

Thesis Title	Analysis of HLA Class II Allele Frequencies in the Kamphaengphet Population using the PCR-SSO Technique
Name	Ratchaneewan Maneemaroj
Degree	Master of Science (Transfusion science)
Thesis Supervisory Committee	Dasnayanee Chandanayingyong, M.D. DR. Henry A.F. Stephens, Ph.D. Sasitorn Bejrachandra, M.D.
Date of Graduation	12 May B.E 2538 (1995)

ABSTRACT

The polymorphism of HLA class II genes (HLA-DRB1,-DRB3,-DRB5,-DQA1,-DQB1 and -DPB1) was investigated in 97 normal Northern Thais (from Kamphaengphet province) using polymerase chain reaction amplification and oligonucleotide (PCR-SSO) typing which is the standard method used for the 11th International Histocompatibility Workshop (IHW). Allele and haplotype frequencies, as well as linkage disequilibrium between HLA class II genes and geographical distribution of HLA class II alleles have been determined.

The results found that, of the 47 DRB1 alleles tested, 23 alleles were observed. DRB1*1202 and DRB1*1502 were most frequently observed

alleles and DR9, DR6, DR4 and DR7 were also relatively frequent in this population (Table 10). The alleles DRB1*01 and DRB1*1001 had very low frequencies. Among the 4 DRB3 and 3 DRB5 alleles tested, DRB3*0202 and DRB5*0102 were the most common alleles of the these two loci (Table 10). DRB3*0201 and DRB5*02 were absent. Of the 8 DQA1 and 17 DQB1 alleles tested, DQA1*0101 and DQA1*0102 and DQB1*0502 were among the most common alleles of the two loci respectively, while DQB1*05032, *0504, *0604, *0605 and *03031 were absent (Table 11). Of the 36 DPB1 alleles tested, DPB1*0501 and *1301 were the most common alleles. The alleles DPB1*0101, *0901, *1901, *2801, *3101 had very low frequencies (Table 12). The most common extended haplotypes in the Kamphaengphet population were DRB1*0901-DQA1*0301-DQB1*03032 and DRB1*1502-DRB5*0102-DQA1*0101-DQB1*0501 (Table 13).

In our studies, allele and haplotype frequencies were similar to those observed in Bangkok (present-day Thais) and Thais from Ramathibodi Hospital. Some differences found in these studies may be a consequence of the many ethnic admixtures found in present-day Thais, or represent rare types in each group. The unusual alleles and haplotypes could be confirmed by further family and DNA sequencing studies. The data presented in this population study should be useful in many fields, such as anthropology, organ transplantation, disease susceptibility, and evolutionary genetics.