VI. SUMMARY

The genotype distribution and nucleotide sequence polymorphism of the VD4 region of *C. trachomatis* were studied in 50 STD high risk women attending the Venereal Disease and AIDS Control Center, Region 10, Chiang Mai province. The genotyping of *C. trachomatis* was determined by using the PCR based RFLP technique. By this method, the VD4 DNA was amplified by using the VD4 specific primers followed by digestion with 4 restriction endonucleases; *Alu* I, *Hind* III, *Dde* I and *EcoR* II. The result was also confirmed by nucleotide sequencing technique. Eight distinct genotypes; D (42%), F (18%), B/Ba (12%), K (10%), H/Ia (8%), G (6%), E (2%) and J (2%) were observed. Looking at the overall genotype distribution, genotype D accounted for almost 50 % of the genital *C. trachomatis* genotype circulated in this area. In the VD4 sequence analysis, 24 samples (48%) comprising genotype F, B/Ba, H/Ia, G, J and E had a sequence identical to the prototypes, while 26 samples (52%) of genotype D and K were sequence variants. The nucleotide substitution was the major mechanism for the mutation observed in this study. In genotype D variants, the guanine was substituted by adenine at position 979. While in the genotype K, the adenine at position 973 was substituted by guanine. All of the nucleotide changes resulted in amino acid transition. This study revealed the information in the molecular epidemiology of *C. trachomatis* and the sequence variation in the antigen coding gene, which may be important for controlling diseases.