HLA-DQA1 genotyping by polymerase chain reaction-single-strand conformation polymorphism (PCR-SSCP) and restriction endonuclease digestion in Papua New Guinea

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ABSTRACT

We have used PCR-SSCP, a technique based on the conformation of single-stranded DNA, to characterize the HLA-DQA1 gene in four geographically diverse population groups in Papua New Guinea. Among the 294 individuals that were studied from Goroka, north coast of Madang, Kimbe and Wanigela, we detected 5 of the 20 known variants of this gene locus. These included alleles 0101, 0102, 0103, 0301 and 0501. Furthermore, variable mobility shifts observed for alleles 0301 and 0501 from Madang suggested a further 3 variants. All 15 combinations of the 5 confirmed alleles were detected and their respective gene frequencies found to be consistent with the groups' ethnic and linguistic diversity. In respect to their frequencies and the observed overall allelic heterozygosity, the distribution in Kimbe showed some similarity to that in the north coast of Madang while Madang and Goroka were the most different. The distribution of alleles 0102 and 0501 was observed to be similar for Goroka and Wanigela as was 0301 for Madang and Wanigela. Our results, confirmed by endonuclease digestion, show PCR-SSCP to be a highly sensitive technique that can be used to characterize HLA-DQ antigens. In addition, the simplicity of the method provides an opportunity for large-scale typing of HLA antigens.