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Sequence register

Sequence analysis of *DPB1*-like genes in cynomolgus monkeys (*Macaca fascicularis*)

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Two sequences of *Mafa-DPB1*-like alleles of the cynomolgus monkey major histocompatibility complex were determined without using cloning techniques. In the present study, eight cynomolgus monkeys belonging to two families (Fig. 1) were selected from the Malaysian colonies at the Tsukuba Primate Center. Using the polymerase chain reaction (PCR)-SSCP method (Hoshino et al. 1992) with a primer set (Kimura and Sasazuki 1992) for the human *DPB1* exon 2, two different homozygous patterns as well as several heterozygous patterns were identified (Fig. 1 A, B). Subsequently, the two sequences of the homozygous DNAs were determined using an automated DNA sequencer. The nucleotide sequences of these two alleles (*Mafa-DPB1*M25* and *M09*; Fig. 2) were closer to those of human *DPB1* alleles (the average percentage identity between the nucleotide sequences of the two macaque alleles and those of human alleles *DPB1*02011, 0401,* and *0101* is 89%; Marsh and Bodmer 1991) than to the human *DPB2* pseudogene (75%; Kapper and Strominger 1986). The findings obtained by comparing the two macaque allele sequences were consistent with the observation that there are many more nonsynonymous than synonymous substitutions at the human *HLA-DPB1* locus. The present results clearly demonstrate that cynomolgus monkeys have *DPB1*-like alleles. It is presumed, therefore, that macaques have at least one *DPB1* locus and that nonsynonymous nucleotide substitutions are prevalent in the gene.

The nucleotide sequence data reported in this paper have been submitted to the GenBank nucleotide sequence database and have been assigned the accession numbers D13335 (*Mafa-DPB1*M09*) and D13336 (*Mafa-DPB1*M25*.)

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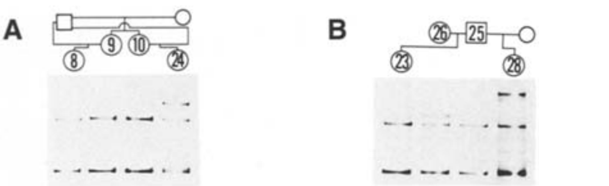

Fig. 1 A, B. Leukocyte DNAs from family members indicated at the *top* (○, females; □, males) were subjected to PCR-SSCP analysis. Since the mobility shifts of each set of single-strande DNA fragments of **A** Nos. 8, 9, and 10 and **B** 23 and 25 were the same, and two bands were observed, they were determined to be homozygotes having equivalent DNA fragments.

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                                       10                                      20
Mafa-DPB1*M25     AG AAT TAC CTG TAC CAG GGA CGG CAG GAA TGC TAC GCG ATT AAC GGG ACA
Mafa-DPB1*M09     -- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

                                           30
Mafa-DPB1*M25 CAG CGC TTC CTG GAG AGA CAC ATC TAC AAC CGG GAG GAG TTC ATG CGC TTC GAC
Mafa-DPB1*M09 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

              40                                      50
Mafa-DPB1*M25 AGC GAC GTG GGG GAG TAC CGG GCG GTG ACA GAG ATG GGA CGG CCT ACT GCG GAA
Mafa-DPB1*M09 --- --- -CC --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

                      60                                      70
Mafa-DPB1*M25 TAC TGC AAC AGC CAG AAG GAC AAA CTG GAG GAG ATG CGG GCA GTG GCG GAC AGG
Mafa-DPB1*M09 --- --G --- --- --- --- --- CGC --- --- --- -A- --- --C -A- -T- --- ---

                              80                                      90
Mafa-DPB1*M25 ATG TGC AGA CAC AAC TAC GAG GTG AAC GAG GCT GTG ACC CTG CAG CGC CGA G
Mafa-DPB1*M09 G-- --- --- --T --- --- --- -G- C-- --- --A --- --- --- -G- --- --- -
```

Fig. 2. Nucleotide sequences of exon 2 in two *Mafa-DPB1* alleles. Sequence identity is indicated by *dashes*.

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