C-863A (rs1800630), C-857T (rs1799724), C-806T (rs4248158) and G-308A (rs1800629) in TNF α gene promoter were determined by DNA sequencing. Serum TNF α was quantified by enzyme-linked immunosorbent assays. The associations of these SNPs and serum TNF α with AF were investigated separately.

Results We did not observe the associations of T-1031C, C-863A, C-857T and C-806T with AF. Patients with AF showed a significantly higher A allele frequency (10.5% vs 6.8%; $p=0.024$) and A carrier genotype frequency (19.3% vs 12.6%; $p=0.026$) for G-308A SNP. Although the G-308A SNP showed a nominal dominant association with AF (OR for the-308A carriers versus-308GG: 1.65; 95% CI 1.06 to 2.56; $p=0.026$), it failed to remain statistically significant after controlling for traditional risk factors. In contrast, serum TNF α levels were significantly associated with AF after adjustment for the covariates (adjusted OR for TNF α levels: 1.14; 95% CI: 1.02 to 1.27, $p=0.023$).

Conclusions An inflammatory state marked by serum TNF α elevation is associated with AF itself. TNF α G-308A polymorphism might act as a weak modifier rather than an independent risk factor in AF development.

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SERUM TNF α LEVELS BUT NOT TNF α GENE PROMOTER POLYMORPHISMS CONFER RISK ASSOCIATION TO ATRIAL FIBRILLATION IN CHINESE HAN POPULATION

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Background Recent findings suggest a link between inflammatory processes and the development of atrial fibrillation (AF). Many studies have investigated the role of C-reactive protein (CRP) in AF, but few have concentrated on the role of tumour necrosis factor- α (TNF α) in its pathogenesis.

Aims The aim was to study the possible associations of the SNPs in TNF α gene promoter and serum TNF α with AF in the Chinese Han population, and thus to help establish the relationship between inflammation and AF.

Methods A pairwise case control study of 301 non-valvular AF patients and 301 health controls was conducted. Five single nucleotide polymorphisms (SNPs), T-1031C (rs1799964),