Gene locus polymorphisms and expression levels of interleukin-1 in lumbar disc disease: a meta-analysis and immunohistochemical study

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Abstract

Background To investigate the association between interleukin (IL)-1 α (rs1800587), IL-1 β (rs1143634) and IL-1RN variable number tandem repeat (VNTR) polymorphisms, expression levels and lumbar disc disease (LDD). **Methods** All relevant articles were searched from 4 databases including PubMed, Embase, Web of Science and China National Knowledge Infrastructure (CNKI). Odds ratios (OR) with 95% confidence intervals (CI) were calculated to evaluate the association between IL-1 gene locus polymorphisms (rs1800587 in IL-1 α , rs1143634 in IL-1 β , VNTR in IL-1RN) and LDD susceptibility. Statistical analysis was conducted by Review Manager (Revman) 5.31 software. Furthermore, qRT-PCR and immunohistochemistry (IHC) were performed to evaluate IL-1 α , IL-1 β and IL-1RN expressions in the normal and degenerated disc. **Results** A total of 15 case-control studies (1455 cases and 2362 controls) were included in our meta-analysis. The pooled results suggested that IL-1 α rs1800587 polymorphism was associated with an increased risk of LDD in overall population (T vs. C, OR=1.21, 95%CI=1.04-1.40, P=0.01). The subgroup analysis found a significant association between IL-1 β rs1143634 polymorphism and LDD in Asian population (T vs. C, OR=0.61, 95%CI=0.39-0.96, P=0.03). Results of qRT-PCR and IHC demonstrated that expressions of IL-1 α and IL-1 β were significantly increased in the degenerated disc. (all P<0.05) **Conclusion** IL-1 α rs1800587 and IL-1 β rs1143634 polymorphisms were significantly associated with LDD in overall population and in Asian population, respectively. The increased expression levels of IL-1 α and IL-1 β may be the important risk factors for LDD.

Introduction

Low back pain (LBP) is a most common musculoskeletal disorder. The annual prevalence of LBP ranges from 15–45%, and 70–85% of all people have LBP at some time in life[1]. The consequences of LBP and related disability are substantial, affecting individuals, families, and health-care systems [2]. It is accepted that lumbar disc degeneration (LDD) is a main risk factor for LBP [3]. Although the pathogenesis of LDD is not fully understood, immune system has been proved to play an important role in development of LDD [4–6]. Interleukin (IL)-1 cytokines are key mediators of immune responses and apoptosis of intervertebral disc cells [7, 8]. Recently, increasing evidence showed that IL-1 gene cluster, including IL-1, IL-1 β and IL-1RN, could be responsible for the appearance or the severity of LDD[9, 10].

To date, several single nucleotide polymorphisms (SNPs) have been identified in the IL-1 gene cluster. The most widely studied of these are IL-1 α rs1800587, IL-1 β rs1143634 polymorphisms and variable number tandem repeat polymorphism (VNTR) of the IL-1RN gene.[11–25] In 2004, Solovieva et al. first reported that IL-1 α rs1800587 and IL-1 β rs1143634 polymorphisms were associated with LDD risk in a Caucasian population [11]. The association of the IL-1 α rs1800587 polymorphism to LDD was subsequently confirmed in Finnish and Danish population studies [15, 16]. However, Spanish, Chinese and Mexican cohort studies were unable to replicate this initial finding [12, 18–20, 23]. For IL-1 β rs1143634 polymorphism, two studies showed a positive association[11, 18], whereas seven demonstrated the null association [12, 13, 15, 16, 19, 21, 22]. A significant association between IL-1RN (VNTR) polymorphism and LDD risk was supported by Ye's and Kim's studies [14, 17]. However, the studies reported by Noponen-Hietala et al.[12] showed no such association. As the conclusions of the available studies were not consistent, we conducted a meta-analysis to provide the comprehensive data on the association between IL-1 gene locus polymorphisms and LDD risk. Furthermore, we used quantitative reverse-transcription PCR (qRT-PCR) and immunohistochemistry (IHC) to evaluate IL-1 α , IL-1 β and IL-1RN expression levels in intervertebral disc between the LDD patients and the control subjects.

Methods

The meta-analysis conformed to the Preferred Reporting Items for Systematic Review and Meta-Analysis Protocols (PRISMA-P) guidelines, and registered in PROSPERO International Prospective Register of Systematic Reviews (CRD42019124118). This study was approved by the Ethics Committee of the First Affiliated Hospital of Guangxi Medical University (2018-KY-NSFC- 025). Written informed consent was obtained from all the participants involved in this study. All procedures were performed in accordance with the guidelines the institutional research committees and with the Declaration of Helsinki.

Search strategy

Four electronic databases, including PubMed, Embase, Web of Science and China National Knowledge Infrastructure (CNKI), were searched by two reviewers (HJ and QX). The following keyword search string was used to identify studies: (IL-1 OR IL 1 OR interleukin-1 OR interleukin 1 OR IL-1RN) AND (polymorphism OR variant OR mutation OR SNPs) AND (disc degeneration OR disc disease OR low back pain). Additional studies were identified through a hand search of references listed in the reports and reviews. No language or publication date restrictions were used. The final literature search was conducted on February 5, 2020.

Inclusion and exclusion criteria

Eligible studies were included in meta-analysis according to the following inclusion criteria: (1) case-control design; (2) LDD diagnosed on the basis of clinical or/and radiologic examinations; (3) the study evaluated the association between IL-1 α rs1800587 or IL-1 β rs1143634 or IL-1RN (VNTR) polymorphisms and LDD risk; (4) genotype of control group conformed to the Hardy-Weinberg balance; and (5) sufficient data were provided to calculate the odds ratios (ORs) and 95% confidence intervals (CI). The exclusion criteria were as follows: (1) comments, reviews, or meta-analysis; (2) repeated publications; (3) study without available data. Based on the inclusion and exclusion criteria, eligible studies were identified independently by two reviewers (HJ and QX). The disagreements were resolved by a third reviewer (QW).

Data extraction

According to a standardized form, two investigators (HJ and QX) independently extracted data on outcomes for each study. The following information were collected from the included studies: (1) first author; (2) publication year; (3) country of enrollment; (4) ethnicity; (5) study design; (6) numbers of cases and

controls; (7) characteristics of participants (gender and age); (8) diagnostic criteria; (9) source of control group; (10) allele or/and genotype frequencies; (11) P value for Hardy-Weinberg equilibrium (HWE) of control.

Methodological quality assessment

Methodological quality of studies was assessed using Critical Appraisal Skills Programme (CASP) [26]. For each question, there were three answers including “no”, “can’t tell” and “yes”, which respectively indicate scored 0, scored 1 and scored 2. The quality score ranged from 0 to 20, and a study with scored 15-20 represented a high-quality study.

Study population

Based on our previous study [27], we collected degenerative disc tissues (n=34) and normal disc tissues (n=21) from the LDD patients and the control subjects, respectively. These disc samples were used to evaluate gene expressions via qRT-PCR and IHC. LDD patients were diagnosed as lumbar disc herniation by physical examination and MRI scan. The control subjects were the patients with traumatic lumbar vertebral fracture, who had no history of low back pain. According to Schneiderman’s classification [28], MRI evaluation of the control subjects showed no significant disc damage and degeneration before surgery (Schneiderman’s classification, Grade 1: 19 cases; Grade 2: 2 cases).

RNA extraction and qRT-PCR analysis

Intervertebral disc tissue was lysed in TRIzol® (Invitrogen Inc, Carlsbad, CA, USA) and total RNA was extracted using an RNeasy® Mini Kit (Qiagen, Valencia, CA, USA) according to the manufacturer’s protocol. Reverse transcription was performed using qScript microRNA cDNA Synthesis Kit (Quantabio, MD, USA). For profiling gene expressions, qRT-PCR was performed, using the primer pairs for IL-1 α (5’-CCTCACCTTCCAGGAGAATGTG-3’ and 5’-GCATCGCCAGATTTTGTAG TG-3’), IL-1 β (5’-CTGTCCTGCGTGTGAAGAT-3’ and 5’-TTCTGCTTGAGAG GTGCTGAT-3’), IL-1RN (5’-TTGTCCTGCTTTCTGTTCTCG-3’ and 5’-CTGTCC TGTGTCAAGTCTGG-3’), and GAPDH (5’-GACATGCCGCCTGGAGAAAC-3’ and 5’-AGCCAGGATGCCCTTTAGT-3’). Samples were normalized to GAPDH expression.

Immunohistochemical assay

Immunohistochemical assay was performed using a standard protocol as previously reported[27]. The sections were treated with 1/200 IL-1 α antibody (ab7632, Cambridge, MA, USA), 1/200 IL-1 β antibody (#2022, Cell Signaling, Danvers, MA, USA), 1/400 IL-1RN antibody (ab123235, Abcam, Cambridge, MA, USA) overnight at 4 °C and incubated with 1/400 secondary biotinylated goat anti-rabbit antibody (Vector Laboratories, Burlingame, CA, USA) for 30 min, followed by treatment with VECTASTAIN Elite ABC Kit (Vector Laboratories, Burlingame, CA, USA). IHC signals were detected by an Olympus BX43 upright microscope (Olympus Optical, Tokyo, Japan), in which 5 typical fields were randomly selected for analysis (400 $\times$ magnifications).

Statistical analysis

The association between IL-1 α rs1800587, IL-1 β rs1143634 and IL-1RN (VNTR) gene polymorphisms and LDD were estimated by odds ratio (OR) and 95% confidence intervals (CI). We evaluated the pooled ORs in five different genetic models. The heterogeneity of statistics was calculated by chi-square-based Q statistics and I^2 statistics. Heterogeneity was considered to be effective, when P was less than 0.10 and I^2 was greater than 50%. If there was significant heterogeneity ($I^2 > 50\%$), the random effect model was used. Otherwise, the fixed effect model was applied. Subgroup analysis of ethnicity was conducted to identify the source of heterogeneity. HWE was detected in control groups using the chi-square test. We performed the sensitivity test to assess the possible influence of one study on the pooled OR. In sensitivity test, studies were removed, in turn, from the overall analysis. Publication bias was tested by Begg’s funnel plot and Egger’s test. The qRT-PCR and IHC assay were calculated by the mean $\pm$ standard error. Statistical difference between two groups was evaluated using unpaired Student t test. $P < 0.05$ was considered to be statistically significant. Statistical analysis was performed by STATA 12.0 software (Stata, College Station, TX) and Revman 5.31 software (Nordic Cochrane Centre, Cochrane Collaboration, Copenhagen, Denmark).

Results

Characteristics of included studies

A flow chart of article selection process is described in Figure 1. A total of 15 studies that met the inclusion criteria were identified in our meta-analysis, including 1455 cases and 2362 controls (IL-1 α rs1800587: 10 studies, 922 cases and 1351 controls), (IL-1 β rs1143634: 10 studies, 1056 cases and 1747 controls), and (IL-1RN VNTR: 3 studies, 290 cases and 507 controls). LDD was diagnosed by MRI scan in all the studies. The characteristics of included studies were shown in Table 1 and 2. All eligible studies were categorized as high quality, with scores > 15 .

IL-1 α rs1800587, IL-1 β rs1143634 and IL-1RN (VNTR) polymorphisms and LDD susceptibility

The meta-analysis of IL-1 α rs1800587, IL-1 β rs1143634 and IL-1RN (VNTR) polymorphisms are presented in Table 3. The pooled result showed rs1800587 was significantly associated with LDD risk in overall population (T vs. C, OR=1.21, 95%CI=1.04-1.40, $P=0.01$) (Figure 2). This significance was across the ethnicity. It was proposed that IL-1 α rs1800587 T allele increased the susceptibility to LDD, and in contrast, IL-1 α rs1800587 C allele was protective. However, IL-1 β rs1143634, IL-1RN (VNTR) polymorphisms were not associated with LDD susceptibility in overall population (all $P > 0.05$). After stratification by ethnicity, the result showed C allele of IL-1 β rs1143634 may be a risk allele for LDD in Asian population (T vs. C, OR=0.61, 95%CI=0.39-0.96, $P=0.03$) (Figure 3).

Sensitivity analysis was performed to examine the impact of each study on the pooled ORs by removing each study in turn (Table 4). For rs1143634, when the study reported by Mu *et al.* was omitted in turn, the heterogeneity was obviously reduced under allele contrast genetic models [13, 19, 22]. For IL-1RN (VNTR), when we omitted the study reported by Ye *et al.* [14], the heterogeneity was significantly reduced under allele contrast genetic models. When the studies deviated from HWE were excluded, our results were robust and consistent. Funnel plots showed no significant evidence of publication bias (Figure 4a and 4b) (all $P>0.05$).

IL-1 α , IL-1 β and IL-1RN expressions and LDD

In contrast to control group, IL-1 α and IL-1 β mRNA levels were increased 2.6 fold and 1.7 fold in LDD group, respectively. IL-1RN mRNA levels were not significant difference between the two groups (all $P>0.05$). IHC analysis showed that significantly higher IL-1 α and IL-1 β expression levels in the LDD group than those in the control group (IL-1 α immunopositive cells: $43.8\pm4.9\%$ vs. $22.5\pm2.8\%$, $P<0.001$; IL-1 β immunopositive cells: $36.4\pm3.7\%$ vs. $21.6\pm2.3\%$, $P<0.001$). However, there were no significant differences in IL-1RN expression between the two groups (IL-1RN immunopositive cells: $21.4\pm3.3\%$ vs. $24.8\pm2.3\%$, $P=0.09$).

Discussion

Our meta-analysis 15 studies, involving 1455 cases and 2362 controls, found the statistically significant associations between IL-1 α rs1800587, IL-1 β rs1143634 polymorphisms and LDD. The pooled analysis indicated that T allele of rs1800587 was significant associated with increased risk of LDD in overall population. This significance was across the ethnicity. Subgroup analysis revealed that IL-1 β rs1143634 polymorphism was associated with LDD in Asian population but not in Caucasian population. The C allele of rs1143634 was identified as a risk allele in the patients with LDD. Furthermore, the results of qRT-PCR and IHC analysis demonstrated that increased IL-1 α and IL-1 β expression levels were found in the degenerated disc. Wang *et al.* initially reported a meta-analysis on IL-1 α rs1800587 and IL-1 β rs1143634 polymorphisms and LDD, which suggested that IL-1 α rs1800587 polymorphism was significantly associated with the risk of disc degeneration [29]. There were several weaknesses in the previous meta-analysis. First, some data extraction errors were found in meta-analysis, such as the allele and genotype frequencies from Solovieva's and Aparicio's studies [11, 18]. Second, the result of pooled analysis was limited by the marginal p values. This may lead to inflate the chance of a false positive association. More importantly, three genetic studies focusing on this topic were published in recent years [23–25], which were not included in Wang's study. Based on the Cochrane guidelines[30], an overlapping meta-analysis is necessary to be updated in time with latest studies. To the best of our knowledge, the current study is the largest sample size of meta-analysis to investigate the association between IL-1 gene locus polymorphisms and LDD.

IL-1 has extensively been studied among proinflammatory mediators, and is believed to play a critical role in the etiology of LDD [8, 31]. There are 3 major members in the IL-1 gene family: IL-1 α , IL-1 β , and IL-1RN. IL-1 α and IL-1 β have a strong influence on apoptosis of intervertebral disc cells, whereas IL-1RN suppresses the effect of IL-1 by competitively inhibiting the binding of IL-1 to the IL-1 receptor [32, 33]. The genetic control of the cytokine function may have an impact on the occurrence and the severity of LDD[8]. We performed an *in silico* analysis for evaluating the possible functional implication of IL-1 α rs1800587, IL-1 β rs1143634 and IL-1RN (VNTR) polymorphisms by using rSNPase (<http://rsnp3.psych.ac.cn/>). The results indicated that rs1800587 and rs1143634 were located within the promoter and exon 5 of IL-1 gene, which may affect the normal production, secretion or function of IL-1. The C to T polymorphism at position-889 of IL-1 α gene (rs1800587) could increase gene expression at mRNA and at protein levels by enhanced promoter activity [34]. Regarding the IL-1 β rs1143634 (T/C) polymorphism, earlier data suggested that a shift from T to C lead to a disruption of the TATA box in exon 5 sequences. The C allele conferred higher expression of the IL1 β gene compared to the T allele [35, 36]. However, the relationship between IL-1 α , IL-1 β polymorphisms and IL-1 α , IL-1 β expressions in LDD patients has not been reported. The results of qRT-PCR and IHC analysis demonstrated that elevated IL-1 α and IL-1 β expression levels were found in the degenerated disc. Compared with other genotypes, TT genotype of rs1800587 and CC genotype of rs1143634 were associated with higher expression levels of IL-1 α and IL-1 β respectively. Thus we postulated that rs1800587 TT and rs1143634 CC genotypes were the genetic risk factors for the progression of LDD, probably by increasing the expression of IL-1 α and IL-1 β [37–39]. Mutations in the introns may affect gene expression and function via effects on mRNA splicing or RNA stability. IL-1RN (VNTR) gene polymorphism, located within a non-regulatory region (intron 2), could not be part of RNA-binding protein site. Thus the functional influence of IL-1RN (VNTR) polymorphism remains unclear. The molecular mechanisms of IL-1 gene locus polymorphisms and expressions in LDD are likely to be more complicated, which need be investigated in the future.

Some limitations in our study should be taken into consideration. First, the sample size is relatively small, which may exert an impact on the statistical power. There is much to be done to ensure the accuracy of this result. Second, we only acquired suitable studies published in English or Chinese. The potential publication bias could not be eliminated as the exclusion of unpublished articles, or articles published in another language. Third, the function information provided by qRT-PCR and IHC is limit to assess the exact mechanisms of disc degeneration. It is necessary to accumulate further evidence to clarify the impact of IL-1 gene locus polymorphisms on LDD.

Conclusion

IL-1 α rs1800587 polymorphism was significantly associated with LDD in overall population, while IL-1 β rs1143634 polymorphism was significantly associated with LDD in Asian population but not in Caucasian population. IL-1 α rs1800587 T allele and IL-1 β rs1143634 C allele could increase the susceptibility to LDD. Elevated IL-1 α and IL-1 β expression levels may be the important risk factors for LDD.

Abbreviations

IL-1: interleukin-6; IHC: immunohistochemistry; LBP: low back pain; LDD: lumbar disc degeneration; SNP: single nucleotide polymorphism; VNTR: variable number tandem repeat polymorphism.

Declarations

Ethical Approval and Consent to participate

The histology study was approved by the Ethics Committee of the First Affiliated Hospital of Guangxi Medical University. All the experimental protocol and the methods were carried out in accordance with the relevant guidelines and regulations, and complied with the principles of the Declaration of Helsinki. Written informed consent was achieved from each participant.

Consent for publication

Not applicable.

Availability of supporting data

Please contact authors for data requests.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

HJ and QJW conceived and designed the study. HJ and QX were involved in the data search and selection of data, analyzed the data and wrote the manuscript. RZ was involved in the data search and selection of data and analyzed the data. JW and DM were involved in the data search and analyzed the data. QX and RZ were involved in the data search and selection of data. XZ analyzed the data and contributed analysis tools. HJ was involved in IHC study. All authors read and approved the final manuscript.

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Tables

Table 1. Characteristics of the case-control studies included in meta-analysis									
First author	Year	Country	Ethnicity	Age (year, mean±sd)		Number cases/controls	Diagnostic criteria	Control group	Outcome measur (SNP genotyping)
				cases	controls				
Solovieva [9]	2004	Finland	Caucasian	41~45	41~45	38/95	MRI	volunteers without LDD	rs1800587, rs114
Noponen- Hietala [10]	2005	Finland	Caucasian	44±13	39±13	155/179	sciatica, MRI	NM	rs1800587, rs114 IL-1RN (VNTR)
Ye [11,12]	2007	China	Asian	42.7	38.4	81/101	sciatica, MRI	volunteers without sciatica	rs1143634, IL-1R (VNTR)
Karppinen [13]	2009	Finland	Caucasian	44	44	45/63	MRI	volunteers without modic changes	rs1800587, rs114
Eskola [14]	2010	Denmark	Caucasian	13.1±0.4	13.1±0.4	66/154	MRI	volunteers without LDD	rs1800587, rs114
Kim [15]	2010	Korea	Asian	49.7±15.4	51.7±9.9	54/227	symptoms, MRI	volunteers without LDD	IL-1RN (VNTR)
Aparicio [16]	2011	Spain	Caucasian	43.9±11.9	68.7 ± 9.2	50/129	symptoms, MRI	patients without LDD	rs1800587, rs114
Kelempisioti [17]	2011	Finland	Caucasian	19	19	150/246	MRI	volunteers without LDD	rs1800587, rs114
Duan [18]	2013	China	Asian	46.5±7.3	48.3±7.7	42/85	symptoms, MRI	patients without LDD	rs1800587
Loncar [19]	2013	China	Asian	48.35±5.14	41.44±5.20	93/96	symptoms, MRI	veterans without LBP	rs1143634
Mu [20]	2013	Croatia	Caucasian	21.94±1.60	22.09±1.68	305/587	symptoms, MRI	soldiers without LBP	rs1143634
Serrano [21]	2014	Mexico	Caucasian	39.22±6.88	39.13±6.80	100/100	MRI	volunteers without LDD	rs1800587
Abdollahzade [22]	2018	Iran	Asian	39.1 ±10.6	NM	76/100	symptoms, MRI	volunteers without LDD	rs1800587, rs114
Chen [23]	2018	China	Asian	42.51±4.42	41.93±4.03	200/200	MRI, pathological analyses	volunteers without LDD	rs1800587
CASP, Critical Appraisal Skills Programme; CT, computerized tomography; LBP: low back pain; LDD: lumbar disc degeneration; NM: not mentioned; MRI, magr resonance imaging									

Table 2. Genotype frequency of IL-1 gene locus polymorphisms in case-control studies														
Authors	Year	Country	Ethnicity	Genotype										P-value for HWE of control
				Case					Control					
				11	12	22	1	2	11	12	22	1	2	
IL-1α (rs1800587)														
Solovieva [9]	2004	Finland	Caucasian	11	21	6	43	33	34	51	8	119	67	0.07
Noponen-Hietala [10]	2005	Finland	Caucasian	62	72	21	196	114	85	77	17	247	111	0.94
Karppinen [13]	2009	Finland	Caucasian	12	26	7	50	40	30	28	5	88	38	0.66
Eskola [14]	2010	Denmark	Caucasian	23	35	8	81	51	72	65	17	209	99	0.69
Aparicio [16]	2011	Spain	Caucasian	22	25	3	69	31	63	61	5	187	71	0.04
Kelempisioti [17]	2011	Finland	Caucasian	64	67	19	195	105	106	114	26	326	166	0.57
Duan [18]	2013	China	Asian	22	17	3	61	23	47	33	5	127	43	0.80
Serrano [21]	2014	Mexico	Caucasian	51	45	4	147	53	55	35	10	145	55	0.22
Abdollahzade [22]	2018	Iran	Asian	33	33	10	99	53	62	62	12	185	86	0.53
Chen [23]	2018	China	Asian	87	78	28	252	134	102	81	14	285	109	0.70
IL-1β (rs1143634)														
Solovieva [9]	2004	Finland	Caucasian	19	12	4	50	20	42	42	9	126	60	0.75
Noponen-Hietala [10]	2005	Finland	Caucasian	81	62	12	224	86	101	67	11	269	89	0.98
Ye [11]	2007	China	Asian	77	4	0	158	4	89	12	0	190	12	0.53
Karppinen [13]	2009	Finland	Caucasian	20	20	5	60	30	32	24	6	88	36	0.63
Eskola [14]	2010	Denmark	Caucasian	31	29	6	91	41	82	53	19	217	91	0.03
Aparicio [16]	2011	Spain	Caucasian	4	16	30	24	76	3	50	76	56	202	0.11
Kelempisioti [17]	2011	Finland	Caucasian	82	53	15	217	83	140	91	15	371	121	0.97
Loncar [19]	2013	China	Asian	283	22	0	145	41	525	61	1	147	45	0.57
Mu [20]	2013	Croatia	Caucasian	55	35	3	588	22	55	37	4	1111	63	0.47
Solovieva [9]	2018	Iran	Asian	39	33	3	111	39	70	58	12	192	82	0.99
IL-1RN (VNTR)														
Noponen-Hietala [10]	2005	Finland	Caucasian	77	65	13	219	91	86	76	17	248	110	0.97
Ye [12]	2007	China	Asian	55	25	1	135	27	83	17	1	183	19	0.90
Kim [15]	2010	Korea	Asian	38	4	0	80	4	193	24	1	410	26	0.78
11, 12 and 22 respectively represent CC, CT and TT for rs1800587, rs1143634; A1A1, A1A2 and A2A2 for IL-1RN VNTR; HWE: Hardy-Weinberg's equilibrium														

Table 3. Association test and heterogeneity test of IL-1 gene locus polymorphisms								
SNPs	Allele contrast	N	Test of association				Test of heterogeneity	
			OR	95%CI	P-value	Statistical Model	P-value	I ² (%)
IL-1α (rs1800587)								
	Overall	10						
	T vs C		1.23	[1.08,1.40]	0.001	FEM	0.79	0
	CT vs CC		1.22	[1.02,1.46]	0.03	FEM	0.82	0
	TT vs CC		1.60	[1.19,2.14]	0.002	FEM	0.51	0
	CT/TT vs CC		1.28	[1.08,1.52]	0.004	FEM	0.82	0
	TT vs CC/CT		1.42	[1.08,1.88]	0.01	FEM	0.55	0
	Caucasian	6						
	T vs C		1.26	[1.06,1.48]	0.007	FEM	0.65	0
	CT vs CC		1.29	[1.03,1.60]	0.02	FEM	0.64	0
	TT vs CC		1.46	[1.02,2.08]	0.04	FEM	0.33	13
	CT/TT vs CC		1.30	[1.06,1.61]	0.01	FEM	0.59	0
	TT vs CC/CT		1.25	[0.89,1.76]	0.19	FEM	0.45	0
	Asian	3						
	T vs C		1.28	[1.02,1.60]	0.04	FEM	0.70	0
	CT vs CC		1.09	[0.79,1.49]	0.60	FEM	0.95	0
	TT vs CC		1.93	[1.15,3.26]	0.01	FEM	0.68	0
	CT/TT vs CC		1.24	[0.92,1.67]	0.15	FEM	0.79	0
	TT vs CC/CT		1.86	[1.13,3.08]	0.01	FEM	0.70	0
IL-1β (rs1143634)								
	Overall	9						
	T vs C		0.99	[0.85,1.16]	0.94	FEM	0.44	0
	CT vs CC		0.93	[0.76,1.14]	0.48	FEM	0.20	28
	TT vs CC		1.10	[0.74,1.64]	0.63	FEM	0.66	0
	CT/TT vs CC		0.95	[0.78,1.16]	0.63	FEM	0.21	26
	TT vs CC/CT		1.13	[0.80,1.60]	0.48	FEM	0.92	0
	Caucasian	7						
	T vs C		1.07	[0.91,1.26]	0.43	FEM	0.90	0
	CT vs CC		1.04	[0.83,1.30]	0.75	FEM	0.38	6
	TT vs CC		1.11	[0.74,1.67]	0.60	FEM	0.56	4
	CT/TT vs CC		1.09	[0.88,1.36]	0.42	FEM	0.81	0
	TT vs CC/CT		1.14	[0.81,1.61]	0.45	FEM	0.87	0
	Asian	2						
	T vs C		0.61	[0.39,0.96]	0.03	FEM	0.44	0
	CT vs CC		0.61	[0.38,0.97]	0.04	FEM	0.40	0
	TT vs CC		0.62	[0.03,15.22]	0.77	FEM	NA	NA
	CT/TT vs CC		0.60	[0.38,0.95]	0.03	FEM	0.39	0
	TT vs CC/CT		0.64	[0.03,15.76]	0.78	FEM	NA	NA
IL-1RN (VNTR)								
	Overall	3						
	2 vs 1		1.15	[0.68,1.94]	0.59	REM	0.12	53

12 vs 11	1.24	[0.68,2.26]	0.48	REM	0.12	53
22 vs 11	0.92	[0.44,1.91]	0.82	FEM	0.87	0
12/22 vs 11	1.21	[0.66,2.22]	0.53	REM	0.10	56
22 vs 11/12	0.92	[0.45,1.88]	0.82	FEM	0.90	0
Asian	2					
2 vs 1	1.51	[0.90,2.25]	0.12	FEM	0.16	49
12 vs 11	1.52	[0.60,3.82]	0.38	REM	0.15	51
22 vs 11	1.57	[0.19,13.10]	0.68	FEM	0.96	0
12/22 vs 11	1.47	[0.57,3.79]	0.42	REM	0.14	54
22 vs 11/12	1.41	[0.17,11.88]	0.75	FEM	0.89	0
SNPs: single nucleotide polymorphisms; N: number of studies included; FEM: fixed effect model; REM: random effect model; OR: odds ratio; 95%CI: 95% confidence interval; NA: not applicable						

Table 4. Sensitivity analysis with each study eliminated for IL-1 α (rs1800587), IL-1 β (rs1143634) and IL-1RN (VNTR) polymorphisms			
Study	Test of heterogeneity		
	OR (95%CI)	P-value	I ² (%)
IL-1α (rs1800587) T/C			
Solovieva [9]	1.23[1.07,1.40]	0.72	0
Noponen-Hietala [10]	1.22[1.06,1.40]	0.72	0
Karppinen [13]	1.21[1.06,1.37]	0.91	0
Eskola [14]	1.22[1.07,1.40]	0.72	0
Aparicio [16]	1.24[1.08,1.41]	0.71	0
Kelempisioti [17]	1.27[1.11,1.47]	0.83	0
Duan [18]	1.24[1.09,1.41]	0.72	0
Serrano [21]	1.26[1.10,1.44]	0.85	0
Abdollahzade [22]	1.24[1.08,1.42]	0.71	0
Chen [23]	1.20[1.04,1.38]	0.78	0
IL-1β (rs1143634) T/C			
Solovieva [9]	1.01[0.86,1.18]	0.37	8
Noponen-Hietala [10]	0.96[0.80,1.14]	0.42	1
Ye [11]	1.01[0.87,1.19]	0.60	0
Karppinen [13]	0.98[0.83,1.15]	0.38	6
Eskola [14]	0.98[0.83,1.16]	0.35	11
Aparicio [16]	1.01[0.86,1.18]	0.36	9
Kelempisioti [17]	0.95[0.79,1.13]	0.45	0
Loncar [19]	1.00[0.85,1.18]	0.35	11
Mu [20]	1.04[0.89,1.23]	0.67	0
IL1-RN (VNTR) A₂/A₁			
Noponen-Hietala [10]	1.38[0.59,3.22]	0.16	49
Ye [12]	0.92[0.67,1.27]	0.76	0
Kim [15]	1.28[0.63,2.57]	0.05	75
OR: odds ratio; 95%CI: confidence interval			

Figures

Figure 1

Literature search strategy and selection of articles. A total of 113 articles were selected for the meta-analysis by searching PubMed, Embase, Web of Science and CNKI, of which 79 articles were excluded after reviewing the title and abstract, 19 articles were excluded after reviewing the full publications. Finally, a total of 15 studies were included in the meta-analysis.

Figure 2

Forest plot of association between IL-1 α rs1800587 polymorphism and LDD risk under allelic contrast model (T vs. C). There was a significant association between rs1800795 and LDD risk in overall population (T vs. C, OR: 1.23, 95%CI: 1.08-1.40, $P=0.001$). OR, odds ratio; CI=confidence interval

Figure 3

Forest plot of association between IL-1 β rs1143634 polymorphism and LDD risk under allelic contrast model (T vs. C). There was a significant association between rs1800797 and LDD risk in Asian population (T vs. C, OR: 0.61, 95%CI: 0.39-0.96, $P=0.03$), but not in Caucasian population (T vs. C, OR: 1.07, 95%CI: 0.91-1.26, $P=0.43$). OR, odds ratio; CI=confidence interval

a

b

Figure 4

Funnel plot analysis for publication bias in selection of studies on IL-1 α rs1800587 (a) and IL-1 β rs1143634 (b) polymorphisms under allelic contrast model. There was no significant publication bias ($P>0.05$).

Figure 5

The expression levels of IL-1α, IL-1β and IL-1RN in the LDD group and the control group. The positive signals were identified in the cytoplasm of nucleus pulposus cells in the LDD group (b, f, j) and the control group (a, e, i). (magnification, 400×). The blue arrowheads show IL-1α, IL-1β and IL-1RN positive cells. Bar charts (c, g, k) show the expression levels of IL-1α, IL-1β and IL-1RN in the two groups. Bar charts (d, h, l) show the mRNA levels of IL-1α, IL-1β and IL-1RN in the two groups. Results are mean ± SD.