Khalili Samani N, Esa Y, Amin SMN, Fatin Mohd Ikhsan N. 2016. Phylogenetics and population genetics of *Plotosus canius* (Siluriformes: Plotosidae) from Malaysian coastal waters. PeerJ 4:e1930 https://doi.org/10.7717/peerj.1930

Phylogenetic Analysis and Population Genetic Study of *Plotosus canius* (Siluriformes, Plotosidae) from Malaysian coastal waters

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Plotosus canius (Hamilton, 1822) is a significant marine species in Malaysia from nutritional and commercial perspectives. Despite numerous fundamental researches on biological characteristics of *P.canius*, there are various concerns on the level of population differentiation, genomic structure, and the level of genetic variability among their populations due to deficiency of genetic-based studies. Deficiency on basic contexts such as stock identification, phylogenetic relationship and population genetic structure would negatively impact their sustainable conservation. Hence, this study was conducted to characterize the genetic structure of *P.canius* for the first time through the application of mitochondrial Cytochrome Oxidase I (COI) gene, cross amplification of Tandanus tandanus microsatellites, and a total of 117 collected specimens across five selected populations of Malaysia. The experimental results of the mitochondrial analysis revealed that the haplotype diversity and nucleotide diversity varied from 0.395 to 0.771 and 0.033 to 0.65 respectively, which pointed out the unlikelihood of mutation effects on gene flow. Moreover, the statistical analysis of microsatellites addressed a considerable heterozygote insufficiency in all populations, with average observed heterozygosity (*H0*) value of 0.2168, which was lower than the standard heterozygosity in marine populations (*H0*= 0.79). This alongside the high *Fis* values estimation, high pairwise differentiation among populations and low within population variations are supposed to be associated with small sample size, and inbreeding system. Besides, the significant finding of this study was the sharing of common haplotype KR086940 at which reflects a historical genetic connectivity between Peninsular Malaysia and Borneo populations due to the geological history of Southeast Asia during Pleistocene era. To put it briefly, the current study has managed to provide an initial genomic database toward understanding of the genetic characterization, phylogenetic, molecular diversification and population structure in *P.canius*, and should be necessary highlighted for appropriate management and conservation of species. Though, further studies must be carried out involving more geographical and sampling sites, larger population size per site, and utilization of more COI genes and nuclear hypervariable markers.

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ABSTRACT: *Plotosus canius* (Hamilton, 1822) is a significant marine species in Malaysia from nutritional and commercial perspectives. Despite numerous fundamental researches on biological characteristics of *P.canius*, there are various concerns on the level of population differentiation, genomic structure, and the level of genetic variability among their populations due to deficiency of genetic-based studies. Deficiency on basic contexts such as stock identification, phylogenetic relationship and population genetic structure would negatively impact their sustainable conservation. Hence, this study was conducted to characterize the genetic structure of *P.canius* for the first time through the application of mitochondrial Cytochrome Oxidase I (COI) gene, cross amplification of *Tandanus tandanus* microsatellites, and a total of 117 collected specimens across five selected populations of Malaysia. The experimental results of the mitochondrial analysis revealed that the haplotype diversity and nucleotide diversity varied from 0.395 to 0.771 and 0.033 to 0.65 respectively, which pointed out the unlikelihood of mutation effects on gene flow. Moreover, the statistical analysis of microsatellites addressed a considerable heterozygote insufficiency in all populations, with average observed heterozygosity (*H0*) value of 0.2168, which was lower than the standard heterozygosity in marine populations (*H0*= 0.79). This alongside the high *Fis* values estimation, high pairwise differentiation among populations and low within population variations are supposed to be associated with small sample size, and inbreeding system. Besides, the significant finding of this study was the sharing of common haplotype KR086940 at which reflects a historical genetic connectivity between Peninsular Malaysia and Borneo populations due to the geological history of Southeast Asia during Pleistocene era. To put it briefly, the current study has managed to provide an initial genomic database toward understanding of the genetic characterization, phylogenetic, molecular diversification and population structure in *P.canius*, and should be necessary highlighted for appropriate management and conservation of species. Though, further studies must be carried out involving more geographical and sampling sites, larger population size per site, and utilization of more COI genes and nuclear hypervariable markers.

KEYWORDS: *Plotosus canius*, Phylogenetic Analysis, Population Structure, COI Gene, Microsatellites, Malaysia

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INTRODUCTION

Plotosus canius (Hamilton,1822) that is known as grey eel-catfish, black eel-tail catfish, canine catfish or Indian catfish (Khan *et al*., 2002; Riede, 2004; Usman *et al*., 2013; Prithiviraj, 2014), were diagnosed as a member of genus *Plotosus*, family Plotosidae (Froese & Pauly, 2015). They are being mainly distributed in estuaries, freshwater rivers, lagoons, and shallow waters of Australia and Southeast Asia (Carpenter, 1999; Prithiviraj & Annadurai, 2012). Grey eel-tail catfish is an amphidromous and demersal bony fish that can live in marine, brackish and freshwater habitats. Their relocation in about 100 km distance range were described as frequent, predictable and cyclical horizontal movement on which could not be categorized as breeding migration (Riede, 2004). Adults could be typically found in estuaries, lagoons and merely in riverine habitats, while their juveniles mostly migrate in massive aggregations toward coastal waters (Carpenter, 1999). After a period of feeding in oceanic littoral zone, fully-grown fishes return to freshwaters in order to prepare themselves for reproduction (Riede, 2004). However, grey eel tail catfish likewise other fish species recently might be endured genetic destruction mostly due to overexploitation (Pauly *et al*., 2002; Collette *et al*., 2011; Usman *et al*., 2013), their population structure could be certainly considered as the best indicator in reliable detection of sustainable and healthy marine environments (Thomsen *et al*., 2012; Bourlat *et al*., 2013).

Genetic structure among marine and terrestrial species is the direct consequence of their biogeography (Leffler *et al*., 2012). As distribution range increases, the effective size of population successively upsurges. Subsequently, after increasing dispersal range, species would be consistently adapted into new habitat that can intensify its genetic variation (Charlesworth & Willis, 2009). However, deterioration of biological variation through accelerated crisis of degeneration in genetic resources is threatening current environmental equations (Krishnamurthy & Francis, 2012). Adding to complication, the accuracy of consistent conservation strategies can extremely restrain by deficiency of reliable knowledge on biodiversity, conservation scales, unidentified anthropogenic degree of ample resolution, as well as biological destruction among taxonomic levels (Butchart *et al*., 2010; Magurran *et al*., 2010; Hoffmann *et al*., 2011). However, the simultaneous scarcities in discovery of biodiversity resources has recently offered a viable incentive to regulate the replicable application in statistic acquisition, conservation, and management protocols (Appeltans *et al*., 2012; Bourlat *et al*., 2013; Leray & Knowlton, 2015).

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To be more specific, the Quantification of population structure at broader scales provides invaluable statistics on patterns of species dynamics, colonization, and isolation (Costello *et al*., 2003). Basically, chronological fluctuations in climate or ecological scale such as recent re-treatment of Pleistocene era are significant parameters in shaping the species extensive association, which might leads to modifications in species dispersal patterns. Besides, precise understanding of historic and contemporary equations can offer the accurate genetic outline of populations toward effective evaluation of population sustainability (Duvernell *et al*., 2008). Therefore, the conservation of sustainable species variation is the most important concern of modern ecological era, regarding the implications of anthropogenic distraction in ecosystems and natural habitats (Pereira *et al*., 2010). Since the destruction in genetic variation can cause the malicious genetic implications (Wright *et al*., 2008), conservation has increasingly gained substantial significance in biological researches at contemporary evolutionary assignments (Primack, 2002). Hence, conservation genetic is greatly advancing as an instructive protocol into the intimidation of recent genetic challenges such as possible distraction of local traits, genetic drift, and inbreeding effects. However the effects of genetic-free parameters like demography, environment and species interactions should not be overlooked (Tallmon *et al*., 2004).

Despite various preliminary studies that have been lately conducted on diverse biological perceptions of *Plotosus canius* including their distribution, morphology and fisheries (Kumar, 2012; Usman *et al*., 2013), fecundity (Khan *et al*., 2002; Usman *et al*., 2013), feeding behaviour (Leh *et al*., 2012), protein structure (Prithiviraj & Annadurai, 2012) and pharmacology (Prithiviraj, 2014), there are some severe concerns on the level of population structure, genetic variation, and the consequences of genetic differentiation among populations of *P.canius* in Malaysia due to lack of genetic researches. Hence, despite their regional significance in Oceania and Southeast Asia (Usman *et al*., 2013), deficiency of genomic research on *P.canius* would certainly have destructive effects on their conservation. Thus, they are undoubtedly in sever necessity for some basic conservation studies especially in Malaysia. As a result, this study was performed to genetically characterize *P.canius* populations of Malaysia through the utilization of the mitochondrial Cytochrome Oxidase I (COI) gene and *Tandanus tandanus* microsatellites, in order to examine the accuracy of employed genetic markers in phylogenetic study, genetic variation assignment, and population genetic structure of *P.canius* in Malaysia.

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MATERIALS AND METHODS

Sample Collection and DNA Isolation

Total of 130 catfish samples demonstrating 2 species of family Plotosidae were directly collected from local fish markets, including of 117 samples of *Plotosus canius* and 13 samples of *Plotosus lineatus*. Sample collection of *P.canius* were performed in 5 various districts throughout Malaysia including: Negeri Sembilan (NSN), Selangor (SGR), Johor (JHR), Sarawak (SWK) and Sabah (SBH) (Figure.1) from May to December 2014, while *P.lineatus* samples were only collected from Selangor. DNA extraction protocol was performed upon sample collection in laboratory via the Wizard® SV Genomic DNA Purification System (Promega, USA), according to manufacturer's protocol instructions by using roughly 20 mg of specimens.

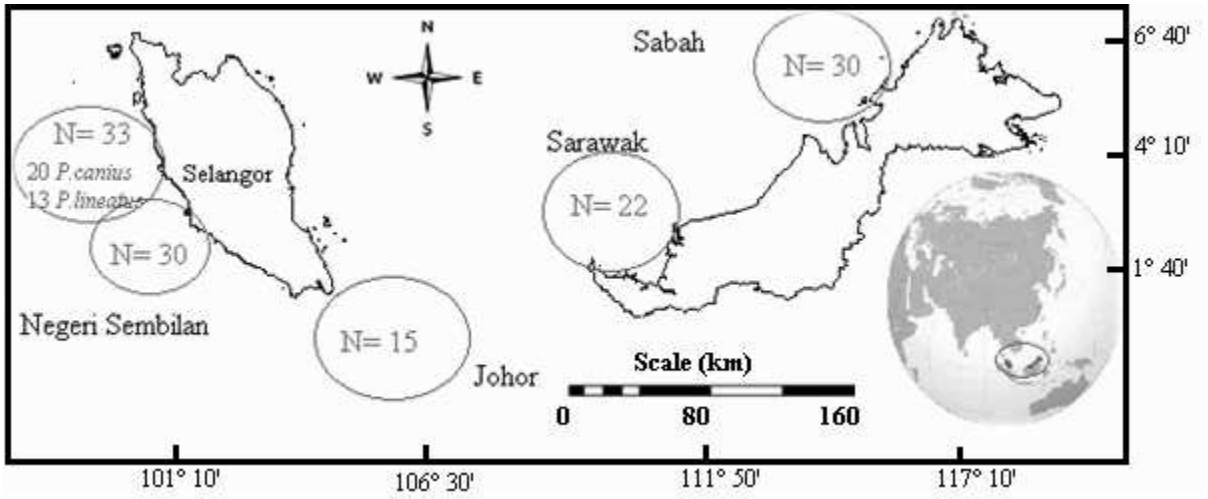

Figure.1) Sampling sites and sample size (N) diagram of *P.canius* and *P.lineatus* in Malaysia.

Statistical analysis of Mitochondrial DNA

To accurately amplify a 655 bp fragment of mitochondrial DNA, PCR amplification were performed by using C_Fish1 primer set (Ward *et al*., 2005) on the 5′ end of COI gene. The amplification protocol were conducted in an overall volume of 25 µl at which contained 0.6 µl of each deoxynucleotide triphosphate (dNTPs), 0.7 µl Taq polymerase, 1.2 µl MgCl2, 0.25 µl of each primers, 2 µl of concentrated genomic DNA, 2.5 µl of Taq buffer and 18 µl of distilled H2O as stated by Ward *et al*. 2005, with slight modification. The PCR reaction was carried out using an Eppendorf Mastercycler based on the following thermal regime: 2 min of 95 °C initial

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denaturation step; 35 cycles of 94 °C denaturation step for 30 s, a 54°C annealing temperature for 45 s and a 72°C extension period of 1 min; followed by 72 °C final extension step for 10 min and a routine 4 °C final hold (Ward *et al*., 2005). In order to confirm that the PCR reaction generated sufficient amplicon proportions, PCR amplification products were visualized using a 2.0 per cent laboratory grade agarose gel containing 5 µl GelRed stain. Amplified products were subsequently isolated and purified upon their visualization and documentation. DNA purification from gel was commonly carried out using the Wizard® SV Gel and PCR Clean-up System (Promega, USA). Purified DNA samples were finally sent to private sector institution (1st Base laboratories Sdn Bhd) for sequencing to generate associated trace files and continuous read lengths intended for genetic and statistical analysis of mitochondrial DNA. Subsequently, trace files were manually end-trimmed using BioEdit software 7.2.5 (Hall, 1999) regarding to their homologous section. Afterwards, ClustalX 2.1 (Thompson *et al*., 1997) was applied to progressively manipulate, align and analyze the DNA sequences. Finally, haplotypes were detected with DnaSP software 5.10.01 (Librado & Rozas, 2009) and deposited into BOLDSYSTEM (international barcode of life) and GenBank.

To comparatively analyze mitochondrial DNA sequences, MEGA 6 program (Tamura *et al*., 2013) were used intending to understand the phylogenetic outlines of COI gene and species, generate sequence alignment and perform evolutionary analysis. Calculation of the pairwise distance was obtained through 1000 bootstrap variance estimation and Tamura-Nei model (Tamura & Nei, 1993). Moreover, overall mean nucleotide distance of sequences was computed using same configuration at each codon positions separately. Subsequently, construction of phylogenetic tree from the highest grade aligned sequences of *P.canius* and *P.lineatus* was prompted in comparison to one haplotype of African sharp tooth catfish *Clarias gariepinus* (ANGBF8254-12) from Thailand as an outgroup through Neighbor-Joining (NJ) method using a mutual 1000 replication bootstrap. Next, Minimum Spanning Network (MSN) was computed using PopART (Bandelt *et al*., 1994) application among obtained sequences of *P.canius*.

Extraction of genetic features from assembly of sequences based on some rudimentary implemented analytical tests was performed through Arlequin software 3.5 (Excoffier *et al*., 2005). As the most crucial objective was to compute the genetic structure, hierarchical analysis

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of molecular variance (AMOVA) and pairwise F_{ST} values of chi square test, population differentiation was successively calculated among five populations of *P.canius* in Malaysia. Analysis of molecular variance was carried out using 1000 permutation to compute distance matrix of sequences, while the same structure were implemented for comparison of all available pair samples and populations through calculation of F_{ST} with 0.05 significance level.

Microsatellite Genotyping

To run measured PCR protocol, optimization of PCR composition were performed at which made positive outcomes based on initial PCR regime using the main protocol for the amplification of *Tandanus tandanus* (Rourke *et al*., 2010) with minor regulation in the amount and concentration of primers, *Taq* DNA polymerase, MgCl2 and dNTPs to enhance the accuracy of the protocol. However, the optimum annealing temperature were practically calculated 55°C similar as original species. To consciously amplify DNA fragments, PCR amplification were performed by using five cross-amplified microsatellites of *T.tandanus* (Rourke *et al*., 2010; Rourke & Gilligan, 2010) on the 5′ end, presented in Table.5. The feasible amplification protocol were conducted in a total volume of 25 µl solution inclosing 0.6 µl of each deoxynucleotide triphosphate (dNTPs), 0.7 µl *Taq* DNA polymerase, 1.2 µl MgCl2, 0.25 µl of each primers, 2 µl of concentrated genomic DNA, 2.5 µl of Taq buffer and 18 µl of distilled H2O as stated by Rourke & Gilligan (2010) with slight modification. The PCR reaction was carried out using a gradient Eppendorf Mastercycler based on the following thermal adjusted protocol: 2 min of 95 °C initial denaturation step; 35 cycles of 95 °C denaturation step for 30 s, a 55°C annealing temperature for 45 s and a 72°C extension period of 1 min; followed by a 72 °C final extension (elongation) step for 10 min and a routine 4 °C final hold (Rourke *et al*., 2010; Rourke & Gilligan, 2010). Afterwards, PCR amplification products were visualized using a 4.0% MetaPhor agarose gel containing 5 µl GelRed staining solution. Subsequently, gel images were subjected to microsatellite screening and approximately 15 µl of the florescent label products were packed and sent to First Base laboratories (private institution) for fragments analysis.

In order to verify any null alleles and scoring error, MICROCHECKER 2.2.3 (Van Oosterhout *et al*., 2004) were applied using diploid data obtained from CONVERT software (Glaubitz, 2004). GENEPOP 4.2 (Rousset, 2008) was employed in order to evaluate the conformity to the "Hardy-

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Weinberg expectations" (HWE) with 10000 permutations for test of exact probability. Observed heterozygosity *(HO)* was estimated using GENALEX 6.5 (Peakall & Smouse, 2012). Successively, FSTAT 2.9.3.2 (Goudet, 1995) was applied to calculate the expected heterozygosity (*HE*), with 15000 permutation actual value test to detect the occurrence probability of any noticeable variations in genetic differentiation among genetic dataset. Afterwards, ARLEQUIN 3.0 (Excoffier *et al*., 2005) were used to analyze the genetic configuration, hierarchical molecular analysis (AMOVA) and pairwise F_{ST} estimations among all five involved populations, using reflection of 95% significance level and 10000 permutations. Assignment of each individual to their genetic groups (*K*) employing admixture model and its associated frequency of allelic data was carried out using the STRUCTURE program 2.1 (Pritchard *et al*., 2000). Next, GENECLASS2 2.0 (Piry *et al*., 2004) was implemented to conduct assignment of individuals into the most plausible inheritance group. Finally, probability of current bottleneck was tested using BOTTLENECK software 1.2.02 (Piry *et al*., 1999).

RESULTS

Phylogenetic and Population Analysis inferred from Mitochondrial DNA

Among overall number of 130 studied specimens using one COI gene, a full mass of 118 reliable sequences (approximately 91%) were identified. Once the sequencing was completed, the C_Fish1 accordingly confirmed as suitable primer set amplifying in *P.canius* and *P.lineatus* DNA samples. Nevertheless, in some cases there were some uncertain base calls, there was no observation of any stop codons nor any instances of insertion or deletion in sequences. Deficiency of structural stop codon more likely supposed to be associated with every amplified mitochondrial sequences, and all that, alongside with the read length of amplified sequences implies that nuclear sequences initiated from vertebrate mitochondrial DNA are not sequenced. Such occasions are based on the fact that nuclear sequences have typically read lengths less than 600-bp (Zhang & Hewitt, 1996). Therefore, the selected COI gene alone was considered for phylogenetic and population structure analysis of *P.canius* and *P.lineatus* in advance.

Preliminary evaluation of verified sequences was mainly generated 20 haplotypes in five populations of *P.canius* and 3 Haplotypes in one population of *P.lineatus* (Table.1). Based on the

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presented data of obtained haplotypes, it can be evidently seen that in *P.canius* samples, KR086940 was found as the most common haplotype in the entire populations from Malaysia, however it was not found in the Negeri Sembilan and the Sabah populations. Moreover, KR086939 was detected as the second common haplotype in *P.canius* populations. The N.Sembilan and the Selangor populations had the most unique haplotypes, while the Johor population had just two shared haplotypes each. In other words, the N.Sembilan and the Selangor population possessed the highest number of identified haplotypes (n = 6), while the N.Sembilan and the Sabah populations had five and four haplotypes respectively.

Species	BOLDSYSTEM Index	GenBank Accession Number	Sampling Site
Plotosus lineatus	NUPM017-14	KP258659	**Selangor**
	NUPM016-14	KP258657	
	NUPM015-14	KP258658	
Plotosus canius	NUPM001-14	KP258648	**Negeri Sembilan**
	NUPM002-14	KP258651	
	NUPM006-14	KP258655	
	NUPM023-15	KR086935	
	NUPM003-14	KP258650	**Sabah**
	NUPM004-14	KP258649	
	NUPM005-14	KP258656	
	NUPM022-15	KR086936	
	NUPM007-14	KP258654	**Selangor**
	NUPM008-14	KP258653	
	NUPM009-14	KP258652	
	NUPM020-15	KR086938	
	NUPM021-15	KR086937	
	NUPM010-14	KP221601	**Sarawak**
	NUPM011-14	KP221602	
	NUPM012-14	KP221603	
	NUPM013-14	KP221604	
	NUPM014-14	KP221605	
	NUPM018-15	KR086940	**Selangor** **Sarawak** **Johor**
	NUPM019-15	KR086939	**Johor** **Negeri Sembilan**

Table. 1) Overview of haplotypes, their sampling sites and accession numbers.

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For the 655 available COI nucleotides, 509 sites (roughly 78 %) were detected as conserved sites, 146 (22%) as variable sites and 136 (21%) identified as parsim-informative sites. The average nucleotide composition in *P.canius* was 29% T, 27.6% C, 25.2%, A, and 18.3% G, while the average C+G content of selected positions was calculated as 45.9%, in *P.lineatus* though, calculation was 28, 28.6, 25, 18.4 and 47% respectively. Translation of all 23 haplotypes for conserved 655 bp fragment was produced 165 amino acids, which presented no signal of pseudogene in their structure. However sample size noticeably varied ranging from 13 to 30 in collected samples of *P.lineatus* and *P.canius* from five different districts in Malaysia, and regarding to the fact that original sample sizes were moderate and some sequences were failed, the actual sample collection is in the desired range recommended by Zhang *et al*. (2010). Basically, in order to detect approximately 80% genetic variation, a collection of 31.9 to 617.8 samples could be needed; although it is far from real laboratory and field work measures; hence it is suggested that at least 10 sample might be desirably sufficient to accurately identify the genetic variability in real phylogenetic studies (Zhang *et al*., 2010). An overview of most crucial outcomes in polymorphism analysis (Table.2) indicated that the number of variable sites are moderately fluctuating from 2 in *P.lineatus* to 54 in *P.canius* samples from Sarawak, While the degree of nucleotide diversity was relatively low (0.00067-0.0391) and as its consequence, the level of polymorphism and genetic variation in populations reasonably presented small portion. Besides, the degree of haplotypes diversity waved from 0.395 (Sabah) to 0.771 (Sarawak).

The Tamura-Nei pairwise distance matrix (Figure. 2) indicated a comparatively high overall interspecies pairwise divergence of 25.2 %, while the least interspecific distance was 0.2 %. The Tamura-Nei intraspecific distance however, ranged from 0.2% to 9.7 % between *P.canius* from Sarawak and Selangor. Nevertheless, the majority of *P.canius* pairwise distances displayed low levels of conspecific divergence roughly around 1 %. The greatest genetic differences was observed between the Selangor and Sarawak (KR086937-KP221604) samples (9.7%), which is moderately reasonable due to their geographical distance. The next significantly high variances was detected between the Sabah-Sarawak pair (KP258656-KP221604) and Negeri Sembilan-Sarawak (KP258654-KP221604), although in later occasion, distance between Sarawak-Sabah sites is extraordinarily closer than Sarawak-Negeri Sembilan.

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Haplotype GenBank Accession Number	*P.canius*					*P.lineatus*
	Selangor ***n*= 20**	**Negeri Sembilan** ***n*= 18**	**Johor** ***n*= 15**	**Sabah** ***n*= 30**	**Sarawak** ***n*= 22**	**Selangor** ***n*= 13**
KP258659						0.078
KP258657						0.153
KP258658						0.769
KP258648		0.056				
KP258651		0.166				
KP258655		0.111				
KR086935		0.056				
KP258650				0.033		
KP258649				0.033		
KP258656				0.766		
KR086936				0.168		
KP258654	0.05					
KP258653	0.1					
KP258652	0.05					
KR086938	0.05					
KR086937	0.1					
KP221601					0.045	
KP221602					0.318	
KP221603					0.136	
KP221604					0.045	
KP221605					0.090	
KR086940	0.65		0.6		0.366	
KR086939		0.611	0.4			
Nucleotide Diversity (Pi JC)	0.00457	0.00184	0.00306	0.00134	0.0391	0.00067
Number of Haplotypes	6	5	2	4	6	3
Haplotype Diversity (Hd)	0.642	0.614	0667	0.395	0.771	0.410
Number of Polymorphic site	14	5	3	4	57	2

Table.2) Summary of 23 observed mitochondrial DNA haplotypes and their distribution, nucleotide diversity, number of haplotypes, haplotype diversity and number of polymorphic sites.

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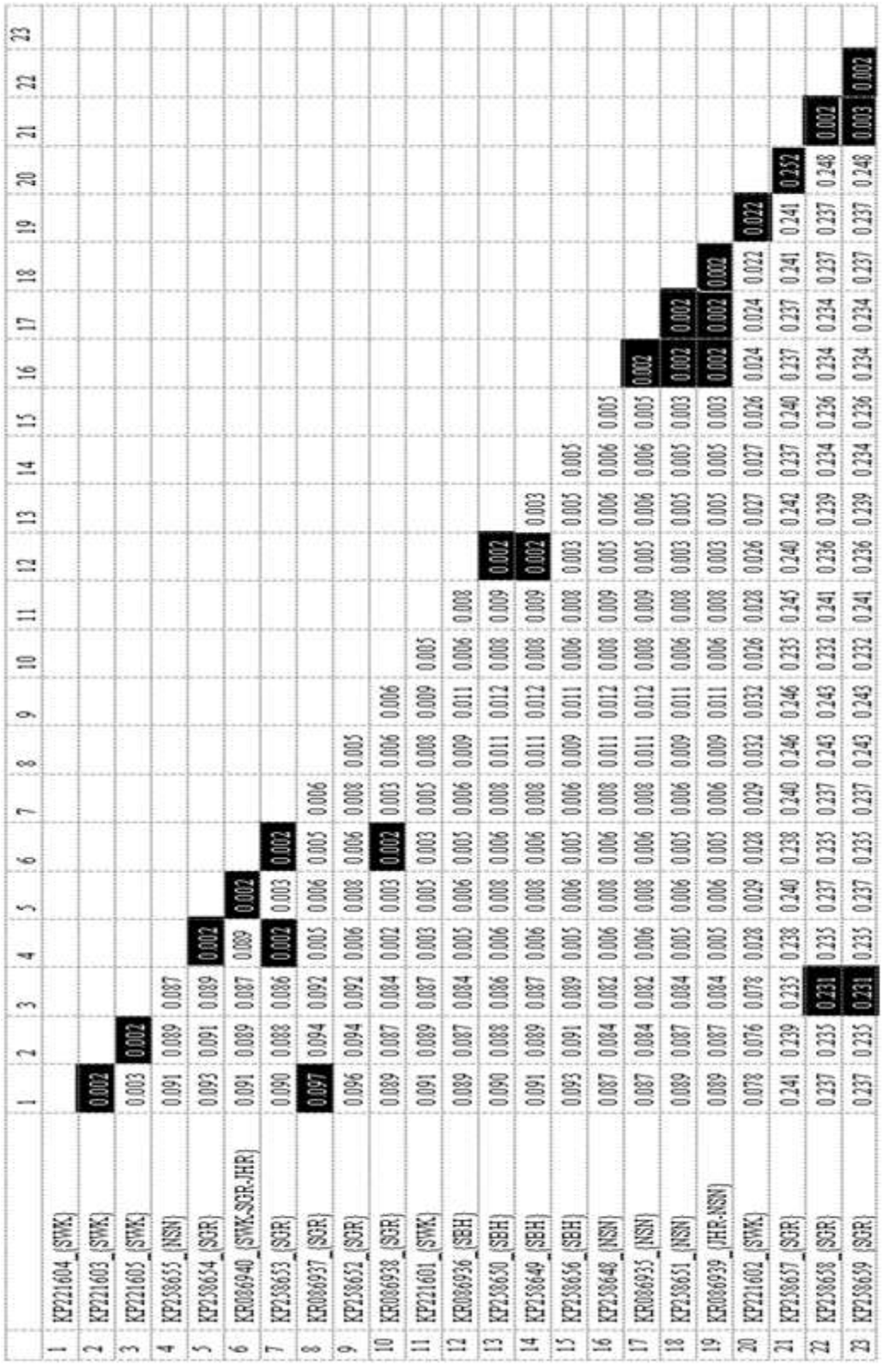

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1	KP221604_{SWK}																							
2	KP221603_{SWK}	0.002																						
3	KP221605_{SWK}	0.003	0.002																					
4	KP238655_{NSN}	0.091	0.089	0.087																				
5	KP238654_{SGR}	0.093	0.091	0.089	0.002																			
6	KR086940_{SWK-SGR-JHR}	0.091	0.089	0.087	0.089	0.002																		
7	KP238653_{SGR}	0.090	0.088	0.086	0.002	0.003	0.002																	
8	KR086937_{SGR}	0.097	0.094	0.092	0.005	0.006	0.005	0.006																
9	KP238652_{SGR}	0.096	0.094	0.092	0.006	0.008	0.006	0.008	0.005															
10	KR086938_{SGR}	0.089	0.087	0.084	0.002	0.003	0.002	0.003	0.006	0.006														
11	KP221601_{SWK}	0.091	0.089	0.087	0.003	0.005	0.003	0.005	0.008	0.009	0.005													
12	KR086936_{SBH}	0.089	0.087	0.084	0.005	0.006	0.005	0.006	0.009	0.011	0.006	0.008												
13	KP238650_{SBH}	0.090	0.088	0.086	0.006	0.008	0.006	0.008	0.011	0.012	0.008	0.009	0.002											
14	KP238649_{SBH}	0.091	0.089	0.087	0.006	0.008	0.006	0.008	0.011	0.012	0.008	0.009	0.002	0.003										
15	KP238646_{SBH}	0.093	0.091	0.089	0.005	0.006	0.005	0.006	0.009	0.011	0.006	0.008	0.003	0.005	0.005									
16	KP238648_{NSN}	0.087	0.084	0.082	0.006	0.008	0.006	0.008	0.011	0.012	0.008	0.009	0.005	0.006	0.006	0.005								
17	KR086935_{NSN}	0.087	0.084	0.082	0.006	0.008	0.006	0.008	0.011	0.012	0.008	0.009	0.005	0.006	0.006	0.005	0.002							
18	KP238651_{NSN}	0.089	0.087	0.084	0.005	0.006	0.005	0.006	0.009	0.011	0.006	0.008	0.003	0.005	0.005	0.003	0.002	0.002						
19	KR086939_{JHR-NSN}	0.089	0.087	0.084	0.005	0.006	0.005	0.006	0.009	0.011	0.006	0.008	0.003	0.005	0.005	0.003	0.002	0.002	0.002					
20	KP221602_{SWK}	0.078	0.076	0.078	0.028	0.029	0.028	0.029	0.032	0.032	0.026	0.028	0.026	0.027	0.027	0.026	0.024	0.024	0.022	0.022				
21	KP238637_{SGR}	0.241	0.239	0.235	0.238	0.240	0.238	0.240	0.246	0.246	0.235	0.245	0.240	0.242	0.237	0.240	0.237	0.237	0.241	0.241	0.252			
22	KP238638_{SGR}	0.237	0.235	0.231	0.235	0.237	0.235	0.237	0.243	0.243	0.232	0.241	0.236	0.239	0.234	0.236	0.234	0.234	0.237	0.237	0.348	0.002		
23	KP238639_{SGR}	0.237	0.235	0.231	0.235	0.237	0.235	0.237	0.243	0.243	0.232	0.241	0.236	0.239	0.234	0.236	0.234	0.234	0.237	0.237	0.348	0.003	0.002	

Figure. 2) Pairwise Tamura-Nei genetic distance in 23 employed haplotypes of *P.canius* and *P.lineatus*.

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Phylogenetic analysis using the 23 haplotypes of the genus *Plotosus* and one haplotype of *C.gariepinus* showed monophyletic status between *P.canius* and *P.lineatus* via the Neighbour-Joining method (Figure. 3). As stated, the three haplotypes from Sarawak population formed a basal clade for *P.canius* using Neighbour-Joining algorithm. Moreover, constructed topology precisely proved the pairwise genetic distances of shared haplotypes, highlighting that KR086940 (SGR, SWK, JHR) have the lowest distance to KP258654 (SGR) and highest to KP221604 (SWK), while KR086939 (JHR, NSN) have the greatest divergence from KP221604 (SWK) and smallest amount from KP258648 (NSN), as their subdivision clades illustrated.

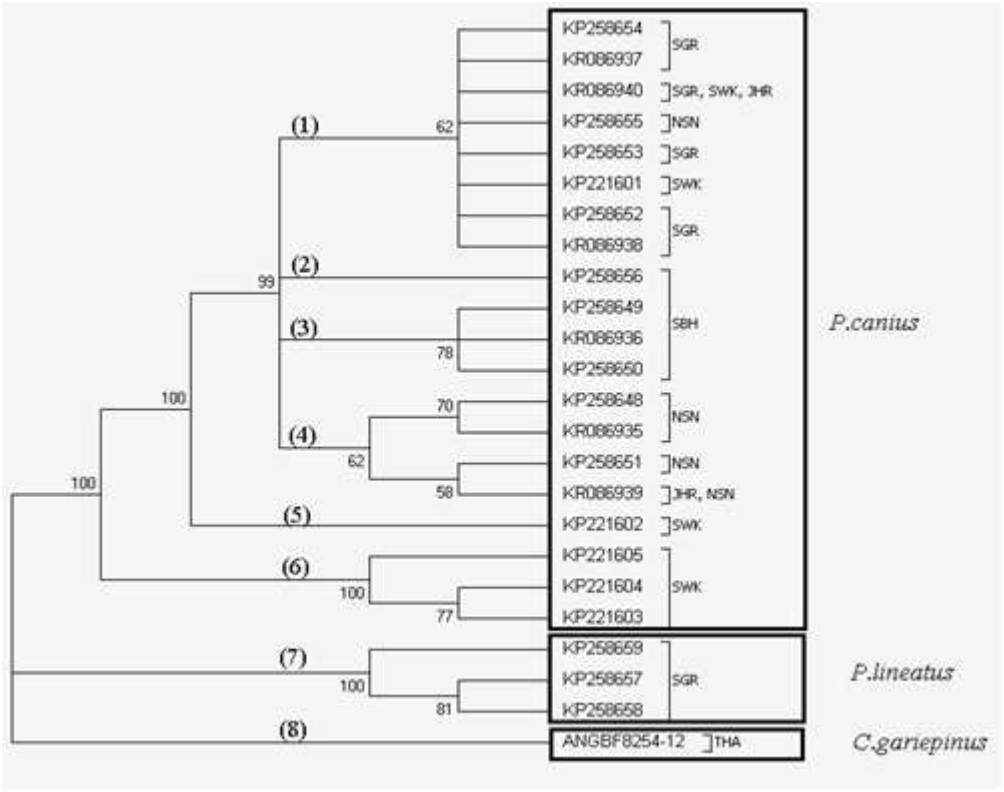

Figure. 3) Summary of Neighbour-Joining relationship in 24 employed haplotypes of *P.canius*, *P.lineatus* and *C.gariepinus* (clades have been indicated by bold numbers in round brackets).

The Minimum Spanning Network (MSN) of 20 haplotypes of *P.canius* (Figure.4) in Malaysia presented more haplotype variability in Sarawak and Negeri Sembilan populations with six and five haplotypes respectively. Indeed, the Sarawak and Negeri Sembilan sequences illustrated a fairly high diversity, while the two haplotypes of Johor possessed the lowest variability. However, the phylogram revealed two relatively irrefutable geographical clades (Sarawak and

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Negeri Sembilan), occurrence of mix haplotypes with other clades indicating that no accurate geographical genetic structure have been certainly detected in studied populations of *P.canius*. Analysis of potential geographical clades have been similarly suggested that all populations are moderately mixed except in Sarawak and Negeri Sembilan. Although there are some possible clades, it was not precisely feasible to clustering the population based on their geographical divisions due to existence of exclusively one connecting mutational steps for most sequences. Hence, analysis was not capable of showing precise separation of geographical clades.

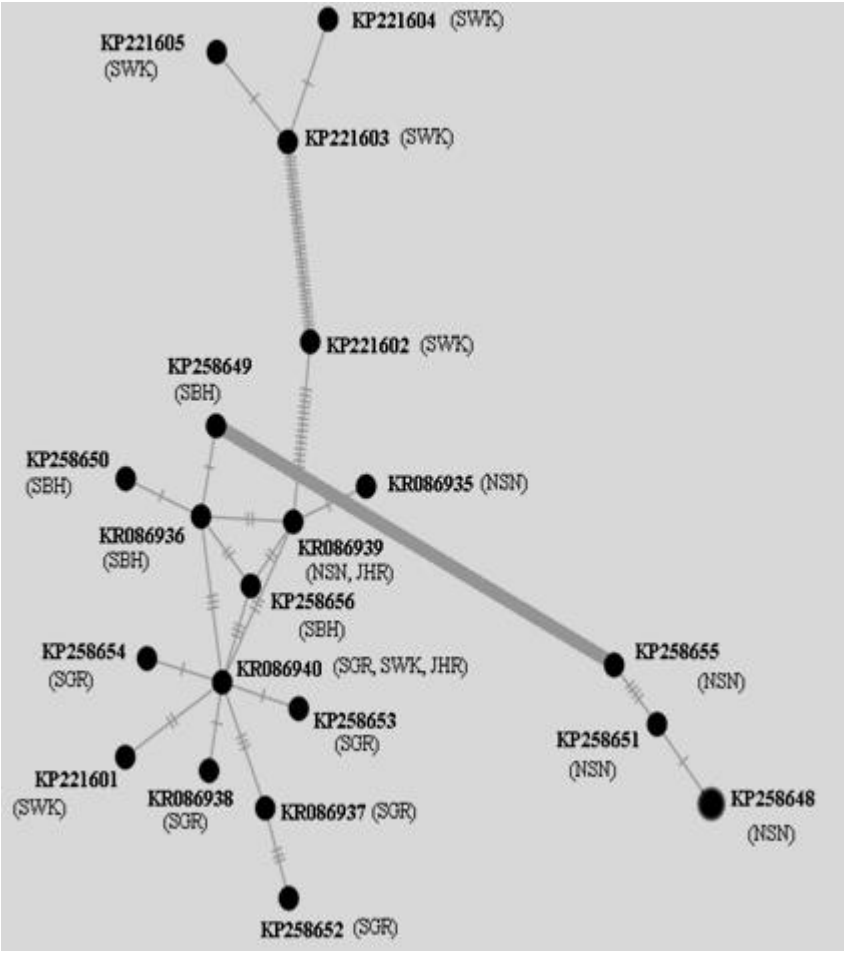

Figure. 4) Minimum Spanning Network (MSN) of 20 haplotypes of *P.canius*.

Analysis of population differentiation inferred from pairwise distance of F_{ST} and Chi-square among studied populations of *P.canius* is displayed in Table.3. Significant genetic variations were detected in all assessments within *P.canius* sequences and two considered species of eel-tail catfishes ($p < 0.001$). However, there were significant distance diversity in genetic variations of almost entire evaluations among populations of Malaysia especially between the Sabah and the

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Negeri Sembilan populations. As expected, the most diversity were identified between *P.canius* populations from the Negeri Sembilan and the Sabah with the rate of 0.62504, which basically means they are nearly genetically divided due to their distance and subsequent decrease in gene flow. However, the lowest genetic distance was detected between Selangor cluster and the Johor clade by the F_{ST} values of 0.05417. Hence, it was considered that maximum sharing of genetic material occurred between Johor and Selangor Populations, while the minimum genetic similarity identified among Sabah and Negeri Sembilan sequences.

	***P.canius* SBH**	***P.canius* JHR**	***P.canius* SGR**	***P.canius* NSN**	***P.canius* SWK**
***P.canius* SBH**	0.00000				
***P.canius* JHR**	0.60156	0.00000			
***P.canius* SGR**	0.43390	0.05417	0.00000		
***P.canius* NSN**	0.62504	0.44097	0.09806	0.00000	
***P.canius* SWK**	0.41533	0.27777	0.29359	0.31333	0.00000

Table. 3) Population pairwise (F_{ST}) values of chi square test for population variation originated with 1000 permutations.

Hierarchical statistics of AMOVA (Table.4) was clearly suggested that roughly 36 % of experimental deviations were inter-population variations, while within population variations were merely responsible for approximately 64 % of overall differentiation.

Source of Variation	**Degree of Freedom**	**Sum of Squares**	**Variance Components**	**Percentage of Variation**
Among Populations	4	77.873	3.09472	35.55
Between Populations	18	100.969	5.60941	64.45

Table. 4) Hierarchical analysis of molecular variance (AMOVA) in *P.canius*.

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Population Genetic results inferred from Genotyping analysis

Fragment analysis were estimated DNA band sizes in *P.canius* that are illustrated alongside with size range in original species (*Tandanus tandanus*), the sequence of each primers and associate annealing temperatures in Table.5.

Primer	Sequence	Size *T.tandanus*	Size *P.canius*	Annealing Temperature
Tan 1-2	F: ´CCGACTGTCAGTGAAAAGGAG3´ R: 5´AGGGTCTGGGAGTGAATGAG3´	216-244	349-385	55°C
Tan 1-7	F: 5´TGTATGGAGCTACTAACAAAACAGG3´ R: 5´TACTCCAGCCCTGAAGGTG3´	181-227	114-125	55°C
Tan 1-10	F: 5´CCTGATTTCTCTCCCAAGG3´ R: 5´AGAAAGGTGGTGCATGTGTG3´	298-310	91-97	55°C
Tan 3-27	F: 5´TGTGGAAGGTTGGGGTTATG3´ R: 5´CGTGATCATGCAAACAGATG3´	215-269	167-168	55°C
Tan 3-28	F: 5´CCCCATTTGCTTTTTCTCTG3´ R: 5´TGTTGAAAGCGGCATGTTAG3´	289-301	280-299	55°C

Table. 5) Five engaged primer sets and their associated size and temperature in *T.tandanus* and *P.canius*.

Genotyping results did not found any signal of null allele nor large allele failure, hence nor scoring inaccuracies due to stuttering. All the five microsatellites loci showed accurate and successful amplification in all populations, although heterozygous alleles were not found in all populations. One microsatellite loci (Tan3-27), was evidently monomorphic in all populations while Tan 1-2, Tan 1-10, Tan 1-7 and Tan 3-28 were polymorphic in at least one population. After implementing the sequential Bonferroni adjustment (Rice, 1989), only four out of the 50 (8%) loci pairs were significant for linkage disequilibrium ($P < 0.05$). Thus, all the five microsatellites loci were considered useful for genetic applications based on the absence of consistent linkage disequilibrium in locus pairs among the studied populations.

Furthermore, after Bonferroni adjustment, nine out of the 25 (36%) microsatellite loci still showed deviation from Hardy-Weinberg Equilibrium (HWE), which might be owing to heterozygote deficiency effects (Table. 6). Heterozygote deficiency could be caused by population structuring, null alleles or inbreeding (Brook *et al*., 2002).

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Locus	N.Sembilan	Sabah	Selangor	Sarawak	Johor	Total* Mean
N	30	30	20	22	15	117
Tan 1-2						
N_a	1	2	1	1	2	4
Ar	1.000	2.000	1.000	1.000	2.000	3.714
H_O	0.0000	0.0000	0.0000	0.0000	0.6000	0.0769
H_e	0.0000	0.4994	0.0000	0.0000	0.4345	0.5974
Fis	-	0.000	-	-	-0.400	
HW	-	1.0000	-	-	0.1791	
Tan 1-7						
N_a	2	2	3	2	1	6
Ar	2.000	2.000	3.000	2.000	1.000	5.844
H_O	1.000	0.0000	0.6000	0.0000	0.0000	0.3590
H_e	0.5085	0.4994	0.6769	0.4947	0.0000	0.7727
Fis	-1.000	1.000	0.116	1.000	-	
HW	0.0000	1.0000	0.5856	1.0000	-	
Tan 1-10						
N_a	1	1	1	1	2	3
Ar	1.000	1.000	1.000	1.000	2.000	2.564
H_O	0.0000	0.0000	0.0000	0.0000	0.4000	0.0513
H_e	0.0000	0.0000	0.0000	0.0000	0.3310	0.3472
Fis	-	-	-	-	-0.217	
HW	-	-	-	-	0.5395	
Tan 3-27						
N_a	1	1	1	1	1	2
Ar	1.000	1.000	1.000	1.000	1.000	1.988
H_O	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
H_e	0.0000	0.0000	0.0000	0.0000	0.0000	0.2242
Fis	-	-	-	-	-	
HW	-	-	-	-	-	
Tan 3-28						
N_a	3	2	3	2	1	8
Ar	3.000	2.000	3.000	2.000	1.000	7.592
H_O	0.4667	1.0000	0.3000	0.0000	0.0000	0.4274
H_e	0.6169	0.5885	0.4769	0.4947	0.0000	0.8393
Fis	0.247	-1.000	0.377	1.000	-	
HW	0.5862	0.0000	0.5771	1.0000	-	

Table. 6) Genetic variation at 5 microsatellite as of five populations of *P.canius* in Malaysia: sample size (*N*), Number of alleles (N_a), allele richness (*Ar*), observed heterozygosity (H_O), expected heterozygosity (H_e), inbreeding coefficient (*Fis*) ($p < 0.05$ symbolic accustomed nominal level (5%) 0.000042, and Hardy-Weinberg expectation (disequilibrium) (HW).

Data from Table. 6 showed that six out of nine deviations were related to Tan1-7 and Tan 3-28 among all the five *P.canius* populations. The fact that the two loci did not show any signal of deviation from HWE in three populations may imply the probability that the estimated deviations could have been originated from either the occurrence of uncertain structure or inbreeding

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among these three population divisions (Pritchard *et al*., 2000). Fairly high level of consistency was detected toward inclusion or exclusion of Tan1-7 and Tan 3-28, accordingly these loci have been retained for further analysis. *Fis* ($P < 0.05$) estimations have been considerably diverse from zero, except in locus Tan 1-2 from Sabah. This alongside with substantial departure from HWE indicates the damaging effect of heterozygote deficiency within associated populations. However, the positive calculated estimations could be translated as decrease in heterozygous levels among offspring in population, mostly owning to non-random mating and its subsequent inbreeding. On the other hand, negative *Fis* estimates might be indication of increasing in heterozygosity level, which could usually occur as a result of random mating system, hence genes should be probably more different (Pritchard *et al*., 2000).

Hierarchical results of microsatellites showed that approximately 64 per cent of experimental variations were originated from inter – population variations, while within individuals variations were only accountable for roughly 28.5 per cent of overall differentiation (Table. 7).

Source of variation	Sum of squares	Variance components	Variation %
Among Populations	191.456	1.02366	63.77361
Among individuals within populations	79.039	0.12422	7.73898
Within Individuals	53.500	0.45726	28.48741

Table. 7) Hierarchical analysis of molecular variance (AMOVA) in *P.canius*.

F_{ST} plot estimations of all involved microsatellites noticeably illustrated that all pairwise calculations presented a fairly high differentiations among populations ranging from 0.29711 between populations of Selangor and Negeri Sembilan to 0.80500 between populations of Sarawak and Johor (Table. 8). The current microsatellite experiment showed that the highest genetic differentiation was between the Johor population and the other populations from Peninsular Malaysia and Borneo. Indeed, the Johor population showed strong deviation from other collected populations, while displayed relatively low intra-population genetic variation (Table. 8), suggesting that the Johor population was less connected to the others during a sizeable period of its evolutionary phase. Likewise, the Sarawak population in the Southwest region of the South China Sea had high F_{ST} values between other populations, signifying the

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restricted gene flow between the Sarawak population and the other populations. The differentiation level among populations of Negeri Sembilan and Selangor (F_{ST} = 0.29711, P< 0.05) showed relatively lower values, even in comparison with their neighbouring populations, theoretically demonstrating the populations that endured inbreeding or genetic drift since their isolation from other populations. Similarly, the Negeri Sembilan and Sabah (F_{ST} = 0.39244, P< 0.05) populations also showed small but significant variances in relation to their close neighbour populations.

		N.Sembilan	Sabah	Selangor	Sarawak	Johor
1	**N.Sembilan**	0.00000				
2	**Sabah**	0.39244	0.00000			
3	**Selangor**	0.29711	0.41039	0.00000		
4	**Sarawak**	0.71934	0.68086	0.72437	0.00000	
5	**Johor**	0.73211	0.68561	0.74834	0.80500	0.00000

Table. 8) Pairwise F_{ST} estimations through *P.canius* populations generated from five microsatellites loci and inclusion of five populations. All calculations were fairly significant ($P < 0.05$) using 10000 permutations.

Levels of genetic variations seem to be widely fluctuated between *P.canius* populations owning to H_e and *Ar* oscillation on which H_e extending from 0.0000 to 0.6769 (Selangor) and *Ar* varied from 1 to 3 (Negeri Sembilan and Selangor). Obviously, two significant clusters could be seen among established populations of *P.canius* in this study, one cluster with low allelic richness and H_e estimations (Johor samples using locus Tan 1-2 and locus Tan 1-10), and another cluster with relatively acceptable H_e and allelic richness (the other four populations using locus Tan 3-28 and locus Tan 1-7). However, the genetic variation in the current study was highly reliant on microsatellites and their sequences as the engaged loci did not specifically develop for *P.canius.* Moreover, allelic frequencies among virtually each combination of population pairs showed highly significant differentiation (F_{ST} < 0.05) (Table. 8), implying that gene flow might be highly restricted among studied populations.

Sampled populations of *P.canius* were basically distributed into five minor clusters using Bayesian analysis. Consequently, the initial highest membership value (q) of the studied populations including Negeri Sembilan, Sabah, Selangor, Sarawak, Johor was estimated as 0.941, 0.983, 0.968, 0.988, and 0.986 respectively (Table. 9). The application of STRUCTURE program subsequently illustrated 4 major *K* (isolated clusters) (Figure. 5). Regarding the fact that

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assessing the expected value of *K* might not be straightforward (Evanno *et al*., 2005), Bayesian structure analysis of the current study revealed the highest probability of *K* for *P.canius* in *K*=2. The four estimated clusters were included Cluster 1: Johor, Cluster 2: N.Sembilan and Selangor, Cluster 3: Sabah, and Cluster 4: Sarawak (Figure. 6).

Populations	Cluster Membership				
	1	2	3	4	5
N.Sembilan	0.005	0.041	0.941	0.010	0.004
Sabah	0.005	0.004	0.005	0.983	0.003
Selangor	0.005	0.968	0.019	0.005	0.004
Sarawak	0.003	0.003	0.003	0.003	0.988
Johor	0.985	0.004	0.004	0.004	0.003

Table. 9) Membership ratio estimated for each population of *P.canius*.

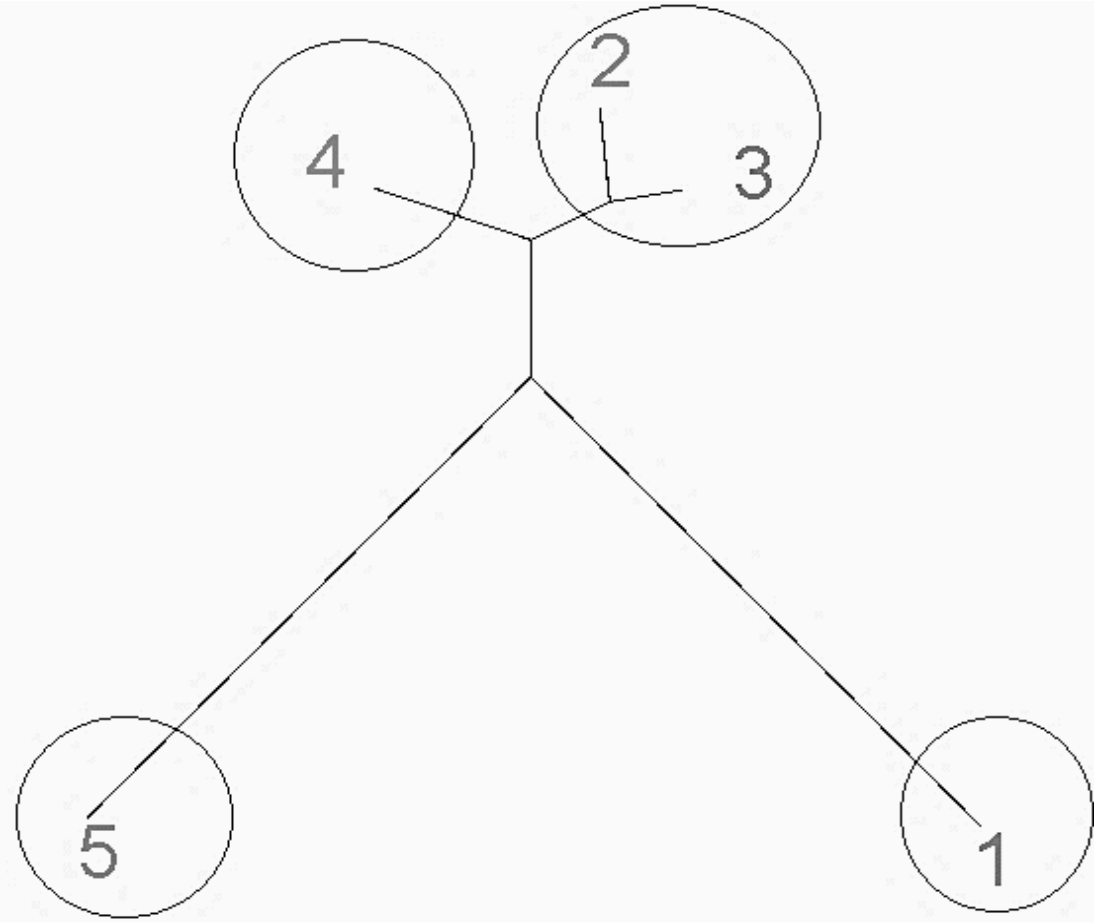

Figure. 5) Tree plot scheme of five engaged populations of *P.canius*.

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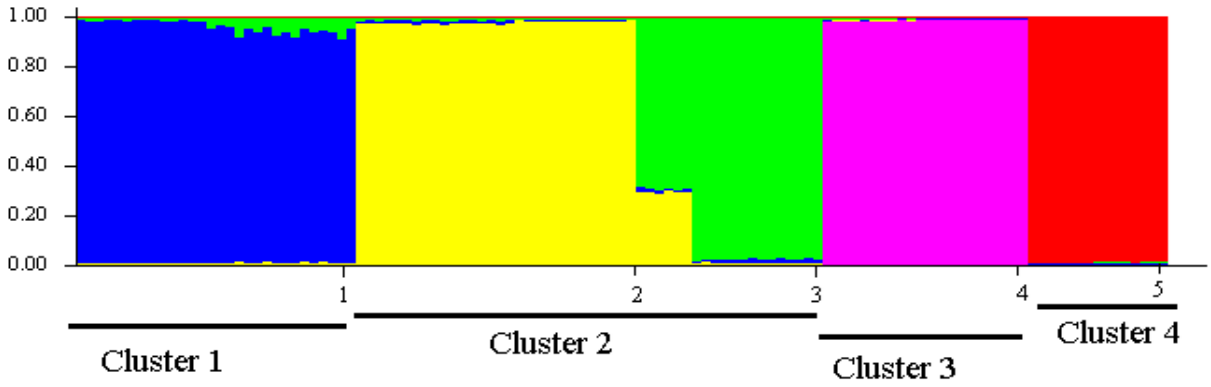

Figure. 6) Population structure of five *P.canius* populations in Malaysia.

Population assignment outcomes evidently revealed that almost all individuals were assigned to their original populations with the probability rate of P> 0.05 (Table. 10). However, the estimation of individual assignment to their populations with the same probabilities revealed the closer rates in comparison levels to other sampling sites. For instance, the Negeri Sembilan population had a relatively closer assignment ratio to the Selangor population.

Assigned Population	CA%	Original Location				
		N.Sembilan (N=30)	Sabah (N=30)	Selangor (N=20)	Sarawak (N=22)	Johor (N=15)
N.Sembilan	100	4.219	70.330	35.873	117.792	92.839
Sabah	100	70.143	4.338	58.286	132.093	96.994
Selangor	100	35.937	58.537	4.715	101.049	83.156
Sarawak	100	115.433	129.921	98.626	3.133	101.070
Johor	100	88.554	92.895	78.807	99.143	2.761

Table. 10) Population assignment based upon five microsatellite loci frequencies in *P.canius* (CA: correct assignment).

Analysis of population bottleneck did not identified substantiating signals of recent population drop in all populations studied using the two phase model (T.P.M) estimations (Table. 11). Furthermore, calculation of the infinite-allele model (I.A.M) comprehensively implied that there was no bottleneck evidence among the studied populations, while the parallel statement was assumed using the stepwise mutation model (S.M.M). Moreover, the shift-mode estimation of allele frequencies was perceived in all five populations, while altogether none of the mutation models were broadly illustrated consistent signals of bottleneck in engaged populations. Therefore, the current experiment could not detect any signals of bottleneck within the *P.canius*

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populations based on three applied models. Nevertheless, outcomes of mutational models consistently suggested the extension in populations due to absence of genetic drift and /or an invasive allele originating from different populations (Piry *et al*., 1999).

	I.A.M	T.P.M			S.M.M	Mode Shift
		60	70	80		
N.Sembilan	0.22672	0.24435	0.26030	0.26596	0.28595	Y
Sabah	0.07656	0.09247	0.09295	0.09683	0.10790	Y
Selangor	0.28119	0.31416	0.34221	0.32656	0.64363	Y
Sarawak	0.17976	0.21249	0.21558	0.20907	0.24057	Y
Johor	0.18105	0.21600	0.24444	0.26510	0.22513	Y

Table. 11) *P* values originated from bottleneck analysis within five populations of *P.canius* (I.A.M: infinite allele model, T.P.M: two phase model, S.M.M: stepwise mutational model, estimation indicate the mutation in stepwise mutational model: Y: yes, N: no) (*Significant values $P < 0.05$).

DISCUSSION

Phylogenetic Analysis of COI Gene

This study has confirmed the efficiency of the COI barcode in identification of eel-tail catfish species. Barcoding fragment has been effectively sequenced mitochondrial DNA isolated from two species of family Plotosidae. Current study provided the first sequence database of *P.canius* to be submitted into barcoding data set. The remarkable concluding outcome of the undergone experiment could be the involvement of two common haplotype. While the most common sequence was KR086940 between populations of Selangor (*n= 7*), Sarawak (*n= 6*), and Johor (*n= 9*), the KR086939 identified as second common haplotype sharing between Johor (*n= 6*) and Negeri Sembilan (*n= 4*). Nevertheless, the most significant finding should be the occurrence of shared haplotype between Selangor, Johor (Peninsular Malaysia) populations and the Sarawak (Borneo) population. The haplotype sharing and their consequent gene flow could practically happen due to several reasons such as breeding migration, mutation, pelagic larvae, and sharing of common ancestors (Frankham, 1996).

Migration is a common behaviour in nearly 3% of all extant fish species (Binder *et al*., 2011). However, there is practically no record on migration and migratory behaviour of family Plotosidae, thus the first assumption of dispersal via migration and ocean current might be highly unlikely since majority of the catfish species cannot endure long distance swimming (more than

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500 kilometers) due to their body shape and structure (Jónsson, 1982). In addition, marine dispersal of eggs, larvae and even juveniles of *P.canius* between two separate ocean currents comprising Straits of Malacca (Selangor and Johor) and South China Sea currents (Sarawak) might also be questionable. In the Strait of Melaka, circulation of currents (particularly in surface) are due to effects of tidal patterns and wind, while the route of both surface and deep layer currents are shown to be relatively the same and toward northwest (Rizal *et al*., 2010). In Johor, however, currents are highly depend on strong winds during monsoon seasons. Indeed, if the monsoon is in its northeast route, the current streams toward South along the coastal region of Malaysia, otherwise, the current will be northward (Mohd Fadzil & Chuen, 2011). Finally, pattern of ocean currents in western South China Sea are largely influenced by season. The circulation in South segment of western current tends to be stable and northward where after separation from coastal region, it forms a northeastern pattern in summer. In fall, however, it strongly flows toward southwest (Fang *et al*., 2012). Therefore, general patterns of aquatic circulation in Strait of Melaka, Johor maritime territory and western area of South China Sea might not strongly implies the probable distribution of grey eel-tail catfish eggs, larvae and juveniles and its consequent gene flow and genetic connectivity.

Considering all possible expectation on genetic variability and gene flow of *P.canius* in Peninsular Malaysia, the second hypothesis of sharing common ancestor due to historical geographic events may reflect the most plausible explanation. Southeast Asia is believed to endured simultaneous glaciation and consequent deglaciation along with its associated decreasing and increasing of marine levels during the Pleistocene period which greatly influenced continental and oceanic configuration (Voris, 2000). During such variations, some regions might be preserved their stable environmental conditions that is nowadays called a refugium on which can greatly affect the gene flow and genetic variability particularly in endemic species (Hobbs *et al*., 2013). Moreover, geographical information proposed that the Pacific and Indian ocean were initially connected directly before the formation of Sundaland (nowadays submerged forming shallow ocean of most Southeast Asia with less than 100m depth) during the Triassic up to the Pleistocene period (Esa *et al*., 2008), hence made such gene flow possible between these comparatively distant locations.

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Hardy-Weinberg Equilibrium and Genetic Diversity

Overall allelic richness revealed quite lower rates using the cross amplified primers ranging from 2 – 8 among the sampled populations in comparison with original species (Rourke *et al*., 2010). Tan 3-28 demonstrated the highest overall allelic rate fluctuating from 1-3 among five populations of *P.canius,* while the lowest level was detected in Tan 3-27. Moreover, the Selangor population showed maximum number of alleles (9), whereas the Johor and Sarawak populations exhibited the lowest (6). Similar instance of low allelic variation have been described in *Bolbometopon muricatum* (Priest *et al*., 2014), *Schizothorax biddulphi* (Palti *et al*., 2012) and *Prosopium cylindraceum* (Mccracken *et al*., 2014). A possible reason for the occurring of low levels of allelic richness might be due to the small employed population size. Hale *et al*. (2012) pointed out the positive effects of sampling size between 25 to 30 individuals per population, however they also mentioned the necessity of 5-100 samples per collection to avoid rare uninformative alleles. Marine vertebrates are believed to present greater allele difference at their microsatellite primers comparing to freshwater populations, which is mostly consistent with their higher population evolutionary size (Neff & Gross, 2001). Their research later revealed that the difference in microsatellite polymorphism among classes and species could be highly dependent upon changes in life history and population biology and moderately to differences happening to microsatellite functions during natural selection. Therefore, it would be probably reasonable that fewer allele number of *P.canius* might be owning to variation in its biology and historic traits, however, the correlation of allelic richness and sample size should not be overlooked.

The average value of observed heterozygosity (H_O) estimated in the five tested microsatellites in *P.canius* were as low as 0.2168, which showed high difference levels in comparison to standard heterozygosity in marine populations (H_O= 0.79) and anadromous fish species (H_O= 0.68) (DeWoody & Avise, 2000). In fact, considerable heterozygote deficiencies were observed in the engaged populations with the exception of the Tan 1-7 and Tan 3-28 loci. Similar temporal pattern of low genetic diversity have been reported for *Pleuronectes platessa* in Island (Hoarau *et al*., 2005) and *Clarias macrocephalous*(Na·Nakorn *et al*., 1999), while in most catfish species higher levels of heterozygosity have been documented as in *Mystus nemurus* (H_O= 0.44-0.57) (Usmani *et al*. 2003). Several decisive issues might influence the genetic variability of marine

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534 species through the variation of Hardy-Weinberg including migration, genetic drift, sample size,
535 over-exploitation, effective size of population and patterns of mating (DeWoody & Avise, 2000).
536 Certainly, *P.canius* should not be presumably considered as long distance migratory marine fish
537 species due to its body structure (Riede, 2004). Alternatively, a possibility of genetic drift in the
538 current study is also suspicious as it basically happens only in small effective size populations
539 that experiencing a period of bottleneck (DeWoody & Avise 2000) at which is completely
540 invalidated in marine species studies like current research.
541
542 Small sample size of collected populations might also be measured as a major parameter in
543 detection of low heterozygosity variation because of the failure to accurately detect the entire
544 extant alleles of the selected populations, hence, deficiency in heterozygote identification
545 (Na·Nakorn *et al*., 1999). Indeed, the current collection size for *P.canius* used for population
546 genetic analysis purposes should be quite small based on Kalinowski (2005), therefore, the
547 hypothesis of deficiency in heterozygote detection due to the low level of sampled specimen
548 could be accepted. The last cause of a low heterozygosity levels and its consequent genetic
549 variation is non-random system of mating behaviour among populations (Brook *et al*., 2002;
550 Balloux *et al*., 2004). Estimation of HWD for the current study however, showed considerable
551 deviation for approximately 36% of the primer/population pairs, which might be due to
552 heterozygote deficiency effects. However, Balloux *et al*. (2004) highlighted that the positive
553 correlation of inbreeding and heterozygosity needs to be examined through application of more
554 polymorphic markers on which demonstrates greater proportion of linkage disequilibrium.
555 Alternatively, the correlation of *Fis* values and inbreeding have been practically assessed and
556 documented in many studies (Balloux *et al*., 2004; Abdul-Muneer, 2005; O'Leary *et al*., 2013).
557 The positive calculated estimations could be translated as a decrease in heterozygous levels
558 among offspring in a population, mostly due to absence of random mating and its subsequent
559 inbreeding. The current study showed considerable significance levels ($P < 0.05$) of *Fis*
560 estimations. This alongside with substantial departure from HWE would indicate the damaging
561 effect of heterozygosity deficit within the populations.
562
563

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565 Analysis of Population Structure

566 A remarkably high levels of genetic structure were detected among populations of *P. canius*
567 ranging from 0.05417 to 0.62504, showing significantly high structuring among studied
568 populations except differences between Johor – Selangor samples (F_{ST} = 0.05417) and Selangor –
569 Negeri Sembilan (F_{ST} = 0.09806). Moreover, AMOVA statistics evidently revealed that
570 approximately 64 % of genetic variations were due to within population variations. Hence, the
571 fairly high F_{ST} rates, significant hierarchical molecular results and consequent higher genetic
572 variances among *P.canius* populations in Peninsular Malaysia and their relatives in Borneo, in
573 addition to the detection of only one sharing haplotype (KR086940), would suggest the absence
574 of contemporary gene flow among them most probably due to the geological modification,
575 consequential rise in marine water levels and historical continental separation during the
576 Pleistocene era (Esa *et al*., 2008; Song, 2012). However, exceptional cases between Selangor –
577 Negeri Sembilan and Selangor – Johor might be inversely interpreted as occurrence of gene flow
578 or migration regarding to fairly close distances rather than extraordinary distance between
579 Borneo and Peninsular Malaysia. The sequential genetic diversity presented in this study could
580 be caused by high haplotype frequencies among the five populations of *P.canius* in Malaysia, in
581 addition to identification of unique sequences in each population (except in Johor). The present
582 patterns of differentiation among catchments is believed to be significantly as a consequence of
583 the Pleistocene associated historical and geological continental and sea level distraction and its
584 subsequent isolation of lands and populations (Esa *et al*., 2008).
585
586 The calculated *Fst* values of five microsatellites in *P.canius* showed significant estimation,
587 indicating substantial genetic structure and differentiation among the studied populations. All
588 populations also showed significantly high assignment rates, followed by a low membership
589 recorded for other population clusters. High rates of proper assignment might indicates strong
590 population differentiation among the studied populations (Paetkau *et al*., 2004). Although the
591 Sabah population demonstrated a close pairwise distance with the Selangor and Negeri Sembilan
592 populations, the Negeri Sembilan and Selangor populations showed the lowest differentiation
593 level (0.29711), and also the highest cluster membership in comparison with other populations.
594 Surprisingly, the highest level of pairwise *Fst* differentiation has been estimated between the

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Johor population and the other four populations, in contrast to the closer geographical distance between the Johor and the Negeri Sembilan populations. Indeed, microsatellite analysis made a relatively counter-outcome in comparison with mitochondrial results, where *Fst* estimation of former populations was estimated as the lowest among the *P.canius* samples. Genetic differentiation detection through microsatellite loci might be influenced by several technical complications. One of the most common practical problems, which is believed to be mostly associated with microsatellite primers (due to higher mutation rate) is well-known as homoplasy (Balloux & Lugon-Moulin, 2002). Homoplasy might diminish the microsatellite-based population differentiation signals. The existence of homoplasy is highly dependent on the occurrence of different identical locus copies, while such identical character is not consequent of mutual ancestor. In fact, the occurrence of homoplasy might be correlated with combination effects of high rates of mutation, outsized population and strong restriction in allele size (Estoup *et al*., 2002). O'Reilly *et al*. (2004) later pointed out that implications of homoplasy in identification of population structure using microsatellite loci are supposedly common in marine species. Nevertheless, further researches have been implied that implications of genetic drift and gene migration might have considerably greater effects on population differentiation analysis in comparison with homoplasy (Estoup *et al*., 2002). Basically, marine vertebrates supposed to have the higher population effective size (N_e) comparing to freshwater species (Hauser & Carvalho, 2008). Besides, genetic drift and effective size are believed to be greatly correlated, hence it is highly probable that neighbouring geographical populations demonstrate the imperceptible population differentiation and structures especially using neutral primers like microsatellites (Larmuseau *et al*., 2010).

CONCLUSION

The current genetic characterization of *P.canius* provided some basic results on their phylogeny and population structure. The phylogenetic and phylogeographic analysis of *P.canius* noticeably constructed accurate clusters in the five population of Malaysia, demonstrating the capability of the chosen mitochondrial COI barcoding gene to potentially assign the genus *Plotosus* into their biological taxa. Indeed, COI analysis resolved the phylogenetic relationships between *P.lineatus* and *P.canius* populations, supporting their taxonomic status as different species. A low mitochondrial differentiation was found among *P.canius* populations with some indication of

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endemism (haplotype restricted only to a particular population) as observed in the Sabah population. Nevertheless, the COI gene revealed sufficient informative interpretation of relationships among the five populations, supporting by reasonable bootstrapping values (>85%). The sharing of haplotypes between a few samples from Peninsular Malaysia and their Sarawak counterpart of Borneo showed the sensitivity of the COI marker to infer the biogeographical history of *P. canius* and potentially other marine taxa in the region.

Microsatellites analyses on the population structure of *P.canius* showed slightly different patterns of structuring in comparison with the COI findings. Nevertheless, both markers detected higher level of among population differentiations than within population variability. In addition, four main clusters or genetic stocks of *P.canius* were identified using the cross species amplification study of *T. tandanus* microsatellites.

Finally, the results from this study has provided valuable understandings on the genetic characterization, molecular phylogeny, evolutionary kinship, and population structuring of *P.canius*, in particular, and the genus *Plotosus*, in general. However, further studies must be conducted using more geographical and sampling sites, larger population sizes per site, and more documented sequences from applicable mtDNA fragments. Furthermore, designing species specific hypervariable nuclear markers such as microsatellite for *P.canius* must be considered in order to accurately analyze the population structure and genetic diversity of *P.canius* before implementation of advanced fisheries and conservation strategies.

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