PCR Analysis Confirms the Presence of NIDDM Susceptibility Loci on Chromosome 2 In the Samoan Population

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October 15, 1999

Background.
Genetic epidemiologic studies have convincingly demonstrated that Non-Insulin Dependent Diabetes Mellitus (NIDDM) has both a genetic and environmental component. Recently, several genome-wide scans have identified NIDDM susceptibility loci, including a region on chromosome 2 in the Mexican-American population. (Hanis et al, 1996). We sought to confirm the presence of susceptibility loci in this region in the American Samoan population.

Methods.
DNA derived from 80 NIDDM-positive American Samoans and 80 NIDDM-negative age-matched controls was amplified using the Perkin-Elmer 9600 PCR Thermocyc1er. Three fluorescent markers (D2SI25, D2S126, and D2S338) were amplified and analyzed using, polyacrylamide gel electrophoresis on the ABI Prism Genotyper (Version 2.1). Data analysis was accomplished using Fisher's Exact Test.

Results.
Overall comparison p-values for each marker were as follows: D2SI26?---0.023 (95% Cl: 0.020-0.026); D2SI25?0.044 (95% CI: 0.041-0.049); D2S338?0.057 (95% CI: 0.052-0.062). Additionally, significant associations were found at specific alleles, with the following adjusted p-values: 99 bp allele at D2S125 (0.012, 13 positives and 2 controls); and 298 bp allele at D2S338 (0.025, 11 positives and 1 control).

Conclusion.
We were able to confirm the presence of at least two NIDDM susceptibility loci (D2S125, D2SI26) in the American Samoan population. The results for the other locus (D2S338) were borderline significant; further analysis of other samples may help clarify whether it is indeed a susceptibility locus. Moreover, we were able to detect specific alleles that showed a significant association with NIDDM. These results would indicate the presence of a gene or genes whose polymorphisms contribute to the NIDDM phenotype. Moreover, these results may be of future clinical diagnostic benefit for identifying at-risk patients within this population.