

## CHAPTER 6: GENERAL CONCLUSION

Overall, 105 Ascomycota, 29 anamorphic fungi and 2 Basidiomycota were recorded from this study and the highest diversity index was recorded from Cape Rachado at 3.79. While Telok Pelandok is 3.77 and 3.25 for Morib. The most common species recorded in this study is *Dactylospira haliotrepha* while species like *Aigialus grandis*, *Aigialus parvus*, *Kallichroma tethys*, *Haloresellinia oceanica*, *Morosphaeria velatispora*, *Quintaria lignatilis*, *Halocyphina villosa* and *Verruculina enalia* are found to be common. All similarity indices calculated between sampling sites were below 0.5. This indicates that the species composition for each study sites is unique. The highest number of index recorded is between Morib and Cape Rachado with 0.370 where both are muddy mangrove forest while the lowest are 0.302 for Telok Pelandok-Cape Rachado. The highest species richness recorded are from Telok Pelandok with 71 species followed by Cape Rachado (68 species) and Morib (40 species).

The molecular analysis provides a strong support that all geographical isolates of *Verruculina enalia* are genetically similar and form a single clade including a single ITS sequence from Liberia that was deposited in GenBank. Constraint analysis rejects our earlier hypothesis that *V. enalia* were genetically diversified according to its geographical origins. However, there are slight variables in Taiwan and Liberia strains but the sequences between the clades differ only for less than 1%. With this, we can conclude that *V.enalia* from South East Asia including Taiwan and Liberia does not evolved long enough to accumulate mutations which makes them identical based on its ITS sequence. However, there was a very minor difference with the Taiwan strains. This could be due to its substrate which were driftwoods collected on a rocky shore while the rest are strictly substrates from mangroves. *Verruculina enalia* is a common tropic and sub-tropic species which are common to the mangroves. It can be considered as a “good

species” as it has very little variation in terms of morphology and in molecular level. At the moment, its cryptic species are still not known. This species is exclusively placed in Testudinaceae and as the most basal clade of the Pleosporales along with *Lepidosphaeria nicotiae* and *Ulospora bilgramii* without any other known sister genera (Schoch *et al.*, 2006; Jones *et al.*, 2009).

From the results obtained, it is impossible to tell the “original source” or the centre of origins for *V.enalia*. As a species that associated with mangrove, the closest theory that could relate with the origin of *V.enalia* is from the theory of the centre of origin for mangroves which is based on the fossil record analysis where mangrove ecosystem are believed to be originated around the Tethys Sea and modern distribution result almost entirely from the vicariance events (Ellison *et al.*, 1999). Tethys Sea is located between the supercontinent of Laurasia and in the north of Gondwana during much of the Mesozoic Era around 251 to 65.5 million years ago.

A different approach of this study might give a better result. This study has indicate that ITS does not show much, if any, variation within species which in this case for the *V. enalia*. A better approach would be to develop hyper variable markers, like microsatellites. Perhaps by using the intergenic spacer (IGS), there will be more variation within species. IGS are sensitive markers of evolutionary change, tracking drift more rapidly than the ITS. For now, it is confirmed that they are all the same species but to address the question, we will need to develop more variable markers.

It is hoped that this study will stimulate further investigations on other species of marine fungi. The cosmopolitan species is a good candidate for biogeographical studies due to its wide distribution nature. A wider biogeographical isolates would give a better overview on the biogeographical aspects of a species and by adding more targeted genes, more analysis could be done in order to give more support for a better findings.