CHAPTER VI

CONCLUSIONS

1. The PCR products of 16S rRNA gene of *T. collina*, *T. fuscobalteata*, *T. laeviceps*, *T. terminata*, and *T. thoracica* are 550 bp.

2. Variation in 16S rRNA gene of *T. collina* and *T. laeviceps* were found when digested with *Dra* I, *Hpy*188 III, and *Ssp* I. Variation in 16S rRNA gene of *T. fuscobalteata*, *T. terminata*, and *T. thoracica* were found when digested with *Dra* I but there were no variation with *Hpy*188 III and *Ssp* I.

3. Digestion of these PCR products of five species (*T. collina*, *T. fuscobalteata*, *T. laeviceps*, *T. terminata*, and *T. thoracica*) with *Dra* I revealed 3, 2, 4, 2 and 2 patterns. Digestion of these PCR products of five species with *Hpy*188 III revealed 4, 1, 2, 1 and 1 patterns. Digestion of these PCR products of five species with *Ssp* I revealed 4, 1, 3, 1 and 1 patterns, respectively.

4. Cluster analysis of *T. collina*, *T. fuscobalteata*, *T. laeviceps*, *T. terminata*, and *T. thoracica* populations (3 restriction enzymes) by UPGMA (unweighted pair group method with arithmetic mean) could be separated into 3, 2, 2, 2, and 2 groups, respectively.

5. These results indicate that the method we used in this study is useful and show additional variation for analysis of population structure and genetic relationships with in five species of stingless bees.