(DNA) samples from test subjects and controls were analysed for the two polymorphisms by polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP). The allele, genotype, and haplotype frequencies were compared in different groups. A meta-analysis was also performed for the CC and GG genotype of both SNPs of interest.

Results: No significant differences were found in frequencies of C allele, CC genotype and C carriers of rs28493229 and rs2290692. Combined CG+GG genotype frequency of rs2290692 was found to be significantly associated with susceptibility of KD (95% Confidence interval (CI) = 1.38-13.83, $p = 0.015$). A meta-analysis did not show a significant association of SNP rs28493229 (Odds ratio = 1.46, CI = 0.96-2.23) and rs2290692 (OR = 1.07, 95% CI = 0.663-1.731) of *ITPKC* and susceptibility to KD.

Conclusion: Combined CG+GG genotype of SNP rs2290692 at 3' UTR of the *ITPKC* gene was found to be significantly associated with susceptibility to KD. Our study did not show a significant association of any allele or genotype with susceptibility to KD. The meta-analysis combining our study with previous studies on these 2 SNPs also failed to show a significant association of different genotypes and susceptibility of KD.

Table:

Table 1. Allele, genotype and carrier frequencies of single nucleotide polymorphisms of rs28493229 and rs2290692

Allele, genotype and carrier frequencies of SNP rs28493229 of <i>ITPKC</i> (n = 100)	KD patients (n = 50) n (%)	Controls (n = 50) n (%)	Odds ratio (95% C.I.)	P value
Allele/ Genotype				
G allele	89 (89%)	92 (92%)	-	-
C allele	11 (11%)	8 (8%)	1.42 (0.49-4.26)	0.468
GG genotype	39 (78%)	42 (84%)	-	-
CG genotype	11 (22%)	8 (16%)	1.48 (0.54-4.19)	0.446
CC genotype	0 (0%)	0 (0%)	-	-
Frequencies of allele and genotype of rs2290692 SNPs in KD patients and controls (n = 100)				
Allele/ Genotype				
G allele	63 (63%)	56 (56%)	-	-
C allele	37 (37%)	44 (44%)	0.747 (0.41-1.36)	0.313
GG genotype	19 (38%)	20 (40%)	-	-
CG genotype	25 (50%)	16 (32%)	1.64 (0.68-4.04)	0.272
CC genotype	6 (12%)	14 (28%)	0.45 (0.14-1.37)	0.173

C.I. Confidence interval, KD- Kawasaki disease

Figure:

Figure 1. Forest plot for the association between (A) CC genotype of rs28493229 and risk of having KD (B) GG genotype of rs2290692 and risk of having KD (C) CG genotype of rs2290692 and risk of having KD

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AB0004

TLR10 SINGLE NUCLEOTIDE POLYMORPHISMS ARE ASSOCIATED WITH HIDRADENITIS SUPPURATIVA IN A CAUCASIAN SPANISH POPULATION (NORTHERN SPAIN)

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Background: Hidradenitis suppurativa (HS) is a chronic, relapsing inflammatory cutaneous disease affecting terminal hair follicles in apocrine-gland bearing skin. The pathogenesis of HS is still unknown, although increasing evidence suggests that the immune system plays an important role. In order to study the role of innate immunity we analyzed several Toll Like Receptors (TLRs) functional single nucleotide polymorphisms (SNPs). To date, only one previous study focused about the role of TLR4 SNPs in HS showing no association with this disease.

Objectives: The main goal of this study was to analyze the role of several TLRs functional SNPs in HS patients and healthy controls, in a Caucasian population from Cantabria (northern Spain).

Methods: Through a case-control study, we analyzed the allele and genotype distribution of the SNPs in 106 patients with HS and 278 age and sex matched healthy control subjects for the following SNPs (TLR1 rs5743611 and rs4833095, TLR2 rs5743704 and rs5743708, TLR6 rs5743810, and TLR10 rs11096955, rs11096957 and rs4129009, by Real-Time PCR using a TaqMan assay.

Results: We did not find any significant difference in the allelic distribution of the different SNPs between HS patients and controls. Regarding genotypes, only TLR10 rs11096955 (dominant, codominant and overdominant), rs11096957 (dominant, codominant and overdominant) and rs4129009 (codominant and overdominant) showed significant differences between HS patients and controls. However, no association was found when we analyzed the different TLR10 haplotypes.

Conclusion: To the best of our knowledge, this is the first study showing an association of TLR10 SNPs with HS.

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AB0005

HLA CLASS II CONFERS RESISTANCE OR SUSCEPTIBILITY TO HIDRADENITIS SUPPURATIVA IN A CAUCASIAN SPANISH POPULATION (NORTHERN SPAIN)

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Background: Hidradenitis suppurativa (HS) is a chronic inflammatory cutaneous disease affecting terminal hair follicles in apocrine glands bearing skin. The pathogenesis of HS remains unknown, although increasing evidence suggests that the immune system plays an important role. To date, two previous studies, did not find any association between HLA and HS.

Objectives: Our aim was to analyze the association of HLA class II with HS in a Caucasian population from Cantabria (northern Spain).

Methods: In this study we analyzed the *HLA-A, -B, -C, DRB1, -DQA1 and -DQB1* allele distribution in 106 HS patients and 262 age- and sex-matched controls from a Caucasian population of Cantabria (northern Spain).

Results: *HLA-A*29* and *B*50* were significantly more frequent in HS patients and *A*30* and *B*37* in controls, but these associations disappeared after correction. On the other hand, *DRB1*07*, *DQA1*02* and *DQB1*02* were significantly more frequent in controls (p 0.026, p 0.0012 and p 0.0005 respectively), and the *HLA* allele *DQB1*03:01* was significantly more frequent in HS patients (p 0.00007) all of them after Bonferroni correction. Furthermore, the *DRB1*07*; *DQA1*02*; *DQB1*02* haplotype was significantly more frequent in controls (p 0.0005).

Conclusion: This is the first study showing an association of HLA-class II with HS. Our results suggest that HLA-II alleles (*DRB1*07*, *DQA1*02*, *DQB1*02* and *DQB1*03:01*) and the *DRB1*07*-*DQA1*02*-*DQB1*02* haplotype could influence on resistance or susceptibility to HS.

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AB0006

HYPOMETHYLATION OF THE PROMOTER REGION OF TLR4 GENE AT A SYSTEMIC LEVEL IN PATIENTS WITH RHEUMATOID ARTHRITIS AND PERIODONTITIS

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Background: Periodontitis (PD) has long been linked with Rheumatoid arthritis (RA) [1]. Epigenetic modifications are being recently explored to explain such associations, DNA methylation being one such important mechanism.

Objectives: To study the effect chronic generalized periodontitis on systemic methylation of TLR4 genes in comparison to only RA and RA with PD patients.

Methods: Twenty-three RA patients, among which 11 patients had chronic generalized PD, 20 patients with only PD and 15 healthy individuals recruited. DNA was isolated from PBMCs of the participants blood, then were first bisulphite converted and then methylation specific PCR were performed using primers for methylated and un-methylated promoters of TLR4. The DNA amplifications were checked in horizontal gel electrophoresis. The methylation signatures were verified by DNA sequencing (Sanger) of the amplified products.

Results: The anti-CCP, DAS-CRP and HAQ DI were higher in patients with both RA and PD (220±40, 5.7±0.2, 1.5±0.1 respectively, p <0.05). Control samples had shown amplification bands for methylated primers of TLR4 but not for un-methylated primers of TLR4. However, only RA, only PD and RA with PD samples, had shown amplification for un-methylated primers and not for methylated primers. These results together with DNA sequencing indicated that 4 CpG sites in the promoter of TLR4 genes were hypo-methylated in the PBMCs of patients whereas those remain methylated in healthy individuals.

Conclusion: The observations indicated that though PD is a localised disease of the gingiva there is a systemic involvement of TLR mediated pathways in them which is similar to those in RA. However, further validation in larger cohort and down-stream signalling molecules needs to be studied.

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AB0007

VALUE OF ULTRASOUND IN ASSESSMENT OF ACTIVE SACROILIITIS IN PATIENTS WITH AXIAL SPONDYLOARTHRITIS

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Background: The inflammatory of the sacroiliac joints (SIJs) called sacroiliitis, is a characteristic of axial Spondyloarthritis (axSpA). The detection of sacroiliitis is meaningful to prevent irreversible changes. The tool of assessment of sacroiliitis including radiographs, computed tomography (CT) and magnetic resonance imaging (MRI). Ultrasound (US) has also been used in the evaluation of sacroiliitis in recent years.

Objectives: We aimed to evaluate the value of US in the assessment of active sacroiliitis in axSpA patients.

Methods: Fifty-one patients fulfilling Assessment of SpondyloArthritis International Society (ASAS) 2009 criteria for the classification of axSpA were recruited¹. All the patients underwent MRI and US evaluation of bilateral SIJs. MRI was performed using the sequences of T1WI, T2WI and fat suppression T2WI (FS-T2WI). MRI sacroiliitis was defined according to ASAS criteria of active sacroiliitis². The Spondyloarthritis research Consortium of Canada (SPARCC) scoring was used to evaluate the inflammatory lesions in SIJs³. US were performed by an ultrasonographer with 10 years of experience in musculoskeletal ultrasound, and resistive index (RI) value was recorded. The US sacroiliitis was defined as the presence of more flow signals at SIJ with an RI $\leq$ 0.75. The HLA-B27, erythrocyte sedimentation rate (ESR) and hypersensitive C-reactive protein (hsCRP) were also evaluated. Consistency rate, sensitivity, specificity, positive predictive values (PPV) and negative predictive values (NPV) for the diagnosis of sacroiliitis by US were calculated, using MRI as the gold standard.

Results: Of the 51 patients, 24 were female and 27 were male. The HLA-B27 positive rate was 90.2% (46/51). The consistency rate of US and MRI sacroiliitis was 55.88 (57/102). The sensitivity and specificity of US for the diagnosis of sacroiliitis were 55.93 (33/59) and 55.81 (24/43) respectively. The PPV and NPV were 63.46 (33/52) and 48 (24/50) respectively. There was no significant difference in ESR and hsCRP between the US positive sacroiliitis and the others ($P=0.7477$ and 0.2268 , respectively). The SPARCC scores have no significant difference between the US positive sacroiliitis and the others ($P=0.2206$). The RI was not significantly associated with the MRI SPARCC score ($P=0.4236$).

Conclusion: US may be an optional method for preliminary screening sacroiliitis. But its reliability as a diagnostic method needs further verification.

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AB0008

THE IMPACT OF STAT4 RS7574865, IL6 RS1800795, IL6R RS2228145 AND RS4845618 ON RHEUMATOID ARTHRITIS SUSCEPTIBILITY IN BELARUSIAN POPULATION

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Background: Rheumatoid arthritis (RA) is a chronic systemic disorder of the connective tissue of still unknown aetiology and complex autoimmune pathogenesis that primarily affects small joints. HLA alleles provide for 11-37% of the RA heritability, suggesting the substantial role of the non-HLA loci in genetic predisposition to RA. Among non-HLA loci, *IL6*, *IL6R* and *STAT4* genes attract attention, however, the data concerning their influence on RA risk are somewhat contradictory.

Objectives: The aim of the study was to analyze the involvement of four SNPs (*STAT4* rs7574865, *IL6* rs1800795, *IL6R* rs2228145 and rs4845618) in RA susceptibility.

Methods: 187 patients diagnosed with RA (mean age 58.2 ± 11.9), and 380 healthy blood donors (mean age 37.18 ± 10.69 years) were included into the