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/la/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.