(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) CC 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.