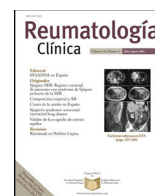




Sociedad Española
de Reumatología -
Colegio Mexicano
de Reumatología

Reumatología Clínica

www.reumatologiaclinica.org



Original Article

The association between interleukin-6 promoter polymorphisms and rheumatoid arthritis by ethnicity: A meta-analysis of 33 studies

Blanca T. Pacheco-Soto^{a,1}, Leonardo M. Porchia^{b,1}, William C. Lara-Vazquez^a, Enrique Torres-Rasgado^a, Ricardo Perez-Fuentes^{a,b}, M. Elba Gonzalez-Mejia^{a,*}

^a Facultad de Medicina, Benemérita Universidad Autónoma de Puebla, 13 Sur 2901 Col. Volcanes, C.P. 72420 Puebla, Pue, Mexico

^b Laboratorio de Investigación en Fisiopatología de Enfermedades Crónicas, Centro de Investigación Biomédica de Oriente, Instituto Mexicano del Seguro Social, Delegación Puebla, Km 4.5 Carretera Federal Atlixco-Metepec, C.P. 42730 Atlixco, Puebla, Mexico

ARTICLE INFO

Article history:

Received 11 November 2019

Accepted 31 March 2020

Keywords:

Interleukin-6
Rheumatoid arthritis
Single nucleotide polymorphism
Meta-analysis
Ethnicity

ABSTRACT

Objective: We performed a meta-analysis to determine the effect Interleukin-6 (IL-6) promoter polymorphism (−174 G>C, −572 G>C, and −597 G>A) have on the development rheumatoid arthritis (RA) by ethnicity.

Material and methods: PubMed, EBSCO, LILACS, and Scopus databases were searched for studies exploring the association between any IL6 polymorphisms and RA until November 2018. Genotype distributions were extracted and, depending on the level heterogeneity, determined by the ψ^2 -based Q test and the Inconsistency Index (I^2), fixed-effects or random-effects models were used to calculate pooled odds ratios (ORs) with 95% confidence intervals (95%CI) for the heterozygous, homozygous, dominant, recessive, and allelic genetic models.

Results: From 708 identified publications, 33 were used in this analysis. For the −174 polymorphism, Asians ($OR_{\text{heterozygous}} = 7.57$, 95%CI: 2.28–25.14, $OR_{\text{homozygous}} = 5.84$, 95%CI: 2.06–16.56, $OR_{\text{dominant}} = 7.21$, 95%CI: 2.30–22.63, $OR_{\text{recessive}} = 5.04$, 95%CI: 1.78–14.28, $OR_{\text{allelic}} = 6.60$, 95%CI: 2.26–19.28, $p < .05$) and Middle East countries ($OR_{\text{heterozygous}} = 2.30$, 95%CI: 1.10–4.81, $OR_{\text{dominant}} = 2.27$, 95%CI: 1.22–4.22, $OR_{\text{allelic}} = 2.29$, 95%CI: 1.24–4.23, $p < .05$) were associated with a significant risk of developing RA. Whereas, for Latinos, the C-allele was associated with a benefit ($OR_{\text{homozygous}} = 0.26$, 95%CI: .08–.82, $OR_{\text{recessive}} = .25$, 95%CI: .08–.80, $p < .05$). For the −572 polymorphism, Asians demonstrated a significant association for the homozygous and recessive genetic models (8 studies, $OR_{\text{homozygous}} = 1.56$, 95%CI: 1.16–2.09, $OR_{\text{recessive}} = 1.63$, 95%CI: 1.08–2.45, $p < .05$). For the −597 polymorphism, no association was observed.

Conclusions: Here, the −174 G>C polymorphism increased the risk of developing RA in Asians and Middle East populations. Interestingly, for Latinos, the polymorphism was associated with a benefit. For the −572 polymorphism, only the Asian population showed an increased risk of developing RA for the CC genotype.

© 2020 Elsevier España, S.L.U. and Sociedad Española de Reumatología y Colegio Mexicano de Reumatología. All rights reserved.

Asociación entre los polimorfismos del promotor de la interleucina-6 y la artritis reumatoide analizado por etnicidad: un metaanálisis de 33 estudios

RESUMEN

Objetivos: Realizamos un meta-análisis para determinar el efecto de los polimorfismos del promotor de interleucina-6 (IL-6) (−174 G>C, −572 G>C, y −597 G>A) sobre el desarrollo de artritis reumatoide (RA) analizado por etnicidad.

Materiales y métodos: En las bases de datos PubMed, EBSCO, LILACS y Scopus se buscaron estudios con la asociación entre polimorfismo de IL-6 y RA publicados hasta noviembre 2018. se obtuvieron las distribuciones de genotipo y de acuerdo al nivel de heterogeneidad el efecto fijo o aleatorio fueron utilizados para calcular los Odds Ratio (OR) con intervalos de confianza del 95% para los modelos genéticos heterocigoto, homocigoto, dominante, recesivo y alélico.

Palabras clave:

Interleucina-6
Artritis reumatoide
Polimorfismo de un solo nucleótido
Metaanálisis
Etnicidad

* Corresponding author.

E-mail address: elba.gonzalezmejia@gmail.com (M.E. Gonzalez-Mejia).

¹ Both authors contributed equally.

Resultados: De 708 estudios identificados, 33 fueron utilizados para este análisis. Para el polimorfismo -174, los países Asiáticos ($OR_{\text{heterocigoto}} = 7,57$, 95%CI: 2,28–25,14, $OR_{\text{homocigoto}} = 5,84$, 95%CI: 2,06–16,56, $OR_{\text{dominante}} = 7,21$, 95%CI: 2,30–22,63, $OR_{\text{recesivo}} = 5,04$, 95%CI: 1,78–14,28, $OR_{\text{alélico}} = 6,60$, 95%CI: 2,26–19,28, $p < 0,05$) y del Medio Oriente ($OR_{\text{heterocigoto}} = 2,30$, 95%CI: 1,10–4,81, $OR_{\text{dominante}} = 2,27$, 95%CI: 1,22–4,22, $OR_{\text{alélico}} = 2,29$, 95%CI: 1,24–4,23, $p < 0,05$) están asociados con el riesgo de desarrollar RA significativamente. Mientras que, para los Latinos, el alelo-C está asociado con un beneficio ($OR_{\text{homocigoto}} = 0,26$, 95%CI: 0,08–0,82, $OR_{\text{recesivo}} = 0,25$, 95%CI: 0,08–0,80, $p < 0,05$). Para el polimorfismo -572, los Asiáticos están asociados significativamente con los modelos genéticos homocigoto y recesivo (8 estudios, $OR_{\text{homocigoto}} = 1,56$, 95%CI: 1,16–2,09, $OR_{\text{recesivo}} = 1,63$, 95%CI: 1,08–2,45, $p < 0,05$). Para el polimorfismo -597, no se observó asociación.

Conclusiones: El polimorfismo -174 G>C aumenta el riesgo de desarrollar RA en población Asiática y Medio Oriente. Curiosamente, para los Latinos el polimorfismo está asociado con un beneficio. Para el polimorfismo -572, solo la población Asiática demuestra una aumento en el riesgo de desarrollar RA con el genotipo CC.

© 2020 Elsevier España, S.L.U.

y Sociedad Española de Reumatología y Colegio Mexicano de Reumatología. Todos los derechos reservados.

Introduction

The world prevalence of rheumatoid arthritis (RA) ranges between 0.5% and 1.0% of the adult population, in which women are four times more likely to develop the disease.¹ RA is a chronic autoimmune disease, characterized by the inflammation of the synovium.² RA can lead to destruction of the patient's joints and prolong/untreated RA can result in multiple organ manifestations, leading to severe disability and even mortality.³ Since RA is a multi-faceted disease, the exact etiology remains elusive. Evidence supports IL-6 as a factor in RA development, such as elevated IL-6 levels are found in RA patients' serum and synovial fluid^{4,5}; moreover, tocilizumab ameliorates disease activity and radiological progression.⁶ For a complete explanation of IL-6's role in RA, please see the review by Srirangan and Choy.⁷

IL-6 is a pro-inflammatory cytokine, released from many types of cells and is a mediator of the acute phase response.⁷ To date, many polymorphisms of the *IL6* gene have been identified; however, the promoter polymorphisms have been shown to affect RA development.^{8–12} Three polymorphisms, -174 G>C (rs1800795), -572 G>C (rs1800796), and -597G>A (rs1800797) have been shown to augment or decrease IL-6 serum levels.^{13,14} Previous meta-analyses have shown that for the Asian population, the -174 G>C polymorphism increases the risk of developing RA^{15–17}; however, for the -572 G>C and -597 G>A polymorphism, the results remain inconclusive. Moreover, with previous meta-analyses, there is an incomplete analysis with respect to Latin America and Middle East countries. Since the latest meta-analyses in 2016 for the -174 polymorphism, which included 13 to 15 studies, there have been 6 additional studies.^{9,18–23} Moreover, it is possible that between 7 and 10 studies were not included with these meta-analyses. Here, we preformed this meta-analysis to elucidate the effect the *IL6* promoter polymorphisms have on the development of RA by ethnicity.

Methods

Search strategy

PubMed, SCOPUS, EBSCO and LILACS databases were searched for all studies that investigated for any *IL6* polymorphisms and RA. The following keywords/index terms and any of their derivations were used: "Interleukin 6 or IL-6 or IFNB2", "rheumatoid", and "variant or SNP or polymorphism or genotype". The search was performed without any language restrictions for publications published until December 15, 2018. Afterwards, the complied publications references were hand searched.

Inclusion and exclusion criteria

Two authors independently determined if each study was to be included. If a disagreement occurred about a publication, a third author analyzed the publication in question. Initially, the titles and abstract were examined to determine if the article focused on RA and IL-6. Afterwards, the publications were thoroughly examined for the *IL6* polymorphisms and the genotype distribution. For inclusion, the studies must have met the following criteria: (1) case-controls studies; (2) examined for any *IL6* polymorphisms; (3) focused on human subjects; (4) RA-confirmed patients using either the American College of Rheumatology or the European League Against Rheumatism²⁴ criteria; and (5) contained information about genotype frequencies. Studies were excluded if they were: (1) not a case-control study; (2) information was used in a previous publication; or (3) meta-analysis, reviews, or editorial articles.

Bias analysis and data extraction

Two authors independently assessed the quality of the studies using the Newcastle–Ottawa Quality Assessment Scale.²⁵ The following aspects of each study were appraised: selection of cases and controls, comparability, and outcome or exposure. For the analysis, the possible quality scores ranged from 0 to 9 (see Supplement information). Studies that scored ≥ 6 were considered as a high-quality study. The following data was collected from each study: first author's name, year of publication, geographical location, diagnosis criteria of RA, technique used to detect the polymorphism, source of controls, and genotype distribution for cases and controls. Before a study was to be excluded for missing information, we attempted to contact the corresponding author by email at least three times.

Statistical analysis

For each study, the Hardy–Weinberg Equilibrium (HWE) was determined by the χ^2 -test for the controls and was considered in agreement when the p -value was > 0.05 . The crude odds ratios (ORs) and 95% Confidence Intervals (95% CI) were used to assess the strength of the association between the *IL6* polymorphisms and the risk of RA. The pooled crude ORs were calculated for allelic (2 vs. 1), dominant (12 + 22 vs. 11), recessive (22 vs. 12 + 11), heterozygous (12 vs. 11), and homozygous (22 vs. 11) genetic models, where for the -174 polymorphism 1 = G (Wild-type) and 2 = C (mutant), for the -572 polymorphism 1 = G (Wild-type) and 2 = C (mutant), and for the -597 polymorphism 1 = G (Wild-type) and 2 = A (mutant).

Heterogeneity was determined using the ψ^2 -based Q-test and its degree was assessed by the Inconsistency Index (I^2). If there was not significant heterogeneity (ψ^2 -based Q-test p -value ≥ 0.10 and $I^2 < 50\%$), the fixed-effects model was used (Mantel–Haenszel method), or if there was significant heterogeneity (ψ^2 -based Q-test p -value < 0.10 and $I^2 \geq 50\%$), the random-effects model was used (DerSimonian and Laird method) to calculate the pooled OR and 95%CI. Sensitivity analysis, removing one study and recalculation of the pooled OR, was conducted to verify the stability of the results. Begg’s funnel plot, Begg–Mazumdar’s test, and Egger’s linear regression test were used to assess for publication bias. For geographic sub-analysis, initially, the studies were categorized based on their country into Northern Africa, Sub-Saharan Africa, Latin America and the Caribbean, Northern America, Central Asia, Eastern Asia, South-eastern Asia, Southern Asia, Western Asia, Eastern Europe, Northern Europe, Southern Europe, Western Europe, or Oceania, according to United Nations M49 standard.²⁶ Afterwards, the regions were grouped into Eastern Europe, Western Europe (Northern, Southern, and Western Europe), Latin America, Asian (Eastern and South-eastern Asia), and Middle East (Northern Africa, Southern and Western Asia). The Middle East category was based on the criteria that most countries identify as Arab and/or Muslim.²⁷ All statistical analyses were conducted by using Comprehensive Meta-analysis v2 (Biostat, Inc., Englewood, New Jersey, USA). Unless noted otherwise, p -values < 0.05 (two-sided) were considered statistically significant.

Results

Selection of eligible studies

After duplicate removal, our literature search resulted in the recovery of 708 publications that focused on the association between the *IL6* polymorphisms and patients with arthritis (Fig. 1). To note, 7 of the hand search articles were identified by the reference list, but the titles were originally in Chinese. After reviewing titles and abstract, 79 publications were considered for full-article examination. Of these publications, 24 were not case-control studies, 10 lacked sufficient data for analysis, 5 focused on the wrong pathology, and 7 were duplicate studies. Therefore, this meta-analysis contains 33 publications, which were divided between the -174 polymorphism (29 studies: cases = 5920 and controls = 6246), the -572 polymorphism (13 studies: cases = 1973 and controls = 1963), and the -597 polymorphism (6 studies: cases = 1278 and controls = 1524). The characteristics of the studies are presented in Table 1. 27.3% of the studies are from Asian countries: China,^{10,11,17,28–31} Taiwan,³² Japan.³³ 18.2% are from Eastern European countries: Russia,^{20,23} Czech Republic,³⁴ Macedonia,³⁵ Poland.^{18,36} 24.2% are from Western European countries: Germany,³⁷ Netherlands,¹² Spain,^{38–40} Sweden⁴¹ and UK.^{42,43} 21.2% are from the Middle East: Egypt,^{9,14,19} Iraq,²² India,^{15,44} and Turkey.⁸ Lastly, 3 studies are from Latin America.^{21,45,46} All the studies used the American College of Rheumatology criteria for RA diagnosis. For only the Pavkova et al. and the Lo et al. studies,

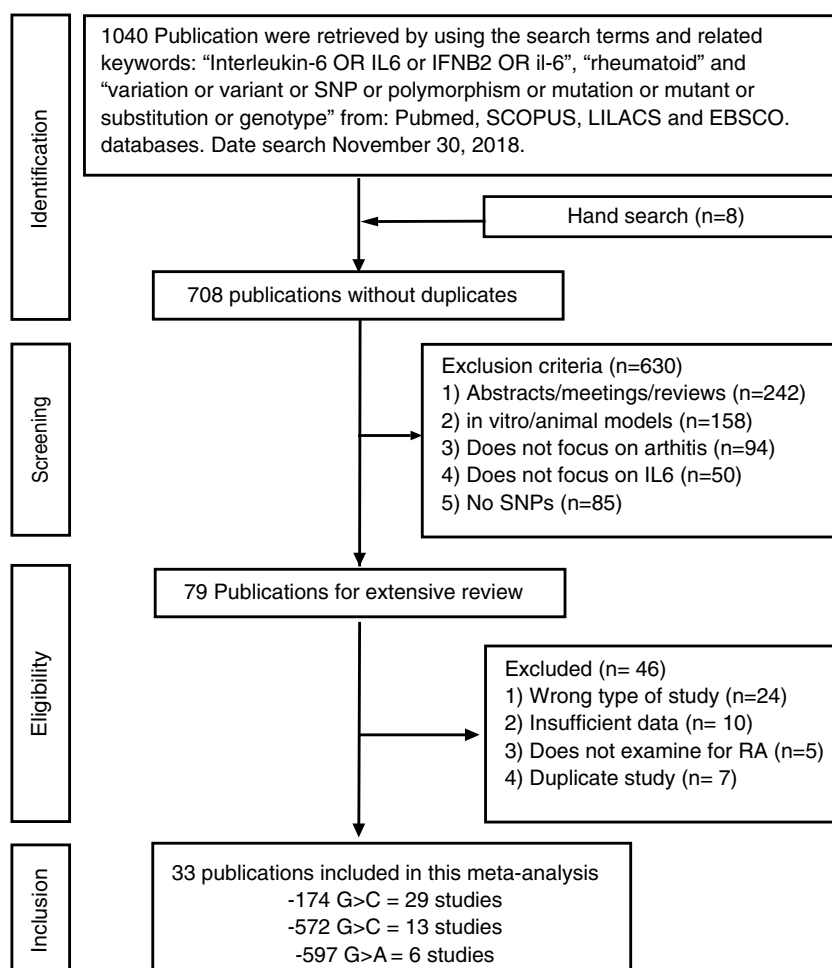


Fig. 1. Flow chart for literature review of studies to be included in the meta-analysis.

Table 1
Characteristics of included studies.

Study	Country (region)	RA criteria	Group ^a	–174 G>C ^b	–572 G>C ^b	–597 G>A ^b	NOS ^d
Ad'hiah 2018	Iraq (Middle East)	ACR	Cases	-/-	1/3/47	-/-	8
			Control	-/-	0/0/45	-/-	
Amr 2016	Egypt (Middle East)	ACR	Cases	44/46/9	26/64/9	-/-	7
			Control	75/23/1	36/58/5 *	-/-	
Arman 2012	Turkey (Middle East)	ACR	Cases	95/62/21	143/31/4	97/59/22	8
			Control	144/80/23 *	194/52/1	133/86/28 *	
Dahlqvist 2002	Sweden (Western Europe)	N/S	Cases	83/121/51	-/-	-/-	7
			Control	57/103/38	-/-	-/-	
Dar 2017	India (Middle East)	N/S	Cases	20/8/6	-/-	-/-	7
			Control	64/16/0	-/-	-/-	
de Souza 2014	Brazil (Latin America)	ACR	Cases	49/14/1	-/-	-/-	8
			Control	29/12/7 *	-/-	-/-	
Emonts 2011	Netherlands (Western Europe)	ACR	Cases	146/133/56	-/-	-/-	7
			Control	146/231/82	-/-	-/-	
Gaber 2103	Egypt (Middle East)	ACR	Cases	24/11/2	-/-	-/-	7
			Control	9/1/0	-/-	-/-	
Gomes-Silva 2018	Brazil (Latin America)	ACR	Cases	68/50/2	-/-	-/-	8
			Control	72/43/5	-/-	-/-	
Guseva 2016	Russia (Eastern Europe)	ACR	Cases	40/62/20	-/-	-/-	8
			Control	85/162/54	-/-	-/-	
Guseva 2018	Russia (Eastern Europe)	N/S	Cases	97/22/1	-/-	-/-	6
			Control	165/3/0	-/-	-/-	
Huang 2007	China (Asia)	ACR	Cases	97/22/1	4/15/101	-/-	8
			Control	165/3/0	13/50/105	-/-	
Julia 2007	Spain (Western Europe)	ACR	Cases	-/-	-/-	115/112/31	8
			Control	-/-	-/-	87/66/28 *	
Kobayashi 2009	Japan (Asia)	ACR	Cases	137/0/0	10/45/82	-/-	8
			Control	108/0/0	8/40/60	-/-	
Li 2009	China (Asia)	ACR	Cases	48/11/1	52/6/2	-/-	8
			Control	82/2/0	52/25/7	-/-	
Li 2014a	China (Asia)	ACR	Cases	247/7/2	23/125/108	249/5/2	8
			Control	329/1/1 *	41/152/138	330/0/1 *	
Li 2014b	China (Asia)	ACR	Cases	613/124/15	-/-	-/-	8
			Control	786/10/2 *	-/-	-/-	
Liu 2013	China (Asia)	N/S	Cases	-/-	12/36/39	-/-	8
			Control	-/-	16/34/15	-/-	
Lo 2008 ^c	Taiwan (Asia)	ACR	Cases	-/-	199: 87/311	-/-	8
			Control	-/-	130: 33/227	-/-	
Lu 2009	China (Asia)	ACR	Cases	120/27/1	5/18/125	-/-	8
			Control	118/2/0	9/36/75	-/-	
Marinou 2007	UK (Western Europe)	ACR	Cases	282/482/166	-/-	-/-	6
			Control	154/226/80	-/-	-/-	
Palomino-Morales 2009	Spain (Western Europe)	ACR	Cases	127/144/40	-/-	-/-	8
			Control	103/94/29	-/-	-/-	
Panoulas 2009	UK (Western Europe)	ACR	Cases	135/176/72	-/-	-/-	7
			Control	148/211/63	-/-	-/-	
Pascual 2000	Spain (Western Europe)	ACR	Cases	75/72/16	-/-	-/-	7
			Control	73/66/18	-/-	-/-	
Pavkova 2014 ^c	Czech Republic (Eastern Europe)	ACR	Cases	144: 159/129	-/-	-/-	8
			Control	200: 232/168	-/-	-/-	
Pawlik 2005	Poland (Eastern Europe)	ACR	Cases	26/53/19	-/-	-/-	8
			Control	25/58/22	-/-	-/-	
Raafat Hamed 2018	Egypt (Middle East)	ACR	Cases	15/8/2	-/-	-/-	7
			Control	25/0/0	-/-	-/-	
Schotte 2015	Germany (Western Europe)	ACR	Cases	17/24/9	46/4/0	17/24/9	7
			Control	30/36/25 *	85/6/0	30/36/25 *	
Shafia 2014	India (Middle East)	ACR	Cases	122/27/1	-/-	-/-	8
			Control	167/30/3	-/-	-/-	
Trajkov 2009	Macedonia (Western Europe)	ACR	Cases	38/30/16	-/-	38/33/13	7
			Control	144/132/25	-/-	153/123/25	
Wielinska 2018	Poland (Eastern Europe)	ACR	Cases	40/65/25	-/-	-/-	7
			Control	37/53/22	-/-	-/-	
You 2013	China (Asia)	ACR	Cases	431/21/0	38/191/222	418/31/3	8
			Control	357/16/0	39/166/168	359/14/0	
Zavaleta-Muñiz 2013	Mexico (Latin America)	ACR	Cases	106/30/1	74/58/5	-/-	8
			Control	80/20/2	62/37/3	-/-	

Abbreviations: ACR: American College of Rheumatology; N/S: not specified; NOS: New Castle-Ottawa Scale.

^a For the controls. HWE was calculated using χ^2 -test. $p < 0.05$ is not in agreement with HWE and indicated with an *.

^b The ratios are given as Wild type, heterozygotes, and homozygote mutant. For the –174 polymorphism, the G-allele is considered the Wild-type and C-allele as the mutant. For the –572 polymorphism, the G-allele is considered the Wild-type and C-allele as the mutant. For the –597 polymorphism, the G-allele is considered the Wild-type and A-allele as the mutant.

^c For the Lo 2008 study and the Pavkova 2014 study, the genotype distribution is represented as total number: Wild-type allelic frequency/mutant allelic frequency.

^d Score was calculated using Newcastle-Ottawa Quality Assessment Scale. A score <6 indicates high bias and indicated with an *.

the data was represented as allelic frequencies.^{32,34} Using the Newcastle-Ottawa scale, none of the studies were determined to contain significant study bias, but the Guseva et al. study⁹ and the Marinou et al. study⁹ could possibly contain potential study bias. For the controls with respect to HWE, 5 studies for the -174 polymorphism,^{8,17,29,37,45} 1 study for the -572 polymorphism,⁹ and 4 studies for the -597 polymorphism^{8,17,37,38} were determined to be not in agreement.

The -174 polymorphism is associated with RA development

The ORs and 95% CIs were calculated for each study for all 5 genetic models (all Forest plots are available as supplement information). Using the selected studies, for the -174 polymorphism, there was significant heterogeneity for all the genetic models; therefore, the random-effects model was utilized (Table 2). When the studies were pooled together, the heterozygous (OR: 1.47, 95%CI: 1.13–1.91, $p=0.004$), dominant (OR: 1.50, 95%CI: 1.15–1.96, $p=0.003$), and allelic (OR: 1.38, 95%CI: 1.13–1.68, $p=0.001$) genetic models demonstrated a significant association. Removing one study did not change the association for any of the genetic models.

Publication bias was assessed by examining the funnel plot. The funnel plots demonstrated no significant asymmetry and the shape of the funnel plots suggested no evidence of publication bias (see Supplement information), even though some over-dispersion can be seen. No correlation was determined by the Begg-Mazumdar's test or bias by Egger's test for the homozygous and recessive genetic models (Table 2); however, there was the presence of publication bias for the heterozygous, dominant, and allelic genetic models (Begg-Mazumdar's test: $p<0.01$, Egger's test: $p<0.01$).

When the cohort was stratified by geographic region, for the Asian population, the -174 polymorphism did demonstrate a strong association for all the genetic models (Table 3). For Middle East countries, the -174 polymorphism showed an association for the heterozygous (OR: 2.30, 95%CI: 1.10–4.81, $p=0.028$), dominant (OR: 2.27, 95%CI: 1.22–4.22, $p=0.010$), and allelic (OR: 2.29, 95%CI: 1.24–4.23, $p=0.008$) genetic models. Interestingly, for Latin America, the -174 polymorphism demonstrated a protective benefit for

the homozygous (OR: 0.26, 95%CI: 0.08–0.82, $p=0.022$) and recessive (OR: 0.25, 95%CI: 0.08–0.80, $p=0.019$) genetic models.

The -572 polymorphism is associated with RA development

For the -572 polymorphism, the homozygous and heterozygous genetic models did not present with a significant level of heterogeneity and were analyzed using fixed-effects, whereas the rest of the genetic models were analyzed with random-effects. Only the homozygous (OR: 1.60, 95%CI: 1.21–2.12, $p=0.001$) and recessive (OR: 1.61, 95%CI: 1.11–2.33, $p=0.012$) genetic models demonstrated a positive association between the polymorphism and the risk of developing RA (Table 2). Removing the Li et al. study⁹ resulted in a significant positive association for the dominant genetic model (OR: 1.32, 95%CI: 1.08–1.63, $p=0.008$), none of the other studies had any effect. For the remaining genetic model, the results were resilient to any change from removing one study. No publication bias was determined by examining the Funnel plot, Egger's bias test, or by Begg-Mazumdar's correlation test.

When stratified by geographic region, it appears that the association was due to the inclusion of studies from the Asian population (Table 4). For the Asian population alone, there was an association between the -572 polymorphism and the development of RA for the homozygous (OR: 1.56, 95%CI: 1.16–2.09, $p=0.004$) and recessive genetic models (OR: 1.63, 95%CI: 1.08–2.45, $p=0.020$). No association was observed for the Middle East region.

No association between the -597 polymorphism and RA development

For the -597 polymorphism, all the genetic models were analyzed with the fixed-effects model, except the allelic genetic model. When the studies were pooled together, there was no effect for any of the genetic models (Table 2). However, removing the Arman et al. study,⁸ a positive association for the heterozygous (OR: 1.33, 95%CI: 1.01–1.74, $p=0.040$) and dominant (OR: 1.30, 95%CI: 1.01–1.68, $p=0.040$) genetic models was observed. No publication bias was determined by examining the Funnel plot, Egger's bias test, or by

Table 2

The association between IL-6 promoter polymorphism and the risk of developing Rheumatoid Arthritis.

Genetic model	Analysis	N ^a	Heterogeneity ^b			Association ^c			Publication Bias ^d	
			Q p-value	I ² (%)	Model	OR	95% CI	p-Value	Begg	Egger
-174 G>C										
Heterozygous	Overall	27	<0.01	82	Random	1.47	1.13–1.91	0.004*	Tau = 0.39, $p<0.01$ *	Bias = 2.78, $p<0.01$ *
Homozygous	Overall	26	<0.01	47	Random	1.13	0.88–1.44	0.337	Tau = 0.12, $p=0.39$	Bias = 0.67, $p=0.14$
Dominant	Overall	27	<0.01	84	Random	1.50	1.15–1.96	0.003*	Tau = 0.31, $p=0.02$ *	Bias = 2.87, $p<0.01$ *
Recessive	Overall	26	0.03	38	Random	1.12	0.92–1.37	0.270	Tau = 0.09, $p=0.49$	Bias = 0.49, $p=0.23$
Allelic	Overall	28	<0.01	85	Random	1.38	1.13–1.68	0.001*	Tau = 0.35, $p<0.01$ *	Bias = 2.73, $p<0.01$ *
-572 G>C										
Heterozygous	Overall	11	0.17	29	Fixed	1.09	0.88–1.35	0.420	Tau = -0.09, $p=0.70$	Bias = -0.94, $p=0.39$
Homozygous	Overall	11	0.21	24	Fixed	1.60	1.21–2.12	0.001*	Tau = -0.13, $p=0.59$	Bias = 0.21, $p=0.80$
Dominant	Overall	12	0.04	46	Random	1.21	0.90–1.63	0.208	Tau = 0.09, $p=0.68$	Bias = -0.11, $p=0.92$
Recessive	Overall	11	<0.01	68	Random	1.61	1.11–2.33	0.012*	Tau = -0.09, $p=0.70$	Bias = 0.56, $p=0.59$
Allelic	Overall	13	<0.01	79	Random	1.18	0.90–1.54	0.246	Tau = 0.03, $p=0.90$	Bias = -0.46, $p=0.75$
-597 G>A										
Heterozygous	Overall	6	0.28	21	Fixed	1.20	0.96–1.51	0.115	Tau = 0.47, $p=0.19$	Bias = 1.91, $p=0.09$
Homozygous	Overall	6	0.25	24	Fixed	1.10	0.79–1.55	0.575	Tau = 0.33, $p=0.34$	Bias = 1.13, $p=0.32$
Dominant	Overall	6	0.15	38	Fixed	1.19	0.97–1.48	0.100	Tau = 0.47, $p=0.19$	Bias = 2.21, $p=0.09$
Recessive	Overall	6	0.14	40	Fixed	1.03	0.75–1.42	0.854	Tau = 0.33, $p=0.34$	Bias = 1.21, $p=0.35$
Allelic	Overall	6	0.02	61	Random	1.21	0.90–1.61	0.205	Tau = 0.47, $p=0.19$	Bias = 2.68, $p=0.10$

Abbreviations: OR: Odds ratio; 95%CI: 95% confidence interval; and I2: Inconsistency Index.

^a N = number of studies included in analysis.

^b Depending on the level of heterogeneity, either Random Effects model or Fixed Effects model was used.

^c The pooled effect was calculated using Comprehensive Meta-analysis software v2.

^d Publication bias was assessed by Egger's bias test (Egger) and Begg and Mazumdar's correlation test (Begg).

* p -Value < 0.05 (two-tailed) were considered significant.

Table 3
The association of the –174 G>C polymorphism on the development of Rheumatoid Arthritis, stratified by ethnicity.

Genetic model	Analysis	N ^a	Heterogeneity ^b			Association ^c		
			Q p-value	I ² (%)	Model	OR	95% CI	p-Value
Asian	Heterozygous	6	<0.01	86	Random	7.57	2.28–25.14	0.001*
	Homozygous	5	0.91	0	Fixed	5.84	2.06–16.56	0.001*
	Dominant	6	<0.01	87	Random	7.21	2.30–22.63	0.001*
	Recessive	5	0.92	0	Fixed	5.04	1.78–14.28	0.002*
	Allelic	6	<0.01	86	Random	6.60	2.26–19.28	0.001*
Middle East	Heterozygous	5	0.02	66	Random	2.30	1.10–4.81	0.028*
	Homozygous	6	0.05	56	Random	3.42	0.94–12.42	0.062
	Dominant	6	<0.01	72	Random	2.27	1.22–4.22	0.010*
	Recessive	6	0.09	48	Random	2.69	0.83–8.66	0.098
	Allelic	6	<0.01	79	Random	2.29	1.24–4.23	0.008*
East Europe	Heterozygous	6	0.93	0	Fixed	0.91	0.72–1.14	0.393
	Homozygous	5	0.18	36	Fixed	1.09	0.81–1.49	0.562
	Dominant	5	0.85	0	Fixed	0.94	0.75–1.17	0.581
	Recessive	5	0.14	43	Fixed	1.15	0.88–1.51	0.307
	Allelic	6	0.56	0	Fixed	1.03	0.90–1.18	0.650
West Europe	Heterozygous	7	0.01	63	Random	0.96	0.76–1.20	0.689
	Homozygous	7	0.40	4	Fixed	0.99	0.82–1.18	0.876
	Dominant	7	0.03	58	Random	0.95	0.77–1.16	0.606
	Recessive	7	0.66	0	Fixed	1.03	0.87–1.21	0.759
	Allelic	7	0.14	37	Fixed	0.99	0.90–1.08	0.732
Latin	Heterozygous	3	0.55	0	Fixed	1.09	0.75–1.57	0.664
	Homozygous	3	0.48	0	Fixed	0.26	0.08–0.82	0.022*
	Dominant	3	0.17	43	Fixed	0.94	0.66–0.35	0.750
	Recessive	3	0.55	0	Fixed	0.25	0.08–0.80	0.019*
	Allelic	3	<0.05	67	Random	0.77	0.44–1.34	0.353

Abbreviations: OR: Odds ratio; 95%CI: 95% confidence interval; and I²: Inconsistency Index.

^a N = number of studies included in analysis.

^b Depending on the level of heterogeneity, either Random Effects (RE) model or Fixed Effects (FE) model was used.

^c The pooled effect was calculated using Comprehensive Meta-analysis software v2.

* p-Value < 0.05 (two-tailed) were considered significant.

Table 4
The association of the –572 G>C polymorphism on the development of Rheumatoid Arthritis, stratified by ethnicity.

Genetic model	Analysis	N ^a	Heterogeneity ^b			Association ^c		
			Q p-value	I ² (%)	Model	OR	95% CI	p-Value
Asian	Heterozygous	7	0.09	46	Random	0.97	0.63–1.49	0.883
	Homozygous	7	0.10	43	Fixed	1.56	1.16–2.09	0.004*
	Dominant	7	<0.01	66	Random	1.23	0.74–2.05	0.416
	Recessive	7	<0.01	78	Random	1.63	1.08–2.45	0.020*
	Allelic	8	<0.01	86	Random	1.20	0.82–1.74	0.351
Middle East	Heterozygous	2	0.12	60	Random	1.08	0.58–2.01	0.806
	Homozygous	3	0.39	0	Fixed	2.42	0.89–6.61	0.084
	Dominant	3	0.27	24	Fixed	1.10	0.76–1.60	0.604
	Recessive	3	0.11	54	Fixed	1.73	0.67–4.48	0.260
	Allelic	3	0.15	46	Fixed	1.15	0.85–1.54	0.367

Abbreviations: OR: Odds ratio; 95%CI: 95% confidence interval; and I²: Inconsistency Index.

^a N = number of studies included in analysis.

^b Depending on the level of heterogeneity, either Random Effects (RE) model or Fixed Effects (FE) model was used.

^c The pooled effect was calculated using Comprehensive Meta-analysis software v2.

* p-Value < 0.05 (two-tailed) were considered significant.

Begg–Mazumdar's correlation test. No sub-analysis could be performed for the –597 polymorphism, due to the few studies.

Discussion

Some studies have shown that IL-6 serum levels are associated with the development of RA¹⁴; moreover, it has been postulated

that the IL6 –174, –572, and –597 polymorphisms are associated with RA development. Here, we show that the –597 polymorphism does not promote RA development; however, the –174 and the –572 polymorphisms do indeed increase the risk of developing RA, especially in Asian and Middle East countries. Unexpectedly, the –174 polymorphism showed a protective effect for Latin American countries.

Previous meta-analyses have shown that the –174 polymorphism does augment the risk of developing RA, especially for Asian populations and not others.^{15–17,47} Our results also confirm this; however, we also found an effect for the –174 polymorphism with countries that are from the Middle East. When the genotype distributions were examined, it appeared that these Middle East and Asian populations had the lowest minor allele frequencies (10% and 1%, respectively), which were different from European populations (~40%). Since the GG genotype is associated with higher serum IL-6 and incremental decreases in serum IL-6 were associated with each additional C-allele,⁴⁸ this would suggest that a large portion of the Europe population would have lower IL-6 serum levels. However, serum IL-6 are also affected by many confounding factors. Serum IL-6 was shown to be affected by age, circadian rhythm, and stress as well as overweight or obesity patients present with elevated serum IL-6 when compared to normal weight subjects.^{49–52} Lastly, it is demonstrated that diets with phytoestrogens decrease serum IL-6,⁵³ whereas, diet with increase carbohydrates or monounsaturated fat augment serum IL-6.^{54,55} Therefore lifestyle, diet, or other factors could significantly affect serum IL-6 level and mitigate the –174 polymorphism's effect associated with RA development.

There are many studies that show differences in the IL-6 serum levels is ethnic dependent. In African Americans, the production of IL-6 was higher compared to Cuban Americans.⁴⁷ Whereas, in Hispanics, especially Mexicans, IL-6 production was demonstrated to be lower than other ethnicities.⁵¹ However, promoter polymorphisms have shown to increase the production of IL-6,¹⁴ but the prevalence of these polymorphisms varying significantly from region to region. For example, Gao et al. reported the prevalence of –174 polymorphism was less frequent in Asian Indian, Afro-Caribbean, Afro-American, and Asians.¹³

Here, we show that, for Latinos, the homozygous mutant of the –174 polymorphism was associated with a protective effect. The mechanism for this result remains elusive. Even though the –174 polymorphism was shown to increase IL-6 production, with a lower basal level, it is possible that the increases are insufficient to augment the risk of developing RA. Moreover, the quality of life and lifestyle in Latin American, which has not fully adopted the Western lifestyle, these confounding factors can mitigate the effect elevated IL-6 causes in developing RA. In support of this, it has been shown that the type of diet affects the production of IL-6 from muscle cells, which indirectly affects immune cell penetration of muscle tissue, promoting prolong IL-6 release.⁵⁶ Diets, in which more carbohydrates are consumed, does mitigate the secondary IL-6 peak, caused by immune cells, after moderate exercise.⁵⁷ Moreover, the more active the subject's lifestyle, the lower IL-6 production.^{58,59} In Latin American countries, it is possible that the lifestyle and quality of life does mitigate the effect the –174 polymorphism has on the development of RA in Latin American. This does posit that some factors such as lifestyle or diet in the presence of elevated IL-6 levels does sensitize a subject to an anti-inflammatory state, leading to the increased release of IL-6 and the development of RA; however, more studies are required to elucidated if the protective effect against RA development is connected to these confounding factors. In a review by Saavedra Ramirez et al., they eloquently explain the enigma of IL-6 in disease pathogenesis and present the possible switch between pro- and anti-inflammatory functions of IL-6.⁶⁰

Three previous meta-analyses did examine for any associations between the –572 and –597 polymorphisms with RA development—one conducted in 2012, which used 2 and 1 studies, respectively, one in 2014, which used 6 and 2 studies, respectively, and one in 2019 that used 6 studies for the –572 polymorphism.^{17,47,61} Since then, numerous studies have examined the association and, in our study using 6 studies, we found no association between the –597 polymorphism and the development of RA. However, removing the Arman et al. study did

indicate that an association could exist. Therefore, more research is required to deduce the association between RA and the –597 polymorphism.

For the –572 polymorphism, using 13 studies, we found that the homozygous mutant does increase the risk of developing RA; however, this result appears to be due the Asian population. This is in disagreement with the Li et al. meta-analysis¹⁷; however, we would say our study is in agreement with the Dar et al. meta-analysis,¹⁵ but their result was based-off of the Huang et al. study, which is included here. Recently, in 2019, a systematic review by Zhang et al., which solely focused on the –572 polymorphism, did determined that the polymorphism is associated with the risk of RA, specially the GG genotype.⁶² We believe that their study presents with similar results, but our study appears to be more inclusive. Here, we have 13 studies, whereas Zhang et al. only used 6 studies, of which all were included in our study, suggesting a possibility of publication/selection bias. Indeed, when we compared the results, we found that for their dominant model (our study's recessive model), the result did not concur, which highly suggests the presence of selection bias. Nevertheless, as we postulated, any effect observed was due to the Asian population and Zhang et al. confirmed our observation.⁶² However, it must be noted that Zhang et al.'s Asian population consisted of 3 studies, whereas our Asian population consisted of 8 studies. This would suggest that our results are more stable than Zhang et al. It could be expected that the Middle East region should have presented with an association; however, with the few studies included here, we could not determine this result.⁶²

With our meta-analysis, some models presented with significant heterogeneity. We believe the cause could be due to the cases and controls, which were not matched by sex (majority of cases were women), age, or type of RA. In a previous study by Donn et al., in juvenile idiopathic arthritis, there was a significant difference in the ratio between systemic onset and enthesitis-related,⁶³ thus indicating that the type of RA could be affected differently. Another cause could be the subject's ethnicity. Even though we performed an ethnic sub-analysis, genetic differences within a country can vary significantly, as indicated in China,^{64,65} Mexico,⁶⁶ Brazil,^{67,68} and India.⁶⁹ The diagnostic criteria used to identify or categorize RA could also act as a source of heterogeneity.

This study has a few limitations. First, as mentioned above, due to the large genetic variation within a country, more studies are required to determine specific effects, such as the protective benefit our results indicated for Latin Americans. Second, our results can only focus on overall risk of developing RA, and stage-specific effects (low, moderate, high or remission) cannot be determined. Third, we calculated crude ORs that were not adjusted.

Here, we show that the –174 polymorphism increased the risk of developing RA for Asians and Middle East populations; interestingly, there was a protective effect for Latinos. As for the –572 polymorphism, only the Asian population was associated with an increased risk of developing RA. No affect was observed for the –597 polymorphism.

Conflicts of interests

The authors declare that they have no conflicts of interests to report.

Acknowledgements

We would like to express their gratitude to Mtro. Ricardo Villegas Tovar, Coordinator of Scientific Production and International Visibility, Benemérita Universidad Autónoma de Puebla. Moreover, we would like to thank Dr. Solbritt Rantapää Dahlqvist, Dr. Irina Anatolyevna Guseva, Dr. Anthony G Wilson, and Dr. Heiko Schotte

for their prompt replies to our emails and the sharing of the data to allow a more conclusive analysis between *IL6* promoter polymorphisms and the development of RA. This study was supported by grants from the Vicerrectoría de Investigación de Benemérita Universidad Autónoma de Puebla (10051909-VIEP2018 to MEGM and 100170644-VIEP2018 to RPF. 100493499-VIEP2018 to ETR).

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.reuma.2020.03.004.

References

- Silman AJ, Pearson JE. Epidemiology and genetics of rheumatoid arthritis. *Arthritis Res.* 2002;4 Suppl. 3:S265–72.
- Miossec P. Rheumatoid arthritis: still a chronic disease. *Lancet.* 2013;381:884–6.
- McInnes IB, Schett G. The pathogenesis of rheumatoid arthritis. *N Engl J Med.* 2011;365:2205–19.
- Baillet A, Gossec L, Paternotte S, Etcheto A, Combe B, Meyer O, et al. Evaluation of serum interleukin-6 level as a surrogate marker of synovial inflammation and as a factor of structural progression in early rheumatoid arthritis: results from a French national multicenter cohort. *Arthritis Care Res.* 2015;67:905–12.
- Robak T, Gladalska A, Stepien H, Robak E. Serum levels of interleukin-6 type cytokines and soluble interleukin-6 receptor in patients with rheumatoid arthritis. *Mediators Inflamm.* 1998;7:347–53.
- Wang J, Platt A, Upmanyu R, Germer S, Lei G, Rabe C, et al. IL-6 pathway-driven investigation of response to IL-6 receptor inhibition in rheumatoid arthritis. *BMJ Open.* 2013;3:e003199.
- Srirangan S, Choy EH. The role of interleukin 6 in the pathophysiology of rheumatoid arthritis. *Ther Adv Musculoskelet Dis.* 2010;2:247–56.
- Arman A, Coker A, Sariöz O, Inanc N, Direskeneli H. Lack of association between IL-6 gene polymorphisms and rheumatoid arthritis in Turkish population. *Rheumatol Int.* 2012;32:2199–201.
- Amr K, El-Awady R, Raslan H. Assessment of the –174G/C (rs1800795) and –572G/C (rs1800796) Interleukin 6 Gene Polymorphisms in Egyptian Patients with Rheumatoid Arthritis. *Open Access Maced J Med Sci.* 2016;4:574–7.
- Lu Y, Yu X. The research on serum level and polymorphism of IL-6 gene. *Chin J Cell Mole Immunol.* 2009;25:725–8.
- Li Y, Sun Z, Wang S, Yang S. The research on interleukin-6 gene promoter polymorphism with rheumatoid arthritis. *Clinical Focus.* 2009;19:1715–7.
- Emonts M, Hazes MJ, Houwing-Duistermaat JJ, van der Gaast-de Jongh CE, de Vogel L, Han HK, et al. Polymorphisms in genes controlling inflammation and tissue repair in rheumatoid arthritis: a case control study. *BMC Med Genet.* 2011;12:36.
- Gao SP, Liang S, Pan M, Sun RL, Chen C, Luan H, et al. Interleukin-6 genotypes and serum levels in Chinese Hui population. *Int J Clin Exp Med.* 2014;7:2851–7.
- Gaber W, Azkalanay GS, Gheita TA, Mohey A, Sabry R. Clinical significance of serum interleukin-6 and –174 G/C promoter polymorphism in Rheumatoid arthritis patients. *Egypt Rheumatol.* 2013;35:107–13.
- Dar SA, Haque S, Mandal RK, Singh T, Wahid M, Jawed A, et al. Interleukin-6-174G> C (rs1800795) polymorphism distribution and its association with rheumatoid arthritis: a case-control study and meta-analysis. *Autoimmunity.* 2017;50:158–69.
- Li B, Xiao Y, Xing D, Ma XL, Liu J. Circulating interleukin-6 and rheumatoid arthritis: a Mendelian randomization meta-analysis. *Medicine (Baltimore).* 2016;95:e3855.
- Li F, Xu J, Zheng J, Sokolove J, Zhu K, Zhang Y, et al. Association between interleukin-6 gene polymorphisms and rheumatoid arthritis in Chinese Han population: a case-control study and a meta-analysis. *Sci Rep.* 2014;4:5714.
- Wielinska J, Dratwa M, Swierkot J, Korman L, Iwaszko M, Wysocka B, et al. IL-6 gene polymorphism is associated with protein serum level and disease activity in Polish patients with rheumatoid arthritis. *HLA.* 2018;92:38–41.
- Raafat Hamed RM, Mohamed SA, Dwedat RA, Elkholy YS, Elgengehy FT. Association of interleukin-6 and its –174G/C promoter polymorphism with clinical and laboratory characteristics of non hepatitis C virus rheumatoid arthritis patients. *Egypt J Med Hum Genet.* 2018;19:235–40.
- Guseva IA, Luchikhina EL, Demidova NV, Avdeeva AS, Soroka NE, Abramov DD, et al. Molecular genetic testing of accp-positive patients with rheumatoid arthritis and high inflammatory disease activity (A remarca study). *Sci Pract Rheumatol.* 2018;56:28–33.
- Gomes-Silva IIF, Rushansky E, Carvalho-Neto FG, Vieira AVB, de Araujo Mariano MHQ, de Souza PRE, et al. Association of methylation and polymorphism of interleukin-6 promoter gene with development of rheumatoid arthritis. *Acta Med Iran.* 2018;56:429–33.
- Ad'hiah AH, Mahmood AS, Al-kazaz A-KA, Mayouf KK. Gene expression and six single nucleotide polymorphisms of interleukin-6 in rheumatoid arthritis: a case-control study in Iraqi patients. *Sci Pract Rheumatol.* 2018;54:639–45.
- Guseva IA, Demidova NV, Soroka NE, Luchikhina EL, Novikov AA, Aleksandrova EN, et al. Investigation of candidate gene polymorphisms in an immune response as markers for the risk of developing rheumatoid arthritis and producing autoantibodies. *Sci Pract Rheumatol.* 2016;54:21–30.
- Aydin SZ, Castillo-Gallego C, Nam J, Freeston J, Horton S, Wakefield RJ, et al. The new ACR/EULAR criteria for rheumatoid arthritis can identify patients with same disease activity but less damage by ultrasound. *Eur J Rheumatol.* 2017;4:118–21.
- Stang A. Critical evaluation of the Newcastle-Ottawa scale for the assessment of the quality of nonrandomized studies in meta-analyses. *Eur J Epidemiol.* 2010;25:603–5.
- United Nation Statistics Division. Standard Country or Area Codes for Statistical Use (M49), <https://unstats.un.org/unsd/methodology/m49/> [accessed 4.05.19].
- Özalp ON. Where is the Middle East? The definition and classification problem of the middle east as a regional subsystem in international relations. *Turk J Polit.* 2011;2.
- Huang XZ, Zhuang JH, Ren YG, Zhou LJ, Zhou Q. Association of interleukin-6 and interleukin-18 gene polymorphism with rheumatoid arthritis in Guangdong Han population. *Nan Fang Yi Ke Da Xue Xue Bao.* 2007;27:1661–4.
- Li X, Chai W, Ni M, Xu M, Lian Z, Shi L, et al. The effects of gene polymorphisms in interleukin-4 and interleukin-6 on the susceptibility of rheumatoid arthritis in a Chinese population. *Biomed Res Int.* 2014;2014:265435.
- Liu X, Xu J, Hu CD, Pan ZL, Zhang YC. The relationship between SNPs in the genes of TLR signal transduction pathway downstream elements and rheumatoid arthritis susceptibility. *Tsitol Genet.* 2014;48:24–9.
- You CG, Li XJ, Li YM, Wang LP, Li FF, Guo XL, et al. Association analysis of single nucleotide polymorphisms of proinflammatory cytokine and their receptors genes with rheumatoid arthritis in northwest Chinese Han population. *Cytokine.* 2013;61:133–8.
- Lo SF, Huang CM, Lin HC, Chen WC, Tsai CH, Tsai FJ. Cytokine (IL-6) and chemokine (IL-8) gene polymorphisms among rheumatoid arthritis patients in Taiwan. *Clin Exp Rheumatol.* 2008;26:632–7.
- Kobayashi T, Murasawa A, Ito S, Yamamoto K, Komatsu Y, Abe A, et al. Cytokine gene polymorphisms associated with rheumatoid arthritis and periodontitis in Japanese adults. *J Periodontol.* 2009;80:792–9.
- Pavkova Goldbergova M, Nemeč P, Lipkova J, Jarkovsky J, Gatterova J, Ambrozkova D, et al. Relation of IL-6 IL-13 and IL-15 gene polymorphisms to the rheumatoid factors, anti-CCP and other measures of rheumatoid arthritis activity. *Int J Immunogenet.* 2014;41:34–40.
- Trajkov D, Mishevska-Perchinkova S, Karadzova-Stojanoska A, Petlichkovski A, Strezova A, Spiroski M. Association of 22 cytokine gene polymorphisms with rheumatoid arthritis in population of ethnic Macedonians. *Clin Rheumatol.* 2009;28:1291–300.
- Pawlik A, Wrzesniewska J, Florczyk M, Gawronska-Szklarz B, Herczynska M. IL-6 promoter polymorphism in patients with rheumatoid arthritis. *Scand J Rheumatol.* 2005;34:109–13.
- Schotte H, Schmidt H, Gaubitz M, Drynda S, Kekow J, Willeke P, et al. Interleukin-6 promoter haplotypes are associated with etanercept response in patients with rheumatoid arthritis. *Clin Rheumatol.* 2015;34:2021–8.
- Julia A, Moore J, Miquel L, Alegre C, Barcelo P, Ritchie M, et al. Identification of a two-loci epistatic interaction associated with susceptibility to rheumatoid arthritis through reverse engineering and multifactor dimensionality reduction. *Genomics.* 2007;90:6–13.
- Palomino-Morales R, Gonzalez-Juanatey C, Vazquez-Rodriguez TR, Miranda-Filloo JA, Llorca J, Martin J, et al. Interleukin-6 gene –174 promoter polymorphism is associated with endothelial dysfunction but not with disease susceptibility in patients with rheumatoid arthritis. *Clin Exp Rheumatol.* 2009;27:964–70.
- Pascual M, Nieto A, Mataran L, Balsa A, Pascual-Salcedo D, Martin J. IL-6 promoter polymorphisms in rheumatoid arthritis. *Genes Immun.* 2000;1:338–40.
- Dahlqvist SR, Arlestig L, Sikstrom C, Lingham S. Tumor necrosis factor receptor type II (exon 6) and interleukin-6 (–174) gene polymorphisms are not associated with family history but tumor necrosis factor receptor type II is associated with hypertension in patients with rheumatoid arthritis from northern Sweden. *Arthritis Rheum.* 2002;46:3096–8.
- Marinou I, Healy J, Mewar D, Moore DJ, Dickson MC, Binks MH, et al. Association of interleukin-6 and interleukin-10 genotypes with radiographic damage in rheumatoid arthritis is dependent on autoantibody status. *Arthritis Rheum.* 2007;56:2549–56.
- Panoulas VF, Douglas KM, Smith JP, Stavropoulos-Kalinoglou A, Metsios GS, Nightingale P, et al. Transforming growth factor-beta1 869T/C, but not interleukin-6-174G/C, polymorphism associates with hypertension in rheumatoid arthritis. *Rheumatology (Oxford).* 2009;48:113–8.
- Shafia S, Dilafoze, Sofi FA, Rasool R, Javeed S, Shah ZA. Rheumatoid arthritis and genetic variations in cytokine genes: a population-based study in Kashmir Valley. *Immunol Invest.* 2014;43:349–59.
- de Souza TR, de Albuquerque Tavares Carvalho A, Duarte AP, Porter SR, Leao JC, Gueiros LA. Th1 and Th2 polymorphisms in Sjogren's syndrome and rheumatoid arthritis. *J Oral Pathol Med.* 2014;43:418–26.
- Zavaleta-Muniz SA, Martin-Marquez BT, Gonzalez-Lopez L, Gonzalez-Montoya NG, Diaz-Toscano ML, Ponce-Guarneros JM, et al. The –174G/C and –572G/C interleukin 6 promoter gene polymorphisms in Mexican patients with rheumatoid arthritis: a case-control study. *Clin Dev Immunol.* 2013;2013:849590.
- Lee YH, Bae SC, Choi SJ, Ji JD, Song GG. The association between interleukin-6 polymorphisms and rheumatoid arthritis: a meta-analysis. *Inflamm Res.* 2012;61:665–71.
- Fishman D, Faulds G, Jeffery R, Mohamed-Ali V, Yudkin JS, Humphries S, et al. The effect of novel polymorphisms in the interleukin-6 (IL-6) gene on IL-6 transcription and plasma IL-6 levels, and an association with systemic-onset juvenile chronic arthritis. *J Clin Invest.* 1998;102:1369–76.

49. Oranskiy SP, Yeliseyeva LN, Tsanaeva AV, Zaytseva NV. Body composition and serum levels of adiponectin, vascular endothelial growth factor, and interleukin-6 in patients with rheumatoid arthritis. *Croat Med J.* 2012;53:350–6.
50. Straub RH, Pongratz G, Hirvonen H, Pohjolainen T, Mikkelsson M, Leirisalo-Repo M. Acute cold stress in rheumatoid arthritis inadequately activates stress responses and induces an increase of interleukin 6. *Ann Rheum Dis.* 2009;68:572–8.
51. Stowe RP, Peek MK, Cutchin MP, Goodwin JS. Plasma cytokine levels in a population-based study: relation to age and ethnicity. *J Gerontol A Biol Sci Med Sci.* 2010;65:429–33.
52. Arvidson NG, Gudbjornsson B, Elfman L, Ryden AC, Totterman TH, Hallgren R. Circadian rhythm of serum interleukin-6 in rheumatoid arthritis. *Ann Rheum Dis.* 1994;53:521–4.
53. Coe CL, Love GD, Karasawa M, Kawakami N, Kitayama S, Markus HR, et al. Population differences in proinflammatory biology: Japanese have healthier profiles than Americans. *Brain Behav Immun.* 2011;25:494–502.
54. Teng KT, Chang LF, Vethakkan SR, Nesaretnam K, Sanders TAB. Effects of exchanging carbohydrate or monounsaturated fat with saturated fat on inflammatory and thrombogenic responses in subjects with abdominal obesity: a randomized controlled trial. *Clin Nutr.* 2017;36:1250–8.
55. Goletzke J, Buyken AE, Joslowski G, Bolzenius K, Remer T, Carstensen M, et al. Increased intake of carbohydrates from sources with a higher glycemic index and lower consumption of whole grains during puberty are prospectively associated with higher IL-6 concentrations in younger adulthood among healthy individuals. *J Nutr.* 2014;144:1586–93.
56. Hennigar SR, McClung JP, Pasiakos SM. Nutritional interventions and the IL-6 response to exercise. *FASEB J.* 2017;31:3719–28.
57. Starkie RL, Arkinstall MJ, Koukoulas I, Hawley JA, Febbraio MA. Carbohydrate ingestion attenuates the increase in plasma interleukin-6, but not skeletal muscle interleukin-6 mRNA, during exercise in humans. *J Physiol.* 2001;533:585–91.
58. Ferrer MD, Capo X, Martorell M, Busquets-Cortes C, Bouzas C, Carreres S, et al. Regular practice of moderate physical activity by older adults ameliorates their anti-inflammatory status. *Nutrients.* 2018;10.
59. Pires MM, Salvador EP, Siqueira-Catania A, Folchetti LD, Cezaretto A, Ferreira SR. Assessment of leisure-time physical activity for the prediction of inflammatory status and cardiometabolic profile. *J Sci Med Sport.* 2012;15:511–8.
60. Ramirez PGS, Duque GMV, Naranjo LAG. Interleucina-6: ¿amiga o enemiga? Bases para comprender su utilidad como objetivo terapéutico. *Iatreia.* 2011;24:157–66.
61. Ji YF, Jiang X, Li W, Ge X. Impact of interleukin-6 gene polymorphisms and its interaction with obesity on osteoporosis risk in Chinese postmenopausal women. *Environ Health Prev Med.* 2019;24:48.
62. Zhang C, Jiao S, Li T, Zhao L, Chen H. Relationship between polymorphisms in -572G/C interleukin 6 promoter gene polymorphisms (rs1800796) and risk of rheumatoid arthritis: a meta-analysis. *Int J Rheum Dis.* 2020;23:47–54.
63. Donn RP, Barrett JH, Farhan A, Stopford A, Pepper L, Shelley E, et al. Cytokine gene polymorphisms and susceptibility to juvenile idiopathic arthritis British Paediatric Rheumatology Study Group. *Arthritis Rheum.* 2001;44:802–10.
64. Chiang CWK, Mangul S, Robles C, Sankararaman S. A comprehensive map of genetic variation in the world's largest ethnic group-Han Chinese. *Mol Biol Evol.* 2018;35:2736–50.
65. Du W, Feng C, Yao T, Xiao C, Huang H, Wu W, et al. Genetic variation and forensic efficiency of 30 indels for three ethnic groups in Guangxi: relationships with other populations. *PeerJ.* 2019;7:e6861.
66. Moreno-Estrada A, Gignoux CR, Fernandez-Lopez JC, Zakharia F, Sikora M, Contreras AV, et al. Human genetics. The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. *Science.* 2014;344:1280–5.
67. Pena SD, Bastos-Rodrigues L, Pimenta JR, Bydlowski SP. DNA tests probe the genomic ancestry of Brazilians. *Braz J Med Biol Res.* 2009;42:870–6.
68. Ramos BR, D'Elia MP, Amador MA, Santos NP, Santos SE, da Cruz Castelli E, et al. Neither self-reported ethnicity nor declared family origin are reliable indicators of genomic ancestry. *Genetica.* 2016;144:259–65.
69. Pathak AK, Kadian A, Kushniarevich A, Montinaro F, Mondal M, Ongaro L, et al. The genetic ancestry of modern Indus valley populations from Northwest India. *Am J Hum Genet.* 2018;103:918–29.