

Candidate gene study of susceptibility to cutaneous leishmaniasis in Sri Lanka

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Abstract

Objectives To investigate the association between selected single nucleotide polymorphisms (SNPs) in TNF, LTA and SLC11A1 genes and risk of endemic cutaneous leishmaniasis (CL) in Sri Lanka through a case-control disease association study. **Methods** An anonymized DNA resource representative of the Sri Lankan population was genotyped initially to establish baseline parameters. This was followed up by genotyping 200 patients and 200 matched controls. Published or modified PCR/RFLP methods were employed for genotyping. **Results** Comparison of the different ethnic groups showed the distribution of alleles of LTA +252 A>G to differ significantly in Tamils and Moors when compared with Sinhalese. The differences seen at allele level were also reflected in the haplotypes defined by these SNPs at the TNF locus. The case-control analysis did not show an association between the SNPs or the haplotypes investigated and CL. The distribution of these variant alleles in other populations, where they are positively associated with leishmaniasis, differed significantly from the Sri Lankan study cohort. **Conclusions** The selected polymorphisms do not predispose to CL in the Sri Lankan population. The study of extended haplotypes at these loci using a sufficiently powered sample collection would elaborate the findings of this study. In the face of an evolving disease pattern in the country with other forms of leishmaniasis now being reported, prevalence of polymorphisms predisposing to these forms calls for heightened surveillance and preparedness. © 2010 Blackwell Publishing Ltd.