

Supplementary Table S1. Primer sequences (5'–3') and expected amplicon sizes for PCR-RFLP genotyping

Gene / Locus	Forward primer (5'–3')	Reverse primer (5'–3')	Expected amplicon (bp)	Notes
IL-1B –31 C/T	AGAAGCTTCCACCAATACTC	AGCACCTAGTTGTAAGGAAG	239	AluI
IL-1B –511 C/T	TGGCATTGATCTGGTTCATC	GTTTAGGAATCTTCCCCTT	305	AvaI
IL-1B +3954 C/T	GTTGTCATCAGACTTTGACC	TTCAGTTCATATGGACCAGA	249	TaqI
IL-6 –174 G/C	CTTTGTCAAGACATGCCAAGTGCT	GCCTCAGAGACATCTCCAGTCC	198	NlaIII
TNF-α –308 G/A	AGGCAATAGGTTTTGAGGGCCAT	TCCTCCCTGCTCCGATTCCG	107	NcoI
IL-10 –819 T/C	ATCCAAGACAACACTACTAA	CCTTTACTTACTAATTCACAC	209	MaeIII
TNF-α –376 G/A	ACACAGCTTTTCCCTCCAAC	GAGGCTGCCCCGATTTCAG	152	MnII
IL-17 rs763780	GCTGTTGAGGTGACTTTGAG	CTGAGGTGAGGTGAGGAGAG	143	BstI
IFN-γ +2108 A/G	GGAAACAGCAAGGCGAAATC	GTTTCACTTCACCGACTTGCT	180	HinfI

Note: Primer sequences and expected amplicon sizes for PCR-RFLP assays. Restriction enzymes and resulting fragment sizes are described for each SNP. For TNF- α –376 G/A, IL-17 rs763780, and IFN- γ +2108 A/G, RFLP enzymes used were MnII, BstI, and HinfI respectively (fragment patterns depend on genotype). All primers were designed based on previously published PCR-RFLP protocols.

Supplementary Table S2. Genotype and allele frequencies of non-significant cytokine gene polymorphisms in UA (n=160) and control (n=280) groups

Gene / Locus	Genotype / Allele	Control (n=280), n (%)	UA (n=160), n (%)	OR (95% CI) ^a	p value
IL-1B +3954 C/T	CC	149 (53.2)	82 (51.3)	1.00 REF	–
	TC	112 (40.0)	66 (41.3)	1.07 (0.71–1.61)	0.821
	TT	19 (6.8)	12 (7.5)	1.15 (0.53–2.48)	0.88
	C allele	410 (73.2)	230 (71.9)	1.00 REF	–
	T allele	150 (26.8)	90 (28.1)	1.07 (0.79–1.45)	0.725
IL-1B –31 C/T	CC	155 (55.4)	91 (56.9)	1.00 REF	–
	TC	112 (40.0)	60 (37.5)	0.91 (0.61–1.37)	0.735
	TT	13 (4.6)	9 (5.6)	1.18 (0.48–2.87)	0.893
	C allele	422 (75.4)	242 (75.6)	1.00 REF	–
	T allele	138 (24.6)	78 (24.4)	0.99 (0.72–1.36)	0.994
TNF-α –376 G/A	GG	139 (49.6)	78 (48.7)	1.00 REF	–
	GA	111 (39.6)	66 (41.3)	1.06 (0.70–1.60)	0.865
	AA	30 (10.8)	16 (10.0)	0.95 (0.49–1.85)	0.984
	G allele	389 (69.5)	222 (69.4)	1.00 REF	–
	A allele	171 (30.5)	98 (30.6)	1.00 (0.75–1.35)	0.961
IL-6 –174 G/C	GG	138 (49.3)	88 (55.0)	1.00 REF	–
	GC	92 (32.9)	48 (30.0)	0.82 (0.53–1.27)	0.433
	CC	50 (17.8)	24 (15.0)	0.75 (0.43–1.31)	0.387
	G allele	368 (65.7)	224 (70.0)	1.00 REF	–
	C allele	192 (34.3)	96 (30.0)	0.82 (0.61–1.10)	0.219
IL-10 –819 T/C	TT	160 (57.1)	102 (63.8)	1.00 REF	–
	TC	90 (32.2)	44 (27.5)	0.77 (0.49–1.19)	0.234
	CC	30 (10.7)	14 (8.7)	0.73 (0.37–1.45)	0.368
	T allele	410 (73.2)	248 (77.5)	1.00 REF	–
	C allele	150 (26.8)	72 (22.5)	0.79 (0.57–1.10)	0.159
IL-17 rs763780	TT	149 (53.2)	80 (50.0)	1.00 REF	–
	TC	112 (40.0)	60 (37.5)	1.00 (0.66–1.51)	0.924
	CC	19 (6.8)	20 (12.5)	1.96 (0.99–3.89)	0.076
	T allele	410 (73.2)	220 (68.8)	1.00 REF	–
	C allele	150 (26.8)	100 (31.2)	1.24 (0.92–1.68)	0.182
IFN-γ +2108 A/G	AA	141 (50.4)	78 (48.7)	1.00 REF	–
	AG	112 (40.0)	66 (41.3)	1.07 (0.71–1.61)	0.844
	GG	27 (9.6)	16 (10.0)	1.07 (0.54–2.11)	0.98
	A allele	394 (70.4)	222 (69.4)	1.00 REF	–
	G allele	166 (29.6)	98 (30.6)	1.05 (0.78–1.41)	0.819