

CHAPTER V

Conclusions

1. Interspecific genetic variation between *T. clareae* and *T. koenigerum* were found at the ITS1-ITS2 region in nuclear ribosomal DNA. A total of nineteen point mutations (ten transitional and nine transversional mutations) and seven insertions/deletions were observed.
2. On the basis of the ITS sequences, sequence divergence between these two taxa was 3.79%. However, intraspecific polymorphisms were not observed in these species.
3. Randomly Amplified Polymorphic DNA (RAPD) analysis of one hundred and twenty-five individual of *T. clareae* and *T. koenigerum* with primers OPA07, OPA11 and OPA12 yielded a total of one hundred and fifty-two genotypes.
4. A UPGMA dendrogram indicated monophyletic status of both *T. clareae* and *T. koenigerum*. It allocated all but E2D and N1D *T. clareae* samples into two different groups depending on the host species implying closer related of *T. clareae* originating from the same than between different hosts.