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Human Leukocyte Antigen Class 1 Phenotype Distribution and Analysis in Persons from Central Uganda with Active Tuberculosis and Latent Mycobacterium tuberculosis Infection

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Abstract : Background: The Ugandan population is heavily affected by infectious diseases and Human leukocyte antigen (HLA) diversity plays a crucial role in the host-pathogen interaction and affects the rates of disease acquisition and outcome. The identification of HLA class 1 alleles and determining which alleles are associated with tuberculosis (TB) outcomes would help in screening individuals in TB endemic areas for susceptibility to TB and to predict resistance or progression to TB which would inevitably lead to better clinical management of TB. Aims: To be able to determine the HLA class 1 phenotype distribution in a Ugandan TB cohort and to establish the relationship between these phenotypes and active and latent TB. Methods: Blood samples were drawn from 32 HIV negative individuals with active TB and 45 HIV negative individuals with latent MTB infection. DNA was extracted from the blood samples and the DNA samples HLA typed by the polymerase chain reaction-sequence specific primer method. The allelic frequencies were determined by direct count. Results: HLA-A*02, A*01, A*74, A*30, B*15, B*58, C*07, C*03 and C*04 were the dominant phenotypes in this Ugandan cohort. There were differences in the distribution of HLA types between the individuals with active TB and the individuals with LTBI with only HLA-A*03 allele showing a statistically significant difference (p=0.0136). However, after FDR computation the corresponding q-value is above the expected proportion of false discoveries (q-value 0.2176). Key findings: We identified a number of HLA class I alleles in a population from Central Uganda which will enable us to carry out a functional characterization of CD8+ T-cell mediated immune responses to MTB. Our results also suggest that there may be a positive association between the HLA-A*03 allele and TB implying that individuals with the HLA-A*03 allele are at a higher risk of developing active TB.

Keywords : HLA, phenotype, tuberculosis, Uganda
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