factor receptor superfamily which is constitutively or inducible expressed on the surface of a variety of immune and non-immune cell types, indicating that this locus might be involved in several autoimmune diseases.

Aim To investigate whether the rs4810485 single-nucleotide polymorphism (SNP) of *CD40* gene is associated with the development of RA and systemic lupus erythematosus (SLE) in the genetic homogeneous population of the island of Crete. The functional significance of this gene polymorphism will also be analysed.

Materials and methods The SLE and RA sample sets consisted of 351 and 272 patients, respectively, while the control group consisted of 670 samples. Genotyping of the rs4810485 SNP was performed by PCR-restriction fragment length polymorphism or using the Sequenom MassArray technology. Genotyping of rs4810485 was performed by PCR-restriction fragment length polymorphism and by the Sequenom MassArray technology. The expression of *CD40* in SLE patients with different genotypes was assessed in peripheral blood mononuclear cells (PBMCs) by flow cytometry. Quantification of *CD40* mRNA was performed by quantitative real time PCR in freshly isolated PBMCs from patients with different genotype.

Results The risk allele G of the *CD40* rs4810485 SNP was more frequent in individuals with SLE and RA than in healthy controls ($p<0.0001$, OR 1.5, 95% CI 1.3 to 1.9 and $p<0.0001$, OR 1.6, 95% CI 1.3 to 1.9 respectively). SLE patients with the rs4810485 G/G genotype had significantly higher CD40 mRNA and protein expression in freshly isolated peripheral blood B cells and monocytes, compared to patients with the G/T or T/T genotype.

Conclusions The CD40 rs4810485 SNP is associated with increased susceptibility to both SLE and RA in a homogeneous Greek population. Identification of shared genetic susceptibility loci may provide insight to their understanding of the pathophysiology of autoimmune diseases. The risk allele G seems to confer susceptibility to clinically distinct disorders through similar or differential effects on disease-specific cell types. Quantitative analysis of the allelic expression of CD40 in SLE patients demonstrated that the risk allele was accompanied by higher expression of CD40 both at mRNA and protein level especially in B lymphocytes and CD14 monocytes.

A33 GENETIC ASSOCIATION AND FUNCTIONAL CONSEQUENCES OF A COMMON SNP IN THE *CD40* REGION WITH SYSTEMIC LUPUS ERYTHEMATOSUS AND RHEUMATOID ARTHRITIS IN A HOMOGENEOUS GREEK POPULATION

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Background There is increasing evidence that different autoimmune diseases may share some common pathogenetic pathways. The *CD40* locus has recently been identified by a genome-wide study as a genetic risk factor for rheumatoid arthritis (RA). *CD40* is a member of the tumour necrosis