

**SPECIES RICHNESS AND GENETIC
DIVERSITY OF THE *ACROPORA*
FAUNA ALONG THE NORTH-WEST
COAST OF SABAH**

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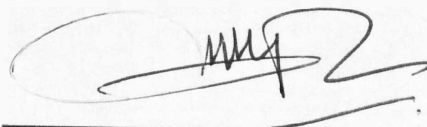


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ABSTRACT

Staghorn corals (*Acropora* Oken, 1815) are the most abundant reef-building corals in Sabah but current knowledge on their species richness is deficient at many localities while baseline data on their genetic diversity are non-existent. In this study, 122 staghorn coral individuals were sampled from coral reefs around Pulau Tiga Park, P. Mantanani, and P. Banggi, Sabah using SCUBA, following which taxonomic assignment was conducted by examining their skeletal morphology. Afterwards, 50 (*M*) representative individuals were subjected to DNA barcoding using nucleotide sequences of the partial cytochrome *c* oxidase subunit-I (*COI*) and cytochrome *b* (*CYB*), and multi-locus microsatellite genotyping using 11 universal markers containing tri-, tetra-, penta-, and hexa-nucleotide repeat motifs. A total of 33 different species were identified from the three localities of which 14 occur in P. Tiga Park, 26 in P. Mantanani, and 22 in P. Banggi. Two species, *Acropora dendrum* and *A. desalwii*, are reported for the first time in Sabah. Meanwhile, the 50 individuals barcoded and genotyped represent the 33 identified species and a morphotype designated as *Acropora* sp. Substitution rate of the staghorn coral *CYB* (mean *p*-distance: 0.38%) was faster than the substitution rate of the *COI* (mean *p*-distance: 0.24%), while the value recorded for the *COI-CYB* was the average of these two rates (mean *p*-distance: 0.32%). Subsequently, haplotype diversity (H_d) with respect to the *CYB* sequences (number of haplotypes: 36; $H_d \pm \text{S.D.} = 0.91 \pm 0.04$) was higher than that with respect to the *COI* sequences (number of haplotypes: 25; $H_d \pm \text{S.D.} = 0.73 \pm 0.07$). The number of *COI-CYB* haplotypes was the highest at 42 ($H_d \pm \text{S.D.} = 0.97 \pm 0.02$), as more nucleotide substitutions were captured. Consequently, the phylogeny of the staghorn corals inferred using the *COI-CYB* sequences exhibited the best resolution but all the trees reconstructed shared a common multifurcating topology, which suggested a polyphyletic evolutionary pattern among the staghorn corals. The discriminatory power of the DNA barcodes currently employed were therefore inadequate for intrapopulation studies, which underlined the potential of the hypervariable microsatellite markers for such investigations. The microsatellite markers used in this study were polymorphic with number of alleles ranging from seven to 23 per locus (mean = 13.5). Estimates of genotypic diversity suggested a state of heterozygote deficit within the Sabah population as the level of observed heterozygosity ($H_o = 0.39 \pm 0.14$) was over two-fold lower in contrast to the levels expected ($H_e = 0.84 \pm 0.08$; Nei's $H_e = 0.83 \pm 0.08$). The lack of genotypic diversity within the Sabah staghorn corals could signal lowered adaptive capacity of the population to extreme changes in their environment that warrants urgent conservation measures. The results presented here further add to current knowledge on the species richness of staghorn corals in Sabah and represent the first quantitative baseline data on their genetic diversity.

ABSTRACT

Staghorn corals (*Acropora* Oken, 1815) are the most abundant reef-building corals in Sabah but current knowledge on their species richness is deficient at many localities while baseline data on their genetic diversity are non-existent. In this study, 122 staghorn coral individuals were sampled from coral reefs around Pulau Tiga Park, P. Mantanani, and P. Banggi, Sabah using SCUBA, following which taxonomic assignment was conducted by examining their skeletal morphology. Afterwards, 50 (*N*) representative individuals were subjected to DNA barcoding using nucleotide sequences of the partial cytochrome *c* oxidase subunit-I (*COI*) and cytochrome *b* (*CYB*), and multi-locus microsatellite genotyping using 11 universal markers containing tri-, tetra-, penta-, and hexa-nucleotide repeat motifs. A total of 33 different species were identified from the three localities of which 14 occur in P. Tiga Park, 26 in P. Mantanani, and 22 in P. Banggi. Two species, *Acropora dendrum* and *A. desalwii*, are reported for the first time in Sabah. Meanwhile, the 50 individuals barcoded and genotyped represent the 33 identified species and a morphotype designated as *Acropora* sp. Substitution rate of the staghorn coral *CYB* (mean *p*-distance: 0.38%) was faster than the substitution rate of the *COI* (mean *p*-distance: 0.24%), while the value recorded for the *COI-CYB* was the average of these two rates (mean *p*-distance: 0.32%). Subsequently, haplotype diversity (H_d) with respect to the *CYB* sequences (number of haplotypes: 36; $H_d \pm \text{S.D.} = 0.91 \pm 0.04$) was higher than that with respect to the *COI* sequences (number of haplotypes: 25; $H_d \pm \text{S.D.} = 0.73 \pm 0.07$). The number of *COI-CYB* haplotypes was the highest at 42 ($H_d \pm \text{S.D.} = 0.97 \pm 0.02$), as more nucleotide substitutions were captured. Consequently, the phylogeny of the staghorn corals inferred using the *COI-CYB* sequences exhibited the best resolution but all the trees reconstructed shared a common multifurcating topology, which suggested a polyphyletic evolutionary pattern among the staghorn corals. The discriminatory power of the DNA barcodes currently employed were therefore inadequate for intrapopulation studies, which underlined the potential of the hypervariable microsatellite markers for such investigations. The microsatellite markers used in this study were polymorphic with number of alleles ranging from seven to 23 per locus (mean = 13.5). Estimates of genotypic diversity suggested a state of heterozygote deficit within the Sabah population as the level of observed heterozygosity ($H_o = 0.39 \pm 0.14$) was over two-fold lower in contrast to the levels expected ($H_e = 0.84 \pm 0.08$; Nei's $H_e = 0.83 \pm 0.08$). The lack of genotypic diversity within the Sabah staghorn corals could signal lowered adaptive capacity of the population to extreme changes in their environment that warrants urgent conservation measures. The results presented here further add to current knowledge on the species richness of staghorn corals in Sabah and represent the first quantitative baseline data on their genetic diversity.

ABSTRAK

KEKAYAAN SPESIS DAN KEPELBAGAIAN GENETIK FAUNA ACROPORA DI SEPANJANG PANTAI BARAT LAUT SABAH

Karang Staghorn (*Acropora* Oken, 1815) adalah komponen utama terumbu karang di Sabah namun maklumat mengenai kekayaan species kumpulan tersebut adalah masih kurang di kebanyakan tempat manakala kadar kepelbagaian genetik karang staghorn di Sabah belum lagi dikaji. Dalam kajian ini, 122 individu karang staghorn telah disampel melalui kerja-kerja penyelaman di kawasan terumbu karang di sekitar Taman Pulau Tiga, P. Mantanani, dan P. Banggi. Spesis sampel-sampel tersebut telah dikenalpasti melalui diagnosis morfologi. Jujukan nukleotida sitokrom c oksidase subunit-I (COI) dan sitokrom b (CYB) telah dipilih sebagai lokus-lokus DNA barcoding manakala sebelas penanda mikrosatelit universal yang mengandungi motif berulang tri-, tetra-, penta-, dan heksa-nukleotida telah digunakan untuk penentuan karang staghorn tersebut. Sebanyak 33 spesis telah dikenalpasti di ketiga-tiga lokaliti tersebut di mana 14 ditemui di Taman P. Tiga, 26 di P. Mantanani, dan 22 di P. Banggi. Dua spesis, *Acropora dendrum* dan *A. desalwii* adalah dilaporkan di Sabah buat pertama kalinya. Aplikasi DNA barcoding dan penentuan mikrosatelit melibatkan sejumlah 50 individu mewakili 33 spesis yang telah dikenalpasti dan satu morfotip dilabel sebagai *Acropora* sp. Jujukan nukleotida CYB (purata jarak berkadar: 0.38%) karang staghorn tersebut bermutasi dengan kadar lebih cepat berbanding dengan COI (purata jarak berkadar: 0.24), manakala kadar bagi jujukan berangkai COI-CYB menunjukkan nilai perantara (0.32%). Sehubungan dengan itu, kepelbagaian haplotip (H_d) berdasarkan jujukan CYB (bilangan haplotip: 36; $H_d = 0.91 \pm 0.04$) adalah lebih tinggi berbanding kepelbagaian haplotip berdasarkan jujukan COI (bilangan haplotip: 25; $H_d = 0.73 \pm 0.07$). Bilangan haplotip COI-CYB adalah paling tinggi (42; $H_d \pm S.D. = 0.97 \pm 0.02$) kerana ia merangkumi mutasi di keseluruhan jujukan COI dan CYB setiap individu. Sehubungan dengan itu, anggaran filogeni karang staghorn Sabah berdasarkan jujukan COI-CYB mempamerkan resolusi lebih tinggi namun semua filogeni dalam kajian ini mempamerkan corak polifiletik. Sebaliknya, penanda mikrosatelit yang digunakan dalam kajian ini adalah polimorfik, terdiri daripada tujuh ke 23 alel bagi setiap lokus (min = 13.5). Analisis genotip karang staghorn dalam kajian ini menunjukkan terdapatnya defisit heterozigot dalam populasi Sabah, di mana tahap heterozigot diperhatikan ($H_o = 0.39 \pm 0.14$) adalah dua kali ganda lebih rendah berbanding dengan tahap yang dijangka ($H_e = 0.84 \pm 0.08$; H_e Nei = 0.83 ± 0.08). Kekurangan kepelbagaian genotip dalam kalangan karang staghorn di Sabah mungkin menandakan bahawa kapasiti populasi tersebut untuk mengadaptasi dalam keadaan persekitaran yang melampau adalah rendah — justeru, langkah-langkah pemuliharaan perlu segera diambil. Hasil kajian yang dibentangkan di sini memaparkan lagi pengetahuan semasa mengenai kekayaan species karang staghorn di Sabah dan ianya mewakili data asas kuantitatif pertama bagi kepelbagaian genetik karang tersebut.

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LIST OF SYMBOLS

| | |
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| π | Measure of the mean (\pm S.D.) of nucleotide diversity within a set of DNA sequences (Nei and Miller, 1990) |
| D | Genetic distance between a set of pairwise microsatellite genotypes (Nei, 1972) |
| \hat{D} | Unbiased measure of genetic distance between a set of pairwise microsatellite genotypes (Nei, 1978) |
| H_d | Measure of mean (\pm S.D.) diversity within a population of haplotypes (Nei and Tajima, 1981) |
| h_e | Uncorrected measure of expected heterozygosity within a microsatellite locus (Levene, 1949) |
| \hat{h}_e | Unbiased measure of expected heterozygosity within a microsatellite locus (Nei, 1978) |
| H_e | Uncorrected measure of mean (\pm S.D.) expected heterozygosity within a set of microsatellite loci (Levene, 1949) |
| \hat{H}_e | Unbiased measure of mean (\pm S.D.) expected heterozygosity within a set of microsatellite loci (Nei, 1978) |
| h_o | Observed heterozygosity in a microsatellite locus (Levene, 1949) |
| H_o | Mean (\pm S.D.) observed heterozygosity within a set of microsatellite loci (Levene, 1949) |
| I | Uncorrected measure of genetic identity between a set of pairwise microsatellite genotypes (Nei, 1972) |
| \hat{I} | Unbiased measure of genetic identity between a set of pairwise microsatellite genotypes (Nei, 1978) |