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Characterizing IgA1 and IgG1 constant region diversity in South Africans

Ncube, Itai T

2021
https://hdl.handle.net/10539/32513

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Abstract

Antibodies consist of five different isotypes which are encoded by different genes. There is evidence that different genotypes of these isotypes can affect antibody function. However, little is known about genotypes in individuals of African descent. Therefore, this study sought to characterise the genetic diversity of *IGHA1* and *IGHG1* genes, the genes that encode IgA1 and IgG1 antibodies which are important in viral infection, in six Black Africans from the Centre for the AIDS Programme of Research in South Africa (CAPRISA) cohort. Genomic deoxyribonucleic acid (DNA) was used to amplify, clone and Sanger sequence these genes and the sequences were compared to reference alleles from the International Immunogenetics information system (IMGT), the global reference database for immunogenetics. Eight novel *IGHA1* alleles were identified. These alleles closely matched the *IGHA1*01* reference allele, with one to four single nucleotide polymorphisms (SNPs). The majority of SNPs were synonymous; however, one novel allele (variant 1) had a R392H amino acid substitution within the CH3 region. Within *IGHG1*, this study identified three alleles that matched known IMGT alleles, and two alleles that were novel. Overall, this pilot study highlights a high level of genetic diversity in this population that may have functional relevance to immune responses in infection and vaccination, and warrants further investigation.