

## Rapid Detection of a Pentanucleotide Deletion Polymorphism in the Human $\alpha_2$ -Macroglobulin Gene

To the Editor:

Alpha-2 macroglobulin ( $\alpha_2$ M) is a serum glycoprotein and a panprotease inhibitor found in various tissues, including plasma and cerebrospinal fluid.  $\alpha_2$ M is thought to inactivate proteinases by a specific trapping mechanism in the so-called "bait" region of the protein (1).  $\alpha_2$ M is also a ligand for the LDL receptor-related protein, and both are up-regulated after brain injury and in regions of the brain affected by Alzheimer disease. Additionally,  $\alpha_2$ M binds to the amyloid  $\beta$  peptide (2, 3), which leads to attenuation of both fibrillogenesis and neurotoxicity (4) and which is cleared by the LDL receptor-related protein. Recently, a pentanucleotide deletion in the 5' splice site of exon 18, which encodes a portion of the  $\alpha_2$ M bait region, has been suggested to be genetically associated with an increased risk for developing Alzheimer disease (5).  $\alpha_2$ M and the  $\epsilon 4$  allele of the apolipoprotein E gene seem to confer a similar degree of risk for developing late-onset Alzheimer disease. The conventional methods for measuring  $\alpha_2$ M are ELISA, immunoblotting, or enzymatic assays, but these methods can not be applied to the detection of  $\alpha_2$ M pentanucleotide polymorphism. The DNA-based method for detecting this polymorphism deletion is not amenable to large-scale screening (5, 6).

The method described below is based on the observation that the  $\alpha_2$ M pentanucleotide deletion polymorphism (6) leads to the loss of the

*HphI* restriction site at the intronic sequence in the 5' splice site of exon 18 (Fig. 1A). The primers amplify a 196-bp region in individuals without the pentanucleotide deletion (Fig. 1B). Genomic DNA was extracted from leukocytes, using HQIAamp (Qiagen), and was amplified by PCR using oligonucleotide primers  $\alpha_2$ MF (5'-GGT GGC AAC TAT TAC ATT CTC TCA-3') and  $\alpha_2$ MR (5'-ACT TAC TTT ACC ACC ACC AAA TCC-3'). In addition to the buffer and nucleotide components, each amplification reaction contained ~200 ng of genomic DNA, 20 pmol of each primer, and 2 U of Taq polymerase (Life Technologies) in a final volume of 50  $\mu$ L. The reaction mixture was first denatured at 94  $^{\circ}$ C for 2 min and then subjected to 35 cycles of PCR (94  $^{\circ}$ C for 1 min, 59  $^{\circ}$ C for 40 s, 72  $^{\circ}$ C for 40 s), after which it was incubated at 72  $^{\circ}$ C for 10 min. A 20- $\mu$ L aliquot of the amplification product was then digested in the presence of 2.2  $\mu$ L of 10 $\times$  buffer and 20 U of *HphI* for at least 2 h at 37  $^{\circ}$ C. Restriction digest products were size fractionated by electrophoresis on a 2% agarose gel with 1 mg/L ethidium bromide for 20 min at 200 V and detected directly under ultraviolet light. (Incomplete digestion may sometimes occur, which can be avoided by a purification step of the PCR product before enzymatic digestion. However, this does not interfere with the scoring of the alleles.) The PCR-amplified digestion products are shown in Fig. 1B along with representative  $\alpha_2$ M genotypes. In a preliminary study of 367 individuals genotyped by this method, the allele frequency of one or two  $\alpha_2$ M alleles was 19.1% in pa-

tients with sporadic late-onset Alzheimer disease compared with 13.8% in age-matched unaffected individuals. We have encountered no difficulties in the samples tested, and we found this method to be well-suited to high-throughput routine clinical screening.

### References

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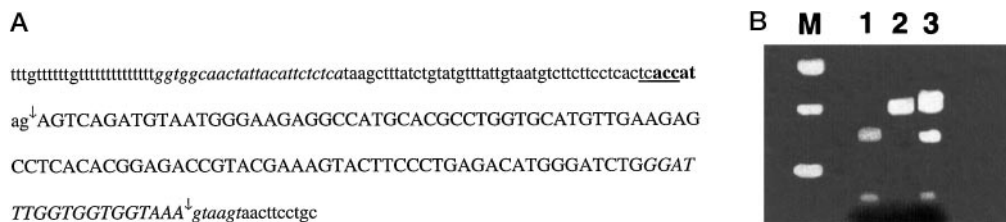


Fig. 1. Sequence (A) and amplification products (B) of exon 18 of the gene coding for  $\alpha_2$ M.

(A) Sequence of exon 18 and partial sequence of flanking introns of the human  $\alpha_2$ M gene (the primer sequence is in *italics*; the pentanucleotide polymorphism in the 5' splicing site of exon 18 is in **bold**; the restriction site of *HphI* is underlined; arrows indicate start/end of coding region of exon 18; capital letters indicate the coding region of exon 18). (B) Photograph of a 2% agarose gel stained with ethidium bromide and viewed through ultraviolet light. Lane M, molecular markers (100, 200, and 400 bp). Lanes 1-3, *HphI* restriction fragment from three possible  $\alpha_2$ M genotypes: lane 1, wild-type allele (130 and 66 bp); lane 2, homozygote for  $\alpha_2$ M polymorphism deletion (191 bp); lane 3, heterozygote for  $\alpha_2$ M polymorphism deletion (191, 130, and 66 bp).