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Lack of evidence for association of two functional SNPs of CHI3L1 gene (HC-gp39) with rheumatoid arthritis

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Abstract

CHI3L1 gene encodes for a glycoprotein (HC-gp39 or YKL40) secreted by synovial fibroblasts, macrophages, neutrophil granulocytes and chondrocytes. Its expression is under the control of NF-kB. It is regarded as an acute phase protein, and its levels are significantly elevated in rheumatic diseases. Furthermore, HC-gp39 has been shown to be recognized by autoreactive T cells in rheumatoid arthritis. In the present study we have examined two functional variants of the promoter region of CHI3L1 gene (CHI3L1-1 (rs4950928) and CHI3L1-2 (rs10399931) that have been reported earlier to be associated with schizophrenia and sarcoidosis. We used TaqMan allelic discrimination assays to study the genotypes of Hungarian patients with rheumatoid arthritis (n=182) and of healthy controls (n=194). No significant association of the investigated SNPs with the disease was found.

Here we report that CHI3L1 SNPs, shown to be involved in the predisposition of schizophrenia, are not associated with rheumatoid arthritis.

Introduction

Rheumatoid arthritis (RA) is a common systemic inflammatory disease affecting approximately 1% of the adult population worldwide [1]. The disease is characterized by inflammation of synovial tissue, progressive cartilage destruction and bone erosion of affected joints. [2]

Despite of significant gains in knowledge of the immunopathology of RA, the exact etiology of the disease remains uncertain [1]. The genetic basis for RA is rather complex with a poorly understood cause. Several studies suggest roles of HLA– DRB1 [3] and PTPN22 [4-6] in RA pathogenesis. Three further RA risk loci have been identified recently, including the STAT4 gene [7-9], loci in the 6q23 [10-11] and TRAF1/C5 [12-13]. As RA is a major cause of disability and is even correlated with increased mortality in severe cases [14]. Identification of genetic risk factors of RA may help to understand basic mechanisms of autoimmunity and may be helpful in the development of targeted diagnostics and therapeutics. Chitinase-3-like1 (CHI3L1) is a glycoprotein also known as human cartilage glycoprotein-39 (HC gp-39) or YKL-40. It has also been suggested to be a growth factor for connective tissue cells as well as a migration-promoting factor for endothelial cells [15].

It is has been first described as a major secretory product of rheumatoid synovial fibroblasts by Nyirkos et al. [16]. Later it was demonstrated to be produced by articular chondrocytes and macrophages [17].

Its expression is under control of NF-kB [18]. CHI3L1 mRNA was shown to be expressed in diseased human osteoarthritic cartilage and osteophyte, while it was not detected in healthy adult cartilage [19]. Peptides derived from HC gp-39 can bind to RA- associated DR4 (DRB1*0401) molecules and are recognized by peripheral blood T cells from patients with RA [20]. Furthermore, elevated levels of CHI3L1 are reported to be associated with inflammatory disorders, such as RA [21-23]. Recently, functional variants of the promoter region CHI3L1 (including rs4950928) have been shown to be associated with susceptibility to schizophrenia [24]. Also, a CHI3L1 gene polymorphism (rs10399931) has been reported to contribute to inter-individual variations of the CHI3L1 levels in sarcoidosis [25]. Given the known elevated levels of CHI3L1 in various inflammatory diseases reported by numerous groups [21-23], in this study we made an attempt to identify a possible disease association of functional single nucleotide polymorphisms (SNPs) of CHI3L1 in a Hungarian cohort of patients with RA and healthy controls.

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Materials and methods

Subjects

We examined 182 patients suffering from RA (156 females, 26 males, mean age 61,98±10,51, range 32-85), treated in the Department of Rheumatology, County Hospital Kecskemét, Hungary. Control subjects (94 males and 100 females; aged 36.8±10.5 years) with no known history of inflammatory arthritis were randomly selected from healthy blood donors (n=192) of the same ethnicity and from the same geographical region as the patients. All study subjects belonged to the Hungarian (Caucasian) population, and all RA patients had the typical symptoms and diagnosis of RA. All RA patients met the American College of Rheumatology criteria for rheumatoid arthritis [26]. During the entire investigation period the guidelines and regulations approved by the local Ethical Committee and the Helsinki Declaration in 1975 were followed; the patients gave their informed consent for use of their anonymized DNA samples for research purposes.

Genotyping

Genomic DNA was extracted from EDTA anticoagulated whole blood-derived buffy coats, after sedimentation at room temperature. A commercial kit QIAamp® DNA blood mini kit (QIAGEN Inc, Chatsworth, CA, USA) was used following the instructions of the manufacturer. Biallelic SNP genotyping was performed with TaqMan allelic discrimination assays (Applied Biosystems) according to the recommendations of the manufacturer. PCR was performed using an ABI 7000 thermocycler, and fluorescent signals were analyzed using an ABI 7000 sequence detector single point measurement and SDS v2.3 software (Applied Biosystems).

The following assays were used for allelic discrimination in the study:

CHI3L1-1 (rs10399931) and CHI3L1-2 (rs4950928). PCR was performed with components including12,5 μ l Mastermix, 9.2 μ l distilled water, 2 μ l DNA (10 ng/ μ l), 1.3 μ l of primers and probes. The total reaction mixture was thus, 25 μ l/well. The following cycle was repeated 45 times: 50^o C – 2 min, 95^o C – 10 min, 95^o C – 15 sec, 60^o C – 1 min.

Clinical and laboratory parameters

Gender, age of onset of the disease, levels of C-reactive protein (CRP), seropositivities for rheumatoid factor (RF) and anti-CCP antibodies, and the current disease activity scores (DAS28) of the patients were documented for all patients with RA. Controls did not suffer from any known joint diseases.

Statistical analysis

Genotypes were determined for all samples, and each SNP was assessed for deviation from Hardy-Weinberg equilibrium. Both allelic and genotypic association tests and Cochran-Armitage tests were performed using an online HWE calculator (<u>http://ihg2.helmholtz-muenchen.de/cgi-bin/hw/hwa1.pl</u>) [27]. Associations with susceptibility to RA were tested by calculating odds ration (OR) and 95% confidence interval (CI).

Results

We tested the possible association of two functional SNPs of the CHI3L1 gene with RA in a Hungarian cohort of patients by using allelic discrimination system. The baseline characteristics of the patients are summarized in Table 1.

Genotype frequencies were determined for both tested SNPs. Allele and genotype frequencies of the SNPs were calculated and are shown in Table 2. No deviation from the Hardy- Weinberg equilibrium (HWE) was observed either in RA patients or in controls. A comparison of allele and genotype frequencies of the polymorphism under study revealed no statistically significant differences between RA patients and healthy controls (Table 3).

After adjusting for age and gender using logistic regression, there was no significant association between the SNP-s and RA (we tested also their interaction) (data not shown).

Discussion

RA is a systemic autoimmune disease with complex genetic background, and dissecting its genetic components may shed light on important mechanism underlying the development of autoimmunity in susceptible individuals.

Several studies examined the role of CHI3L1 and reported to be associated with inflammatory disorders, such as RA [21-23]. Recently, the promoter SNP of the CHI3L1 gene (rs4950928) was found to be associated with elevated serum CHI3L1 levels as well in asthma, bronchial hyperresponsiveness, and measures of pulmonary functions [29]. The same polymorphism was also demonstrated to be associated with schizophrenia [27].

The elevated levels and suggested role of CHI3L1 in the regulation of cytokine signaling as well as its protective role in inflammatory environments [28] were compelling to hypothesize that functional polymorphisms of the CHI3L1gene might be associated with RA.

Surprisingly, there were no significant differences in the distributions of alleles and genotypes between the RA patients and controls. Haplotype analysis of these two polymorphisms did not show differences between the two groups either.

We also carried out power analysis in order to refine our conclusions. Assuming a dominant model, the sample size in the study (377), and a significance level 0.05, we investigated the power for the estimated allele frequency range (22%-29.5%) and the estimated OR range (<4). We found that the power diminished below OR=2, thus, based on our data, we can not exclude associations with RA below this level. Our present data argue that the reported elevated CHI3L1 levels in RA might be consequences rather than causative components of the inflammatory processes in RA. However, further SNPs of the CHI3L1 gene need to be tested in order to entirely rule out the association of the gene with RA susceptibility.

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Conflict of interest

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The authors declare that they have no conflict of interest.

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Table 1.

		Cases in this study n=182	Controls n=194	
Age of onset of the	disease	53.26 (12.52)	NA	
Sex***	female	156	100	
	male	26	94	
log RF [#]		3.56 (1.62)	ND	
log RF [#] log anti-CCP ^{&}		3.53 (1.85)	ND	
DAS-28		5.17 (1.27)	ND	
ESR ^{##}		19.64 (17.92)	ND	

Values are given as mean (standard deviation). Abbreviations: NA: not applicable; ND: not determined *** P < 0.001 for the different ratios of genders for cases and controls "RF levels (expressed as IU/ml) [&] anti-CCP levels were expressed as U/ml ## ESR- erythrocyte sedimentation rate was expressed in mm/h

Table 2. Genotype and allele frequencies of CHI3L1polymorphisms in patients with RA and controls

SNP	Allele	Case (frequency %)	Control (frequency %)	Genotype	Case (frequency %)	Control (frequency %)	HWE (p value Case)	HWE (p value control)
CHI3L1-1	С	280 (76.4)	302 (77.8)	CC	108(59.34)	116 (59.79)	0,897 ^x	0.524 ^x
rs4950928	G	84 (23.1)	86 (22.2)	CG	64 (35.16)	70 (36.08)	0,898#	0.517#
				GG	10 (5.49)	8 (4.12)	0,837 [§]	0.677 [§]
CHI3L1-2	С	259 (72.4)	281 (70.8)	CC	93 (51.09)	100 (51.54)	0.627 ^x	0.528 ^x
rs10399931	Т	106 (27.6)	107 (29.2)	CT	73 (40.10)	81 (41.75)	0.628#	0.524#
				TT	17 (9.34)	13 (6.70)	0.596 [§]	0.593 [§]

X Pearson test

Llr test

§ Exact test

HWE: Hardy Weinberg equilibrium

Risk allele	Allele freq. difference	Heterozygous	Homozygous	Allele positivity	Armitage's trend test
CHI3L1-1	OR=1.053	OR=0.982	OR=1.343	OR=1.019	OR=1.085
Allele 2	C.I.= [0.748-1.483]	C.I=[0.640-1.507]	C.I=[0.511-3.527]	C.I=[0.675-1.539]	P=0.76296
	p=0.76510	p=0.93382	p=0.54884	P=0.92870	
CHI3L1-1	OR=0.949	OR=0.731	OR=0.745	OR=0.740	OR=0.925
Allele 1	C.I=[0.674-1.336]	C.I=[0.272-1.968]	C.I=[0.284-1.957]	C.I=[0.285-1.918]	P=0.76296
	P=0.76510	P=0.53447	P=0.54884	P=0.53382	
CHI3L1-2	OR=1.085	OR=0.969	OR=1.406	OR=1.030	
Allele 2	C.I.=[0.790-1.489]	C.I=[0.634-1.481]	C.I.=[0.648-3.053	C.I.=[0.687-1.542]	OR=1.122
	p=0.61385	p=0.88452	p=0.38743	p=0.88780	P=0.61300
CHI3L1-2	OR=0.922	OR=0.689	OR=0.711	OR=0.701	
Allele 1	C.I.=[0.672-1.265]	C.I.=[0.313-1.516	C.I.=[0.328-1.544]	C.I=[0.331-1.488]	OR=0.895
	p=0.61385	p=0.35308	p=0.38743	p=0.35331	P=0.61300

Table 3. Tests for association with RA (C.I:95% confidence interval)

Allele frequency difference:- [1]<->[2] &[2]<->[1], Homozygous :- [11+]<->[22] &[22]<->[11] Heterozygous :- [11]<->[12]& [22]<->[12], Allele positivity :- [11]<->[12+22] and[11+12]<->[22] C.I.: confidence interval, OR : odds ratio