뇌신경재활

게시일시 및 장소 : 10 월 18 일(금) 13:15-18:00 Room G(3F)

질의응답 일시 및 장소 : 10 월 18 일(금) 16:21-16:25 Room G(3F)

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Association Between IL1RN Gene Polymorphisms and Post-Stroke Infection

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Background and Purpose

Neurogenic dysphagia due to acquired brain lesions, such as stroke and hemorrhage, is one of the leading causes of chronic disability. Dysphagia can be observed in about 40-60% of post-stroke patients, and about 20-30% of them might suffer from recurrent aspiration pneumonia. There are studies reporting that many genes may affect the outcome of stroke. Among those genes, Interleukin-1 receptor antagonist (IL-1ra) is known as an endogenous immunomodulatory cytokine encoded by IL1RN on chromosome 2, that inhibits the actions of IL-1α and IL-1β. Elevated plasma IL-1ra is known to predict infection early after stroke. Therefore, polymorphisms in IL1RN that affect the production of IL-1ra may influence post-stroke infection risk. Furthermore, there is a report that polymorphisms in IL1RN may predispose to vascular disease, such as coronary heart disease. However, the role of minor C allele of rs4251961 single nucleotide polymorphism (SNP) in IL1RN is controversial. This study aimed to explore whether minor C allele of rs4251961 in IL1RN is associated with the risk of post-stroke infection in stroke patients with dysphagia, and whether it is associated with the vascular diseases.

Method

A total of 218 subjects who met the inclusion criteria, and who agreed to undergo gene study were enrolled in the study. Blood samples were obtained from the subjects and genotyping for IL1RN rs4251961 was carried out. Genotypes of the subjects were classified into TT, CT, and CC types. Infection events, such as aspiration pneumonia, urinary tract infection, colitis, and other infections were recorded. The history of complications (admission to intensive care unit, history of intubation, septic shock, etc.) was also recorded.

Results

Data from 206 participants were available for final analysis. The baseline characteristics of patients with and without the minor (C) allele of the rs4251961 SNP in IL1RN are shown on

Table 1. There were no significant differences in age, sex, stroke type, diabetes, hypertension, atrial fibrillation, and coronary heart diseases between the patients with minor C allele of the rs4261961 and those without. Post-stroke infection risk also did not show significant differences between two groups (Table 2).

Conclusion

Based on our results, genetic polymorphism of IL-1RN gene failed to effectively reflect the post-stroke infection risk during follow-up period in stroke patients. Unlike previous study, minor C allele of rs4261961 did not revealed statistically significant association with vascular disease. The risk of post-stroke infection and vascular diseases may be affected by multifactorial reasons. Further long-term studies and studies of genetic polymorphism of other genes on infection are warranted.

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Table 1. Baseline Characteristics of patients with and without the minor C allele of the rs4261961 SNP in IL1RN

		TT (n=177)	CT (n=27)	CC (n=2)	p-value	TT (n=177)	CT or CC (n=29)	p-value
Age		65.0 [55.0;73.0]	62.0 [57.5;73.5]	63.5 [53.0;74.0]		65.0 [55.0;73.0]	62.0 [56.0;74.0]	
Sex	Male	113 (63.8%)	21 (77.8%)	2 (100.0%)	0.216	113 (63.8%)	23 (79.3%)	0.156
	Female	64 (36.2%)	6 (22.2%)	0 (0.0%)		64 (36.2%)	6 (20.7%)	
Stroke type	Infarct	99 (55.9%)	18 (66.7%)	2 (100.0%)	0.527	99 (55.9%)	20 (69.0%)	0.316
	Hemorrhagic	72 (40.7%)	9 (33.3%)	0 (0.0%)		72 (40.7%)	9 (31.0%)	
	Combined	6 (3.4%)	0 (0.0%)	0 (0.0%)		6 (3.4%)	0 (0.0%)	
DM		77 (43.5%)	7 (25.9%)	1 (50.0%)	0.218	77 (43.5%)	8 (27.6%)	0.158
HBP		132 (74.6%)	15 (55.6%)	2 (100.0%)	0.082	132 (74.6%)	17 (58.6%)	0.12
Afib		26 (14.7%)	6 (22.2%)	0 (0.0%)	0.5	26 (14.7%)	6 (20.7%)	0.582
CHD		23 (13.0%)	4 (14.8%)	0 (0.0%)	0.83	23 (13.0%)	4 (13.8%)	1
Recurrence of Stroke		33 (18.6%)	8 (29.6%)	0 (0.0%)	0.321	33 (18.6%)	8 (27.6%)	0.386
CHD + Recurrence of Stroke		51 (28.8%)	11 (40.7%)	0 (0.0%)	0.293	51 (28.8%)	11 (37.9%)	0.439

Table 2. Infection of patients with and without the minor C allele of the rs4261961 SNP in IL1RN

	TT (n=177)	CT (n=27)	CC (n=2)	p-value	TT (n=177)	CT or CC (n=29)	p-value
Total infection	125 (70.6%)	17 (63.0%)	1 (50.0%)	0.605	125 (70.6%)	18 (62.1%)	0.478
Aspiration Pneumonia	93 (52.5%)	14 (51.9%)	1 (50.0%)	0.995	93 (52.5%)	15 (51.7%)	1
Urinary Tract Infection	40 (22.6%)	6 (22.2%)	1 (50.0%)	0.654	40 (22.6%)	7 (24.1%)	1
Colitis	22 (12.4%)	1 (3.7%)	0 (0.0%)	0.358	22 (12.4%)	1 (3.4%)	0.269
Infection with complication	30 (16.9%)	2 (7.4%)	0 (0.0%)	0.368	30 (16.9%)	2 (6.9%)	0.268
Multiple Infection	70 (39.5%)	10 (37.0%)	0 (0.0%)	0.511	70 (39.5%)	10 (34.5%)	0.754