdiagnosis. The sample size of the present study (n = 1046) is more than twice as large as that of Jun et al. (n = 387) [20] and that of Schwartz et al. (n = 481) [44].

The power calculation showed that when genotypic relative risk was set at 1.69 for homozygous risk allele carriers under the multiplicative model of inheritance the power was more than 0.80 for four SNPs (rs2069763, rs2069762, rs2243250 and rs2243267). However, our sample size did not have sufficient statistical power for the other three SNPs (rs2069772, rs2227282 and rs2243283). Therefore, we could not exclude the possibility that our negative results for these SNPs were due to type II error.

In conclusion, the present study suggests that *IL2* and *IL4* do not contribute to vulnerability to schizophrenia in the Japanese population. To draw a definitive conclusion, however, further studies using larger sample sizes and sufficient markers will be needed in different ethnic populations.

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