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Figure 4.30 a) Distribution of *Dactylospora haliotrepha* b) Distribution of 100 *Halorosellinia oceanica* c) Distribution of *Kallichroma tethys* d) Distribution of *Lulworthia grandispora* e) Distribution of *Halocyphina villosa* f) Distribution of *Verruculina enalia*. (a-f) Species distribution of 6 common marine mangrove fungi. Data based on published literature by Besitulo *et al.*, 2010 (Phillipines), Sakayaroj *et al.*, 2011 (Thailand), Jones and Puglisi, 2006 (Florida, USA), Pang *et al.*, 2011 (Taiwan), Hyde, 1988 (North Sumatra, Indonesia), Nambiar and Raveendran, 2009 (Kerala, India), Abdel Wahab, 2005 (Egypt), Hyde, 1988 (Brunei), Jones and Abdel Wahab, 2005 (Bahamas), Tan *et al.*, 1989; Leong *et al.*, 1991 (Singapore) and Jones and Vrijmoed, 2003 (Hong Kong).

Figure 4.31 Species abundance distribution of marine fungi collected from 3 105 study sites. CR= Cape Rachado, TP= Telok Pelandok and MO= Morib (Species sequence are in decreasing order of % of abundance).

Figure 5.1 Genomic DNA extracted from *V.enalia* isolated from Malaysia, 107 Taiwan, Hong Kong, Philippines and Singapore using the method of Pang et al. (2003) and Sakayaroj et al. (2005) visualized on 1% (w/v) of TAE agarose gel. A) ISB0201-Tioman Island, Malaysia B) ISB0301- Kukup, Malaysia C) ISB0361-Bagan Lalang, Malaysia D) ISB0362- Bagan Lalang, Malaysia E) ISB3532- Sai Kung, Hong Kong F) ISB3533- Sai Kung, Hong Kong G) ISB2952- Samal, Philippines H) ISB2953- Samal, Philippines I) ISB2954- Samal, Philippines K) ISB5059- Sai Kung, Hong Kong L) ISB1350- Three Fathom Cove, Hong Kong M) ISB0657- Jici Rockyshore, Taiwan N) ISB0658- Jici Rockyshore, Taiwan.

Figure 5.2 PCR amplification of ITS1-5.8S-ITS2 region from V.enalia isolated 108 from Malaysia, Taiwan, Hong Kong, Philippines and Singapore. Representation of isolates showing amplification of the entire ITS1-5.8S-ITS2 region. The PCR products had a molecular weight of 500-550 bp. A) ISB0658 B) ISB0657 C) ISB1350 D) ISB1350 E) ISB5059 F) ISB5059 G) ISB0201 H) ISB0301 I) ISB3532 J) ISB3533 K) ISB5059 L) ISB1350 M) ISB0361 N) ISB0362 O) ISB2952 P) ISB2953.

Figure 5.3 A single most parsimonious tree inferred from the ITS1-5.8S-ITS2 110 sequences data. The tree was produced using branch-swapping algorithm with the Multiple trees option (MULTITREES) disabled (tree length=178 steps, C. I. =1.000, R.I. =1.000). Maximum parsimony tree was produced by the unweighted parsimony analysis where gaps are treated as missing data. Sixteen taxa were used and a *Phoma* sp. was chosen as the outgroup taxa. One tree was resulted with a

tree length = 178, a consistency index (C.I.) = 1.000, a retention Index (R.I.) = 1.000 and rescaled consistency index (R.C.) = 1.0000 Two clades were resulted; the first clade consisted of 13 isolates (ISB2954, ISB2953, ISB2952, ISB0362, ISB0361, ISB5059, ISB1350, ISB3533, ISB3532, ISB1349, ISB0301, ISB0201 and GQ203796) with a moderate bootstrap support and the second clade consisted only 2 isolates (ISB0658 and ISB0657) with a weak bootstrap support. The pairwise matrix (Table 4.2) shows the sequences within both clades are identical, while sequences between the clades differ only for less than 1%.

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List of Abbreviations and Symbols

UV- ultraviolet EDTA- ethylene diamine tetra-acetic acid DCA- detrended correspondence analysis °/_{oo –} part per thousand MA- million years ago ITS- internal transcribed spacer rDNA- recombinant deoxyribonucleic acid IWP- Indo West-Pacific ISEA- Island South East Asia Ha- hectares DIC- differential interference contrast CMA/SW- cornmeal agar/seawater rRNA- recombinant nucleic acid LSU- large subunit ribosomal CO1- cytochrome c oxidase subunit 1 ng- nano gram µM- micro molar mM- mili molar L- litre g- gram dNTP- Deoxyribonucleotide triphosphate PCR- polymerase chain reaction w/v- weight/volume bp.- base pair **OD-** optical density NCBI- National Centre for Biotechnology Information