

CHAPTER 6: CONCLUSION

The RAPD method is easy, fast and it allows a good discrimination of two individuals of the same species. It can detect genetic variation even at intracolonial level where other techniques such as RFLP or allozyme may face some limitations. RAPD may be used as a tool to develop individual fingerprints for *G.changii* as it can also detect intrapopulational variation. The use of RAPD to detect minor variations between individuals of the same species and these minor variations may not be detected using other techniques. This enables the use of RAPD as a tool for developing individual fingerprints.

Furthermore, common bands found among the *G.changii* can be developed into specific genetic markers for species identification. Future studies can explore the possibilities of obtaining RAPD probes for *Gracilaria* species with a more detailed study on these common bands. Even though RAPD has some limitations, it is, however, an easy and rapid technique for identifying closely related species by using the RAPD probe. Specific bands can be used to identify qualitative trait loci (QTLs) or gene for certain traits at an individual level. The genetic differences between two individual which are of the same species but demonstrated different characteristic such as resistant to certain diseases can be detected. The gene obtained can then be cloned and use as probe for the future.

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However, in biogeographical studies of *G. changii*, no geographical boundary can be defined as RAPD analysis showed that intrapopulation variation was as great as interpopulational variation. However, OPA 13 separated Thailand and Malaysian *G. changii* into two groups.

In interspecific relationship studies, RAPD analysis was found to be useful in the study of phylogenetic relationships among species of *Gracilaria*. Primer OPA 11 was able to separate *Sargassum* species from all the *Gracilaria* samples. It also distinguished among the *Gracilaria* species tested. The RAPD data generated with OPA11 showed the possibilities of hybridisation between *Gracilaria changii* with both *Gracilaria salicornia* and *Gracilaria edulis*. Further studies can be conducted to assess the possibilities of this hybridisation. It is suggested that a wider range of samples of each species to be examined in order to generate a more detailed and less biased dendrogram. However, this approach may be an easy, fast and useful technique in identifying other closely related algal species of potential value in genetic improvement programmes.

RAPD data alone does not provide sufficient information for phylogenetic studies. Other techniques such as gene sequencing, RFLP or allozyme analysis should be carried out to obtain a combined data, which gave a more reliable information. Amplified Restriction Fragment Polymorphism (AFLP) is an alternative new technique, which provides a more reliable and stable DNA fingerprinting. Results obtained from the AFLP analysis can be correlated to both

the RAPD data and the taxonomic data and this will give a better description and assessment of biological diversity and phylogenetic relationship.

The significant findings of this study may be summarised as follows:-

1. OPA11 (CAATCGCCGT) and OPA13 (CAGCACCCAC) distinguish *Gracilaria* samples from *Sargassum* samples.
2. OPA13 distinguish the Malaysian *Gracilaria changii* from that collected from Thailand.
3. OPA13 distinguish *Gracilaria changii* from *Gracilaria salicornia* and *Gracilaria edulis*.
4. OPA11 shows that there is a possibility of hybridisation between *Gracilaria changii* and *Gracilaria salicornia* or between *Gracilaria changii* and *Gracilaria edulis*.