

VI. SUMMARY

The genotype distribution and nucleotide sequence variation of the MOMP gene of *C. trachomatis* were carried out from 34 STD high risk patients who resided in Chiang Mai and surrounding areas. The genotyping of *C. trachomatis* was performed by means of the RFLP analysis of the VD4-MOMP gene, which was confirmed by nucleotide sequencing of the whole MOMP gene. The results from these two methods were simultaneous. However, the genotype D/Da/L1 and H/Ia/J could not be separated into individual genotypes by the VD4 PCR-RFLP technique, since they had identical VD4 sequences. Seven genotypes of *C. trachomatis* were identified as F (26.5%), D (23.5%), K (17.6%), E (14.7%), G (5.9%) and J (2.9%). Among those, genotype F and D were predominantly observed. From the nucleotide sequence analysis, 21 samples (61.8%) had a nucleotide sequence different from their prototypes, while 13 (38.2%) were identical. The nucleotide substitution seemed to be a major mechanism for the sequence variation observed in this study.