

## CHAPTER VI

### CONCLUSIONS

1. The extracted DNA of thirty-seven giant galanga accessions from different areas in Thailand using SDS extraction procedure was enough to PCR amplification.
2. Randomly amplified polymorphic DNA (RAPD) analysis of giant galanga originally screened with twenty-two arbitrary primers, 8 primers (OPA20, OPB18, OPC09, OPD02, OPD11, OPG13, OPK12 and OPAX17) produced a total of 73 polymorphic bands. Band sizes ranged from 0.75 to 2.5 kb.
3. A UPGMA dendrogram of thirty-seven giant galanga using RAPDs divided the accessions into five major clusters. The first cluster consisted of two red-medium cultivated rhizome accessions. The second cluster consisted of one red-medium cultivated and one red-medium wild rhizome accessions. The third cluster included two red-medium cultivated and one white-medium cultivated rhizome accessions. The fourth was the largest cluster, including 13 cultivated- and 4 wild accessions, most of which had red-medium rhizome. The fifth cluster included two wild- and eleven cultivated accessions that six white-, six red- and one yellow rhizome accessions.
4. The dendrogram showed no relation with their morphological characters such as type, color of rhizome and collection sites which were indicated by the regions of Thailand.
5. RAPD was shown to be highly capable of evaluating genetic variability in giant galangas. The information presented in this study may be served as a basis to establish evolutionary and genetic relationships among giant galanga cultivars for the plant selection and improvement.