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## Mutations in Insulin-Receptor Gene

### Val<sup>996</sup> Allele in White NIDDM Patients

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The insulin-receptor (IR) gene plays a critical role in allowing cells to respond to insulin (1), and insulin resistance is a prominent feature of non-

insulin-dependent diabetes mellitus (NIDDM; 2). The involvement of the IR defects in the etiology of diabetes mellitus has been suggested by the findings of

mutations in the IR gene in rare patients with genetic syndromes of severe insulin resistance (3-12). Odawara et al. (7) have described a case of young Japanese male with insulin resistance and acanthosis nigricans in which valine is substituted for glycine at position 996 (GTC instead of GGC) in the tyrosine kinase domain of the IR gene. Whether this mutation also contributes to the etiology of the common forms of NIDDM is unknown. Therefore, we determined the prevalence of the Val<sup>996</sup> allele of the IR gene in a population of white NIDDM patients.

We studied a population of 103 NIDDM patients referred to the Diabetic Clinic of our Medical School. Diagnosis of NIDDM was made according to National Diabetes Data Group criteria. All subjects gave their informed consent to participate in the study. Subjects had a mean  $\pm$  SE age of  $56.9 \pm 1.06$  yr and a body mass index of  $28.12 \pm 0.45$  kg/m<sup>2</sup>. Their diabetes duration was  $12.97 \pm 0.85$  yr. Forty-three were men and 60 were women. We used a modification of the polymerase chain reaction (PCR) procedure that permits the rapid identi-

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fication of mutations at sites not recognized by restriction endonucleases (13). We altered the sequence of the sense primer such that amplification of DNA containing a G, but not any other nucleotide, at position 3116 of the IR gene, would generate a recognition site for the enzyme *Msp* I. This region was amplified as follows: 200 ng of genomic DNA from each patient were amplified in 50  $\mu$ l of PCR buffer (10 mM Tris-HCl [pH 8.3], 1.5 mM MgCl<sub>2</sub>, 50 mM KCl, 0.001% gelatin) containing 20 pmol of each oligonucleotide primer (nucleotides 3089 to 3115, sense strand; nucleotides 3191 to 3217, antisense strand) and 10 nmol of each deoxyribonucleotide triphosphate; one unit of thermus aquaticus DNA polymerase (Perkin Elmer Cetus, Norwalk, CT) was added and 100  $\mu$ l of mineral oil was layered over the samples. The samples were incubated at 95, 55, and 72°C, respectively, for 45, 50, and 50 s; this cycle was performed 36 times in a DNA-RNA amplifier (Biostar Violet, Rome, Italy). The amplified DNAs were restricted with *Msp* I and analyzed by electrophoresis in 2.5% agarose.

Because all the DNAs were digested by *Msp* I showing the presence of a G at position 3116 of the IR gene, we never detected Val<sup>996</sup> allele in our diabetic patients.

Our data are consistent with a very low prevalence of the Val<sup>996</sup> allele of the IR gene (<1/206 alleles) in the NIDDM population. Further studies are needed to establish the prevalence of

other IR gene mutations among diabetic individuals.

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