

HLA-DQ alleles in patients with cutaneous leishmaniasis in Sri Lanka: a preliminary report

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Introduction

Leishmaniasis is an endemic disease in Sri Lanka with localized cutaneous leishmaniasis (LCL) continuing to be the predominant form to be reported. *L. donovani*, the parasite isolated from cutaneous lesions in Sri Lanka, is commonly known to cause the visceral form of the disease, in foci around the world. Polymorphisms of human leucocytes antigen (HLA) system have been implicated in susceptibility as well as the phenotype of leishmaniasis.

Objectives

The objective of this study was to determine the association of class II alleles of HLA with LCL in the Sri Lankan population. The preliminary findings are presented.

Methods

A DNA resource consisting of DNA extracted from the venous blood of 200 patients with cutaneous leishmaniasis and 200 age, sex and ethnicity matched controls has already been established. DNA of 40 patients and 30 controls from the above sample collection were genotyped for alleles of HLA-DQB1 by a PCR-SSP low resolution method.

Results

The allele distribution in cases and controls were as follows: Cases- HLA-DQB1*02: 12.5%, HLA-DQB1*03: 28.75%, HLA-DQB1*05: 25%, HLA-DQB1*06: 33.75%.

Controls - HLA-DQB1*02: 6.7%, HLA-DQB1*03: 26.7%, HLA-DQB1*05: 35%, HLA-DQB1*06: 31.6%. The above allele frequencies did not differ significantly between cases and controls ($P > 0.05$).

Conclusions

The preliminary analysis is underpowered to support or refute the hypothesized association. Genotyping the rest of the sample collection is on going in our laboratory.

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