



Eco-Economically Indispensable Borneo-Endemic Flora and Fauna: Proboscis Monkey (*Nasalis larvatus*), Malaysian Mahseer (*Tor tambroides*), Engkabang (*Shorea macrophylla*), Sarawak Rasbora (*Rasbora sarawakensis*) and Sago Palm (*Metroxylon sagu*)

Kit Lim LW*

Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

***Corresponding author:** Leonard Whye Kit Lim, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia, Tel: +6012-2497983; Email: lwkl1993@gmail.com

Mini Review

Volume 5 Issue 3

Received Date: June 07, 2022

Published Date: June 23, 2022

DOI: 10.23880/izab-16000381

Abstract

The Borneo Island is the third-largest island and one of the greenest islands on earth. It is the natural habitat to various endemic flora and fauna such as the proboscis monkey (*Nasalis larvatus*), Malaysian mahseer (*Tor tambroides*), engkabang (*Shorea macrophylla*), Sarawak rasbora (*Rasbora sarawakensis*) and sago palm (*Metroxylon sagu*). In this mini review, we ventured into the current research, eco-economical aspects and potentials of each species and further provided future perspectives and recommendations to drive future research to greater heights besides supporting conservation endeavours.

Keywords: Proboscis Monkey; Malaysian Mahseer; Engkabang; Sarawak Rasbora; Sago Palm

Introduction

The Borneo Island is the third-largest island and one of the greenest islands on earth. It is the natural habitat to various endemic flora and fauna such as the proboscis monkey (*Nasalis larvatus*), Malaysian mahseer (*Tor tambroides*), engkabang (*Shorea macrophylla*), Sarawak rasbora (*Rasbora sarawakensis*) and sago palm (*Metroxylon sagu*). In this mini review, we ventured into the current research, eco-economical aspects and potentials of each species and further provided future perspectives and

recommendations to drive future research to greater heights besides supporting conservation endeavours.

Proboscis Monkey (*Nasalis larvatus*)

The proboscis monkey is the most primitive colobine evidenced from its unique diploid number of $2n=2x=48$ and its morphology [1-3]. What differs proboscis monkey from other primates are their high swimming capability, huge elongated nose, digestive physiology (they are foregut fermenter, unlike other primates), as well as four-chambered

large stomachs [4]. In 2019, Lim, et al. [5] had isolated and characterised genome-wide putative liver-specific enhancers in this species. Interestingly, they discovered that some of the liver-specific transcription factors are highly responsible for the enhancer activity elevation (AP-1, C/EBP- β and HNF-1) and reduction (HNF-3 β) [5]. These findings were deemed imperative as it serves as a stepping stone and important reference for future regenerative therapy and molecular treatments for humans [6], apart from establishing the proboscis monkey as one of the primate model organisms.

Malaysian Mahseer (*Tor tambroides*)

The Malaysian mahseer (or empurau) is food, ornamental and sport fish all-in-one, and its price is exorbitant due to its unique flesh taste and texture [7]. Wild empurau is much more expensive than their farmed counterparts as wild fishes feed on illipe nuts that are high in lipid content, thus the wild fish flesh has fruity sweetness. Majority of the empurau research focused on the growth performance and it was not until recently that the genetics and genomics of this fish are being explored thoroughly. Lim, et al. [8] improved the phylogenetic resolution of the Javan and Malaysian mahseers via mitogenomes sequencing, and they further identified several potential mitogenome markers useful for haplotype identification of empurau from unknown locations. Lau, et al. [9] sequenced the transcriptomes of the Javan and Malaysian mahseers not long after. Besides, Lau, et al. [7] explored the microbiome and metagenome of healthy and diseased empurau via 16S rRNA markers. Not long ago, Lau, et al. [9] sequenced, assembled and characterised the entire nuclear genome of this fish species. All in all, these data generated are essential for future evolutionary, taxonomy and conservation of this fish species.

Engkabang (*Shorea macrophylla*)

The engkabang is not only producing quality timber for the wood industry, but also producing lipid-filled nuts important for food and cosmetics manufacturing (as reviewed by Lim, in press). Kamarudin, et al. [10] attempted to improve the fatty acid contents of farmed juvenile empurau fishes via illipe oil (engkabang fat) diets but failed, as juveniles fed with 0% illipe oil has the highest muscle n-3 and n-6 polyunsaturated fatty acid retention values [10]. Chew, et al. [11] had just recently sequenced the chloroplast genome of this tree species and further characterized the genome in terms of microsatellite, long repeat, structural features, comparative genomics, as well as phylogeny. Surprisingly, this tree species was found to cluster with *Parashorea macrophylla*, *Parashorea chinensis*, *Shorea leprosula*, *Shorea pachyphylla* and *Shorea macrophylla* in a clade with bootstrap values exceeding 98% [11].

Sarawak Rasbora (*Rasbora sarawakensis*)

The Sarawak rasbora shared the same family (Cyprinidae) with the famous model organism, zebrafish. Lim, et al. [12] examined the phylogenetic and expression of ATP-binding cassette transporter genes in this fish species. They concluded that the Sarawak rasbora is one of the most feasible candidate as an alternative vertebrate model organism to complement future zebrafish researches. Aminan, et al. [13] further investigated the genetic relationship of this fish species with other rasbora from the same family via the combination of both morphometric and molecular tools. The cryptic diversity of rasbora fishes was greatly improved with the inclusion of molecular tools like genetic markers [3]. Later, Lim, et al. [14] sequenced and characterized the whole mitogenome of this fish species. They unravelled that the phylogenetic resolution has been improved with the availability of several newly sequenced mitogenomes of rasbora fishes from the same family, namely *Rasbora tornieri*, *Rasbora hobelmani*, *Trigonopoma pauciperforatum*, and *Rasbora myersi* [15-18].

Sago Palm (*Metroxylon sagu*)

The sago palm is another all-in-one unique tree as it compacts its starch within its trunk and every organ of this tree can be utilized in various industries like food, polymer, bioprocess, microbiology, computational biology, genetics and genomics, population genetics as well as furniture manufacturing (as reviewed by Lim, et al. [19]). This tree is also widely deemed as the future tree of life and food security that can ease the global food hunger crisis, contributed by its high salt tolerance and disease resistance characteristics [20]. In 2020, Lim et al. [21] evaluated and documented the organellar genome copy number variations across different growth stages, organs, phenotypes and main localities in Sarawak, Malaysia. Not long after, Lim, et al. [22] sequenced and characterized the whole chloroplast genome of this tree species. In 2021, Lim, et al. [23] conducted a genome survey of sago palm before performing a hybrid genome assembly recently.

Future Perspectives and Conclusion

The future research of all the aforementioned eco-economical Borneo-endemic flora and fauna species is as limitless as the sky's limit. For instance, the proboscis monkey can be further established as one of the most primitive primate model organism to facilitate the regenerative and personalized medical therapy in human. The culture of proboscis monkey organs in lab may be useful for organ replacement and transplantation in human in the near future. The Malaysian Mahseer, et al. research can be further elevated with the genome wide identification of growth and immune related genes (such as the ATP-binding cassette transporter

genes, emulating that of Lim, et al. [24] on striped catfish) so that the growth of fish can be accelerated and shortened and at the same time diminishing the occurrence of diseases that can impact the fish farming industry profit. The future engkabang research can move forward with the investigation of which part of the fruit is consumed by the wild empurau fishes that had contributed towards the fruity sweetness in the fish flesh. To further improve the research advancement in Sarawak rasbora, some zebrafish related ecotoxicological and promoter mutational researches Yeaw, et al. [25-28] can be emulated to discover their similarities and differences in terms of gene arrangement and toxic removal. The sago palm researches in the field of genomics can be further enriched with the sequencing of mitogenome that is known to be highly replicative and involves tedious assembly work. Besides, pest and virus related work emulating that of Jee, et al. [29], Lim, et al. [30] and Lim, et al. [31] is also as imperative as this could help planters to minimize profit loss of sago palm and engkabang. In short, the Borneo Island offers a myriad of rich resources yet to be explored fully. The flora and fauna species reviewed in this study is just the tip of the iceberg as we focused only on those that are research established and have eco-economical values [32-36]. It is hoped that these resources can be rightfully and completely geared towards their full potential with the right research initiatives without compromising the conservation endeavours.

References

- Chiarelli B (1966) The chromosome complement of *Nasalis larvatus* (Wurm 1781). *Experientia* 22(12): 797.
- Soma H, Bernischke K, Robinson KP (1974) The chromosomes of proboscis monkey (*Nasalis larvatus*). *Chromosome Information Service* 17(1): 24.
- Stanyon R, Camperio Ciani A, Sineo L, Morescalchi MA (1992) The G-banded chromosomes of the proboscis monkey (*Nasalis larvatus*) compared with the macaque (*Macaca mulatta*). *Anthropology Contemporary* 15(1): 101-104.
- Lim LWK, Chung HH, Chong YL, Lee N.K (2019a) Enhancers in proboscis monkey: A primer. *Pertanika Journal of Tropical Agricultural Science* 42(1): 261-276.
- Lim LWK, Chung HH, Chong YL, Lee NK (2019b) Isolation and characterization of putative liver-specific enhancers in proboscis monkey (*Nasalis larvatus*). *Pertanika Journal of Tropical Agricultural Science* 42(2): 627-647.
- Lim LWK, Chung HH, Chong YL, Lee NK (2018a) A survey of recently emerged genome-wide computational enhancer predictor tools. *Computational Biology and Chemistry* 74(1): 132-141.
- Lau MML, Lim LWK, Ishak SD, Abol Munafi A, Chung HH (2021a) A Review on the Emerging Asian Aquaculture Fish, the Malaysian Mahseer (*Tor tambroides*): Current Status and the Way Forward. *Proceedings of the Zoological Society* 74: 227-237.
- Lim LWK, Chung HH, Lau MML, Aziz F, Gan HM (2021a) Improving the phylogenetic resolution of Malaysian and Javan mahseer (Cyprinidae), *Tor tambroides* and *Tor tambra*: Whole mitogenomes sequencing, phylogeny and potential mitogenome markers. *Gene* 791: 145708.
- Lau MML, Lim LWK, Chung HH, Gan HM (2021b) The first transcriptome sequencing and data analysis of the Javan mahseer (*Tor tambra*). *Data in Brief* 39: 107481.
- Kamarudin MS, Bami ML, Arshad A, Saad CR, Ebrahimi M (2018) Preliminary study of the performance of crude illipe oil (*Shorea macrophylla*) as a dietary lipid source for riverine cyprinid *Tor tambroides*. *Fisheries Science* 84: 385-397.
- Chew IYY, Chung HH, Lim LWK, Lau MML, Gan HM, et al. (2018) Complete chloroplast genome of *Shorea macrophylla* (engkabang): Structural features, comparative and phylogenetic analysis. *Plant Diversity*.
- Lim LWK, Tan HY, Aminan AW, Jumaan AQ, Mokhtar MZ, et al. (2018b) Phylogenetic and expression of ATP-binding cassette transporter genes in *Rasbora sarawakensis*. *Pertanika Journal of Tropical Agricultural Science* 41(3): 1341-1354.
- Aminan AW, Lim LWK, Chung HH, Sulaiman B (2020) Morphometric Analysis and Genetic Relationship of *Rasbora* spp. in Sarawak, Malaysia. *Tropical Life Sciences Research* 31(2): 33-49.
- Lim LWK, Kamar CKA, Roja JS, Chung HH, Liao Y, Lam TTY, Chong YL (2020a) Sequencing and characterisation of complete mitogenome DNA for *Rasbora sarawakensis* (Cypriniformes: Cyprinidae: *Rasbora*) with phylogenetic consideration. *Computational Biology and Chemistry* 89: 107403.
- Chung HH, Kamar CKA, Lim LWK, Roja JS, Liao Y, et al. (2020a) Sequencing and characterization of complete mitogenome DNA of *Rasbora tornieri* (Cypriniformes: Cyprinidae: *Rasbora*) and its evolutionary significance. *Journal of Genetics* 99: 67.
- Chung HH, Kamar CKA, Lim LWK, Liao Y, Lam TTY, et al. (2020b) Sequencing and characterisation of complete mitogenome DNA for *Rasbora hobelmani* (Cyprinidae) with phylogenetic consideration. *Journal of Ichthyology* 60: 90-98.

17. Chung HH, Lim LWK, Liao Y, Lam TTY, Chong YL (2020c) Sequencing and Characterisation of Complete Mitochondrial DNA Genome for *Trigonopoma pauciperforatum* (Cypriniformes: Cyprinidae: Danioninae) with Phylogenetic Consideration. *Tropical Life Sciences Research* 31(1): 107-121.
18. Lim LWK, Roja JS, Kamar CK, Chung HH, Liao Y, et al. (2019c) Sequencing and characterization of complete mitogenome DNA for *Rasbora myersi* (Cypriniformes: Cyprinidae: Rasbora) and its evolutionary significance. *Gene Reports* 17: 100499.
19. Lim LWK, Chung HH, Hussain H, Bujang K (2019d) Sago palm (*Metroxylon sagu* Rottb.): Now and beyond. *Pertanika Journal of Tropical Agricultural Science* 42(2): 435-451.
20. Lim LWK, Chung HH (2020) Salt Tolerance Research in Sago Palm (*Metroxylon sagu* Rottb.): Past, Present and Future Perspectives. *Pertanika Journal of Tropical Agricultural Science* 43(2): 91-105.
21. Lim LWK, Chung HH, Hussain H (2020b) Organellar genome copy number variations and integrity across different organs, growth stages, phenotypes and main localities of sago palm (*Metroxylon sagu* Rottboll) in Sarawak, Malaysia. *Gene Reports* 21: 100808.
22. Lim LWK, Chung HH, Hussain H (2020c) Complete chloroplast genome sequencing of sago palm (*Metroxylon sagu* Rottb.): Molecular structures, comparative analysis and evolutionary significance. *Gene Reports* 19: 100662.
23. Lim LWK, Chung HH, Hussain H, Gan HM (2021b) Genome survey of sago palm (*Metroxylon sagu* Rottboll). *Plant Gene* 28: 100341.
24. Lau MML, Lim LWK, Chung HH, Gan HM (2022b) The first draft genome assembly and data analysis of the Malaysian mahseer (*Tor tambroides*). *Aquaculture and Fisheries*.
25. Yeaw ZX, Lim LWK, Chung HH (2020) Mutagenesis Analysis of ABCB4 Gene Promoter of *Danio rerio*. *Trends in Undergraduate Research* 3(2): a44-a52.
26. Yusni NZ, Lim LWK, Chung HH (2020) Mutagenesis Analysis of ABCG2 Gene Promoter of zebrafish (*Danio rerio*). *Trends in Undergraduate Research* 3(2): a53-59.
27. Lai PN, Lim LWK, Chung HH (2021) Mutagenesis analysis of ABCB8 gene promoter of *Danio rerio*. *Trends in Undergraduate Research* 4(1): a1-8.
28. Lim LWK, Chung HH, Ishak SD, Waiho K (2021c) Zebrafish (*Danio rerio*) ecotoxicological ABCB4, ABCC1 and ABCG2a gene promoters depict spatiotemporal xenobiotic multidrug resistance properties against environmental pollutants. *Gene Reports* 23: 101110.
29. Jee MS, Lim LWK, Dirum MA, Hashim SIC, Masri MS, et al. (2017) Isolation and characterization of avirulence genes in *Magnaporthe oryzae*. *Borneo Journal of Resource Science and Technology* 7(1): 31-42.
30. Lim LWK, Hung IM, Chung HH (2022c) Cucumber mosaic virus: Global genome comparison and beyond. *Malaysian Journal of Microbiology* 18(1): 79-92.
31. Lim LWK, Liew JX, Chung HH (2020) Piper yellow mottle virus: A deep dive into the genome. *Gene Reports*.
32. Lau MML, Kho CJY, Lim LWK, Sia SC, Chung HH, et al. (2022a) Microbiome Analysis of Gut Bacterial Communities of Healthy and Diseased Malaysian Mahseer (*Tor tambroides*). *Malaysian Journal of Microbiology* 18(2): 170-191.
33. Lim LWK (2020) Engkabang (*Shorea macrophylla*): Butter, timber and something better. *Tropical Life Sciences Research*.
34. Lim LWK, Chung HH, Chong YL, Lee NK (2018a) A survey of recently emerged genome-wide computational enhancer predictor tools. *Computational Biology and Chemistry* 74(1): 132-141.
35. Lim LWK, Lau MML, Chung HH, Hussain H, Gan HM (2022a) First high-quality genome assembly data of sago palm (*Metroxylon sagu* Rottboll). *Data in Brief* 40: 107800.
36. Lim LWK, Chung HH, Gan HM (2022b) Genome-Wide Identification, Characterization and Phylogenetic Analysis of 52 Striped Catfish (*Pangasianodon hypophthalmus*) ATP-Binding Cassette (ABC) Transporter Genes. *Tropical Life Sciences Research* pp: 1-34.

