V. CONCLUSION AND SUGGESTION

A. Conclusion

Based on the results of the study and discussion, it can be concluded that:

1. The RAPD analysis produced 23 DNA markers with 19 polymorphic and 4 monomorphic markers, resulting in a high polymorphism level of 81.7%. Each primer generated different numbers of polymorphic and monomorphic bands, with primers OPA-02, OPA-10, OPB-11, and OPU-19 showing 100% polymorphism. These profiles indicate significant genetic differences among the six *Nepenthes* species analyzed.

2. The UPGMA dendrogram constructed from the RAPD data shows that *N. reinwardtiana* is the most genetically distinct species. *N. spathulata* and *N. maxima* form a separate cluster, while *N. sumatrana*, *N. mirabilis var. globosa*, and *N. adrianii* are grouped together, with *N. mirabilis var. globosa* and *N. adrianii* being the most closely related pair. These results reflect varying levels of genetic similarity among the species.

B. Suggestion

Further studies involving the use of more RAPD primers are needed to better reveal genetic relationships among *Nepenthes* species and provide a more accurate understanding of their genetic diversity. Expanding the genetic dataset will also help clarify evolutionary patterns within the genus.