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Alleles carried at positions –819 and –592 of the *IL10* promoter affect transcription following stimulation of peripheral blood cells with *Streptococcus pneumoniae*

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Abstract IL-10 inhibits the production of many pro-inflammatory cytokines. Polymorphisms in the *IL10* gene promoter at positions –1082G→A, –819C→T and –592C→A occur as three haplotypes, *ATA*, *GCC* and *ACC*. These influence several infectious and inflammatory diseases including community-acquired pneumonia, where a role for IL-10 is suggested by fluctuations in plasma levels of the cytokine. However, the effects of the haplotypes on IL-10 production are unclear. We stimulated peripheral blood mononuclear cells (PBMC) from at least five individuals homozygous for each of the three haplotypes with lipopolysaccharide (LPS, 10 µg/ml) or heat-killed *Streptococcus pneumoniae* (10⁷cfu/ml) and measured IL-10 mRNA by RT-PCR. Following *S. pneumoniae* stimulation, PBMC with the *ATA* haplotype had higher IL-10 mRNA levels than those with the *GCC* haplotype at 4 h (independent *t*-test; *P*=0.024), or the *ACC* haplotype at 4 h (*P*<0.0001) and 8 h (*P*=0.007). Following LPS stimulation, IL-10 mRNA levels were not significantly influenced by the *IL10* haplotype, but similar

trends were observed, consistent with the variable outcome of published studies. The results suggest that the –819 and/or –592 alleles affect transcription.

Keywords Interleukin 10 · Lipopolysaccharide · *Streptococcus pneumoniae* · Promoter polymorphisms

Interleukin-10 [IL-10; cytokine synthesis inhibitory factor (CSIF)] is a multifunctional anti-inflammatory cytokine produced by monocytes, macrophages, B cells, T cells and mast cells (de Waal Malefyt and Moore 1998). IL-10 inhibits the production of pro-inflammatory cytokines including TNFα, IL-1, IL-6 and IL-8 (de Waal Malefyt et al. 1991). In sepsis, septic shock and community-acquired pneumonia (CAP), IL-10 serum levels correlate with the intensity of the inflammatory response, the severity of injury and the clinical outcome (Marchant et al. 1994; Gomez-Jimenez et al. 1995; Glynn et al. 1999). This suggests that dysregulation of IL-10 may affect clinical outcome.

Family studies attribute up to 75% of differences in IL-10 production to genetic factors (Westendorp et al. 1997). The *IL10* gene is located on Chromosome 1, with multiple single nucleotide polymorphisms (SNP) in the distal and proximal promoter regions (Eskdale et al. 1998). SNP at positions –1082G→A, –819C→T and –592C→A relative to the transcription start site occur as three haplotypes, *GCC*, *ACC* and *ATA* (Turner et al. 1997). These SNP are associated with various inflammatory diseases including CAP (Gallagher et al. 2003; Schaaf et al. 2003), inflammatory bowel disease (Tagore et al. 1999), rheumatoid arthritis (Hajeer et al. 1998), primary Sjogren's syndrome (Hulkkonen et al. 2001), multiple organ dysfunction in patients with sepsis (Reid et al. 2002) and meningococcal sepsis (van der Pol et al. 2001).

The effects of the *IL10* promoter haplotypes on IL-10 production are unclear. Crawley et al. (1999) and Koss et al. (2000) exposed whole blood to LPS and found that individuals with the *ATA* genotype produced significantly less IL-10 than non-*ATA* carriers. However, Schaaf et al.

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(2003) associated the -1082A allele with decreased IL-10 protein levels in similar whole blood assays, while Keijsers et al. (1998) associated low levels with the -1082G allele. Carriage of the ATA haplotype was associated with high IL-10 plasma levels in neonates (Helminen et al. 2001), but this was not apparent in adults with or without injections of LPS (Fijen et al. 2001; Hulkkonen et al. 2001).

A limitation of these studies as models of CAP is that cells were stimulated with the Gram-negative cell wall component, LPS. While Gram-negative bacteria can cause CAP, *Streptococcus pneumoniae* is more often responsible (Marrie 2000). Moreover many studies have analyzed IL-10 protein in plasma or culture supernatants, rather than mRNA production where the effects of promoter polymorphisms are likely to be clearest. IL-10 protein levels may be affected by factors that modulate translation, secretion and utilization of the cytokine, independent of the *IL-10* promoter haplotype. Here we investigated whether IL-10 mRNA levels in cultured peripheral blood mononuclear cells (PBMC) are influenced by SNP in the proximal promoter of *IL10* after stimulation with *S. pneumoniae* or LPS.

Ninety-three healthy Caucasian volunteers from Perth (Western Australia) were genotyped (Table 1), and 16 individuals homozygous for the 3 known haplotypes (ATA, GCC, ACC) were selected for further study (Table 2). These were hospital and laboratory staff, had no chronic illness and were not on any medications or affected by any acute medical condition at the time of this study. They gave written informed consent and the Medical Ethics Committee of the Royal Perth Hospital approved the study. Typing for the -1082, -819 and -592 polymorphisms was performed by a single base extension in multiplexed reactions using Sequenom's Mass ARRAY technology (Ross et al. 1998). The -819 and -592 polymorphisms were found to be in complete linkage disequilibrium (Table 1).

Table 1 Frequencies of *IL10* genotypes ($n=93$ subjects)

| <i>IL10</i> haplotype | Allele at position | | | Haplotype frequency |
|-----------------------|--------------------|------|------|---------------------|
| | -1082 | -819 | -592 | |
| 1 | GG | CC | CC | 0.13 |
| 2 | AA | CC | CC | 0.05 |
| 3 | AA | TT | AA | 0.08 |
| 4 | AA | CT | AC | 0.15 |
| 5 | GA | CT | AC | 0.28 |
| 6 | GA | CC | CC | 0.31 |

Table 2 Homozygous individuals selected for study of IL-10 mRNA

| <i>IL10</i> haplotype | Allele at position | | | Males (n) | Females (n) | Median age (years) | Age range (years) |
|-----------------------|--------------------|------|------|---------------|-----------------|--------------------|-------------------|
| | -1082 | -819 | -592 | | | | |
| 1 | G | C | C | 2 | 3 | 34 | 24-49 |
| 2 | A | C | C | 4 | 2 | 42 | 22-56 |
| 3 | A | T | A | 2 | 3 | 26 | 24-48 |

PBMC from the five or six individuals with each *IL10* haplotype were then stimulated for 4 and 8 h with *S. pneumoniae* or LPS. PBMC were isolated by density gradient centrifugation of heparinized blood on Ficoll-Hypaque and stored in liquid nitrogen in 10% DMSO/90% heat-inactivated (HI) fetal calf serum (FCS). Thawed PBMC were washed once and resuspended at 0.5×10^6 cells/ml in RPMI/10% HI FCS. Aliquots of 500 μ l were placed into 6 ml round-bottom polypropylene tubes with 500 μ l RPMI/10% HI FCS with or without 10 μ g/ml LPS (from *Escherichia coli* 0111:B4; Sigma) or 10^7 cfu/ml heat-killed *S. pneumoniae*, prepared as described previously (Temple et al. 2003), and incubated for 4 and 8 h (37°C, 5% CO₂).

Expression of IL-10 mRNA was measured by real time RT-PCR. RNA was extracted from PBMC using the RNeasy Mini Kit (Qiagen, Clifton Hill, Victoria, Australia). RNA (6 μ l) was used for first-strand cDNA synthesis using Omniscript reverse transcriptase (Qiagen) and oligo (dT₁₅) primers (Promega, Australia) in a final volume of 20 μ l. IL-10 mRNA was quantitated with a forward primer spanning the exon 2-3 junction (5'-TTAAGGGTTACCTGGGTTGC-3') and a reverse primer spanning the exon 3-4 junction (5'-GGGAAGAAATC-GATGACAGC-3'), yielding a 191 bp product. β -Actin was amplified with a forward primer spanning the exon 2-3 junction (5'-GATGACCCAGATCATGTTTGA-3') and a reverse primer spanning the exon 3-4 junction (5'-GACTCCATGCCAGGAAGGAA-3'), yielding a 459 bp product. For amplification using the LightCycler (Roche, Indianapolis, Ind., USA), the reaction mixture contained 5 μ l cDNA, 20 ng/ μ l primers (Geneworks, Adelaide, South Australia), 0.25 μ g/ μ l bovine serum albumin (CSL Biosciences, Parkville, Victoria, Australia), 0.08 mM dNTP, 2.0 mM MgCl₂ pH8.9 (IL-10) or 2.5 mM MgCl₂ pH8.9 (β -actin), 2 μ l SYBRGreen 1 (Sigma, St Louis, Mo., USA), 1.5 U Platinum *Taq* DNA polymerase (Invitrogen Life Technologies, Mount Waverley, Victoria, Australia) in 20 μ l. Cycling conditions for IL-10 were 95°C for 5 min; 45 cycles of 96°C for 1 s, 65°C for 5 s, 72°C for 15 s; 96°C for 1 min, 60°C for 5 s, 99°C for 1 min and 40°C for 30 s. For β -actin, the annealing temperature was 64°C and 35 cycles were run. 2% agarose gels containing ethidium bromide were used to confirm amplification of a single product of the correct size. Negative controls were run without cDNA template. Serial 10-fold dilutions of pGEMT-Easy plasmids (Promega, Annandale, NSW, Australia) containing the amplified region of each gene were used to establish standard curves. The method of least squares was used to calculate the initial template concentration using the

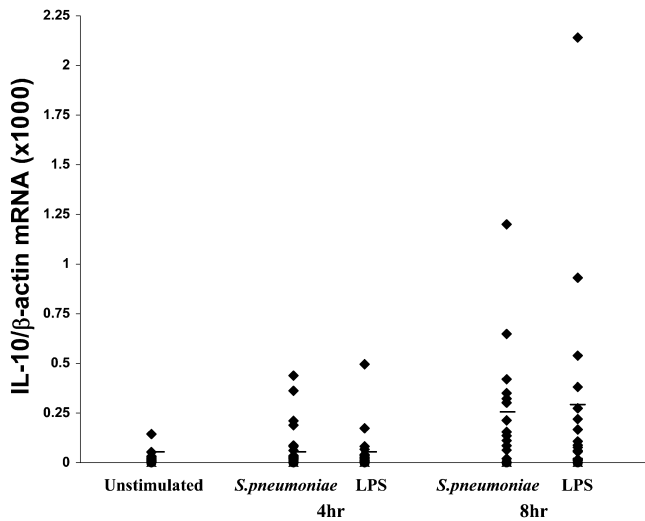


Fig. 1 IL-10 mRNA levels in PBMC (0.5×10^6) from healthy subjects ($n=16$) stimulated with *Streptococcus pneumoniae* (10^7 cfu/ml), or LPS ($10 \mu\text{g/ml}$), for 4 and 8 h. Bars represent the geometric means of duplicate experiments (independent *t*-tests using SPSS v10.1)

Lightcycler software. The inter-assay correlation coefficient was 0.97 ± 0.02 .

Levels of IL-10 mRNA from the 16 individuals assayed were elevated at 4 h, and continued to increase at 8 h (*S. pneumoniae*, $P=0.01$, LPS, $P=0.036$; compared to unstimulated cells) (Fig. 1). There was no significant difference between cells stimulated with *S. pneumoniae* or LPS.

Following *S. pneumoniae* stimulation, PBMC with the *ATA* haplotype had higher IL-10 mRNA levels than those with the *GCC* haplotype at 4 h ($P=0.024$), or the *ACC* haplotype at 4 h ($P<0.0001$) and 8 h ($P=0.007$) (Fig. 2a). A similar trend was evident after LPS stimulation (Fig. 2b), but the differences were not significant ($P>0.05$).

After stimulation with *S. pneumoniae* PBMC with the *IL10*-819TT or *IL10*-592AA haplotype had higher IL-10 mRNA levels (4 h, $P=0.001$; 8 h, $P=0.004$) than those with *IL10*-819CC or *IL10*-592CC (Table 3). In contrast, no significant associations were observed with LPS stimulation. IL-10 mRNA levels were not affected by *IL10*-1082 (Table 3).

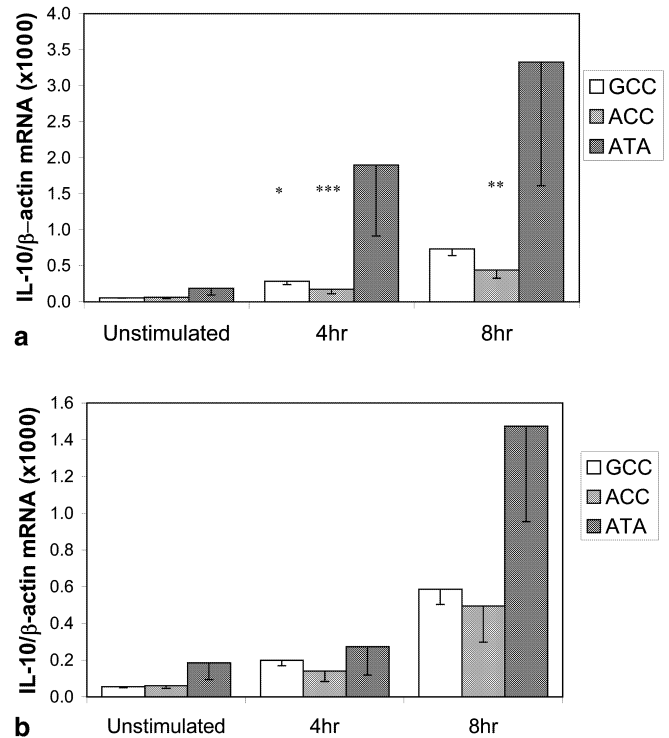


Fig. 2 IL10 mRNA levels after stimulation with **a** *S. pneumoniae* (10^7 cfu/ml) and **b** LPS ($10 \mu\text{g/ml}$) for 4 and 8 h. Results are presented as the geometric means and 95% confidence intervals for duplicate assays of 5–6 samples per group. * $P<0.05$, ** $P<0.01$, *** $P<0.001$, compared with the *ATA* haplotype (independent *t*-tests using SPSS v10.1)

These results establish that *IL10* promoter haplotypes influence IL-10 mRNA levels in stimulated PBMC from healthy subjects. *S. pneumoniae*-stimulated PBMC with the *ATA* haplotype produced more IL-10 mRNA than those with the *ACC* and *GCC* haplotypes after 4 and 8 h. LPS stimulation generated similar trends but no differences were significant. This may account for some variation between published studies.

The haplotypic association shown here can be explained by the SNP at -819 and/or -592 . These are in complete linkage disequilibrium and lie within positive and negative regulatory regions, respectively (Kube et al. 1995). The -819T and -592A may increase stimulated transcriptional activity by influencing transcription factor binding. However this has not been demonstrated exper-

Table 3 IL-10 expression is higher in cells from IL-10 -819TT and IL-10 -592AA donors

| Stimulus | Locus | Haplotype comparison | IL-10 mRNA | |
|----------------------|---------------------------|----------------------|------------|-----------|
| | | | 4 h* | 8 h* |
| LPS | $-1082(\text{rs}1800896)$ | AA vs GG | $P=0.964$ | $P=0.738$ |
| | $-819(\text{rs}3021097)$ | TT vs CC | $P=0.352$ | $P=0.184$ |
| | $-592(\text{rs}1800872)$ | AA vs CC | $P=0.352$ | $P=0.184$ |
| <i>S. pneumoniae</i> | $-1082(\text{rs}1800896)$ | AA vs GG | $P=0.295$ | $P=0.535$ |
| | $-819(\text{rs}3021097)$ | TT vs CC | $P=0.001$ | $P=0.004$ |
| | $-592(\text{rs}1800872)$ | AA vs CC | $P=0.001$ | $P=0.004$ |

* Differences in means assessed by independent *t*- tests using SPSS v10.1

imentally and other loci should also be considered. For example, nine extended haplotypes, formed by the distal promoter SNP $-3575T \rightarrow A$, $-2849G \rightarrow A$, and $-2763C \rightarrow A$ and the proximal *IL10* SNP ($-1082G \rightarrow A$, $-819C \rightarrow T$, and $-592C \rightarrow A$, including $-1330G \rightarrow A$) have been demonstrated in Caucasians (Gibson et al. 2001). In addition, two microsatellites (*IL-10.R/IL-10.G*) associated with differential *IL-10* protein secretion form four haplotype families with the *IL10* haplotypes at positions -1082 , -819 and -592 (Eskdale et al. 1998; Eskdale et al. 1999).

Although we have established the *IL10-819TT:I-L10-592AA* haplotype as a determinant of high *IL-10* transcription, it is still not clear whether levels of *IL-10* protein are affected. Previous studies have obtained variable results using LPS as the stimuli and measuring protein levels of *IL-10* (Crawley et al. 1999; Hulkkonen et al. 2001). Our results concur with those of Helminen et al. (2001), who found high plasma *IL-10* from neonates with the *ATA* haplotype. More comprehensive studies are required.

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