UNIVERSITI PUTRA MALAYSIA

ENVIRONMENTAL CHARACTERIZATION AND METAGENOMICS ANALYSIS OF BIOTIC AND ABIOTIC FACTORS IN NORTH SELANGOR PEAT SWAMP FOREST, MALAYSIA

SAADU HAMIDU

FS 2021 22

ENVIRONMENTAL CHARACTERIZATION AND METAGENOMICS ANALYSIS OF BIOTIC AND ABIOTIC FACTORS IN NORTH SELANGOR PEAT SWAMP FOREST, MALAYSIA

By

SAADU HAMIDU

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Doctor of Philosophy

September 2020

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Doctor of Philosophy

ENVIRONMENTAL CHARACTERIZATION AND METAGENOMICS ANALYSIS OF BIOTIC AND ABIOTIC FACTORS IN NORTH SELANGOR PEAT SWAMP FOREST, MALAYSIA

By

SAADU HAMIDU

September 2020

Chairman : Associate Professor Mohammad Noor Amal Azmai, PhD
Faculty : Science

The North Selangor Peat Swamp Forest (NSPSF), like all other peatland ecosystems are subjected to various of threats such as forest fire, wild animal poaching, expansion of area for agricultural and industrial activity, canal construction, deforestation, and air, water and land pollutions. Moreover, limited fundamental studies have been conducted in this unique ecosystem, especially in the aspect of microbial ecology that associated with the continuous anthropogenic activities of the protected forest.

In general, this study determines the environmental characterization and metagenomics analysis of biotic and abiotic factors in North Selangor Peat Swamp Forest, Selangor, Malaysia. Firstly, this study determines the current environmental variables of undisturbed and disturbed areas. Secondly, the composition and diversity of bacterial communities in the fish gut contents, water and soil of undisturbed and disturbed areas were identified. Thirdly, the taxa and functional genes biomarkers of bacteria in soil samples of undisturbed and disturbed areas were determined. Lastly, this study identified the relationships between the environmental variables and bacterial taxa biomarker from soil of undisturbed and disturbed areas.

In order to understand the impacts of natural and human induced factors on the bacterial communities in NSPSF, two areas namely NSPSF (undisturbed) and its nearby (disturbed) areas were selected in this study. In each area, three sites were selected, namely Sungai Karang Peat Swamp Forest site 1 (SKPSF-1), Raja Musa Peat Swamp Forest (RMPSF) and Sungai Karang Peat Swamp Forest site 2 (SKPSF-2) for undisturbed area, while for disturbed area, paddy field (PF), forest fire (FF) and oil palm plantation (OP) areas were selected. The environmental variables of anthropogenic activities, forest characteristics and water physico-chemical parameters in undisturbed and disturbed areas were determined. Following that, the metagenomics techniques was utilized to assess the composition, diversity, taxonomical biomarkers and functional genes of bacteria in the undisturbed (U) and disturbed (D) samples of fish gut contents (UF and DF), water (UW and DW) and soil (US and DS) in the study areas, as well as to relate these metagenomics findings with the measured environmental variables.

The findings on anthropogenic activities revealed that the disturbed areas have higher scores in water (WP), land (LP) and noise (NP) pollutions and agricultural activity (AA). Other anthropogenic activities that recorded in disturbed areas were distance from human settlement (DHS), state of accessibility (SA), and deforestation (DL), and these were the predominant anthropogenic activities in disturbed area. Whereas, construction activities (CR) cut across all the sites. The higher seedling percentage (PS) in OP was observed and conversely, the percentage of trees (PT) and number of falling trees (FT) appeared to be correspondingly higher in SKPSF-1. The PF in the disturbed area was characterized by high relative light intensity (RLI). Conversely, RLI was relatively lower in the undisturbed area. The undisturbed area indicates lower dissolved oxygen (DO) values and notably increases from undisturbed to disturbed areas, particularly in PF and OP. The FF was an exception, which was observed to have comparatively lower DO concentration. Some of anthropogenic activities such as DHS, SA, DL and AA correlated closely with NH_3-N and Fe in the disturbed area, while sign of fire (SF) in the undisturbed area was associated with NO_3^-.

The metagenomics analyses in undisturbed and disturbed areas revealed a rich and diverse bacterial community across the 18 samples of fish gut contents, water and soil. Moreover, the alpha indexes showed significant difference ($p < 0.05$) between the disturbed and undisturbed sites of each sample. The rarefaction among the samples showed curves, at points where the number individual organisms increase, but the number of species remain constant in the study area. The Proteobacteria appeared to be the most dominated phyla, followed by unassigned taxa, Firmicutes and Actinobacteria, and they were relatively significance in disturbed area of DF and DS samples. The finding showed significant differences in relative abundance of some phyla between undisturbed and disturbed areas. The higher relative abundance of some taxa such as *Novosphingobium* in UW and *Desulfobacter* in DS indicates the presence of pollutants in undisturbed and disturbed areas. Similarly, phylum Acidobacteria was apparently present throughout the undisturbed samples and was the most common bacterial group detected in undisturbed area.

Furthermore, among the three samples (soil, water and fish gut content), the soil samples recorded higher difference between the OTUs in undisturbed and disturbed areas. Hence, differential features of bacterial community in the soil were predicted. The metagenomics taxonomic features of soil samples showed ACK_M1, Hydrogenophilaceae and *Thiobacillus* were taxa biomarker that prevalent in undisturbed samples, whereas, the taxa biomarker identified in disturbed area were p_WPS_2, Planctomycetaia and Gemmatales. The discriminatory metagenomics features detected KO biomarkers through LEfSe which were notably higher in DS

samples, and most of them were associated with chemotaxis and related electron transfer. Whereas, majority of the KO biomarkers in US samples were linked with transport, adhesion of proteins and iron. The functional biomarkers detected in DS samples were connected to synthesis of proteins and amino acid related enzymes such as DNA replication, translation factors, RNA polymerase and aminoacyl_tRNAbiosynthesis were observed. In contrast, most of the functional biomarkers depicted in US samples related to metabolism and degradation of chemicals like ascorbate and alderate metabolism, C5_branched dibasic acid metabolism, biosynthesis and biodegradation of secondary metabolites, and dioxin degradation. Metagenome contribution by gene family in soil samples revealed Enterobacteriaceae and Aeromonadaceae, to be associated with K03088. However, only Moraxellaceae was predicted in DS sample which was linked to K03406. The higher number of taxa biomarker and metagenomic contribution by genes family were predicted in the DS samples. Thus, it suggests the presence of consortium of bacteria with synergistic or antagonistic actions of bacteria in the disturbed area, and this could have been the source of ecological difference between disturbed and undisturbed area of NSPSF.

Redundancy analysis was used to analyse and summarise the relationships between the anthropogenic activities, forest characteristics and water physico-chemical factors with bacterial taxa biomarker of soil samples in undisturbed and disturbed areas. The taxa biomarker connected to five anthropogenic activities of SA, AA, CR, DL and DHS including c_TK17, *Legionella*, p__WPS_2, *Spirochaeta* and *Acinetobacter* in DS samples. Interestingly, similar taxa biomarker particularly C__TK17, g__*Legionella*, p__WPS_2, g__*Spirochaeta* and g__*Acinetobacter* as obtained in anthropogenic factors were also were strongly linked to the two forest characteristics of RLI and PS that found in DS samples. Whereas, the members of Hydrogenophilaceae, *Thiobacillus*, *Candidatus Rhodoluna* and f__ACK_M1 and Methylococcales were the biomarkers that more localized in US samples with closer association to NO_3^-, turbidity and water depth.

In this study, some recommendations were proposed such as to regulate indiscriminate construction of canals, roads, and other buildings in the both undisturbed and disturbed areas. As such, environmental impact assessment should be carried out and this recommendation should be adhered prior to any project in and around NSPSF. On the forest characteristics, the seedlings could be complemented through artificial nurseries in undisturbed areas which recorded low PS. Despite the differences in environmental factors between disturbed and undisturbed areas, no significant difference obtained between the two areas in term of the bacterial diversity and composition. Interestingly, NO_3^-, turbidity and water depth have strong associations with taxa biomarker in undisturbed area. Thus, suggesting that change in these three factors could likely affect the distribution and abundance of species within the bacterial biomarker identified in NSPSF. Indeed, further study on metagenomics analysis of biotic and abiotic factors could be carried out to exploit the effects of seasonal variation on environmental conditions of NSPSF. Additionally, the unclassified taxa of bacterial community in NSPSF could also be investigated to bring out its taxonomical and functional features. This study could potentially provide guidelines for effective identification, remediation and restoration of degraded peat swamp forest, as well as give the insight in ecological monitoring and conservation of NSPSF and its environment.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

PENCIRIAN PERSEKITARAN DAN ANALISIS METAGENOMIK FAKTOR BIOTIK DAN ABIOTIK DI HUTAN PAYA GAMBUT UTARA, MALAYSIA

Oleh

SAADU HAMIDU

September 2020

Pengerusi : Profesor Madya Mohammad Noor Amal Azmai, PhD
Fakulti : Sains

Hutan Paya Gambut Selangor Utara (NSPSF) adalah salah satu ekosistem tanah gambut yang mengalami pelbagai ancaman seperti kebakaran hutan, pemburuan haiwan liar, perluasan kawasan untuk kegiatan pertanian dan perindustrian, pembinaan terusan, penebangan hutan, dan pencemaran udara, air dan tanah. Tambahan pula, kajian asas yang telah dilakukan di dalam ekosistem unik ini adalah terhad, terutamanya di dalam aspek ekologi mikrobiologi yang berkaitan dengan aktiviti antropogenik yang berterusan dalam hutan terlindung ini.

Secara umumnya, kajian ini menentukan pencirian persekitaran dan analisis metagenomik faktor biotik dan abiotik di Hutan Paya Gambut Utara Selangor, Selangor, Malaysia. Pertama, kajian ini menentukan pembolehubah persekitaran semasa kawasan tidak terganggu dan terganggu. Kedua, komposisi, diversiti dan penanda bio taksa bakteria oleh bakteria komuniti dalam kandungan usus ikan, air dan tanah di kawasan tidak terganggu dan terganggu dikenalpasti. Ketiga, taksa dan gen berfungsi bakteria di dalam kandungan tanah di kawasan tidak terganggu dan terganggu ditentukan. Akhir sekali, kajian ini mengenalpasti perhubungan di antara pembolehubah persekitaran dan penanda bio taksa bakteria dari tanah, dari kawasan tidak terganggu dan terganggu.

Untuk memahami kesan faktor semula jadi dan manusia pada komuniti bakteria di NSPSF, dua kawasan, iaitu NSPSF (tidak terganggu) dan kawasan berdekatannya (terganggu) telah dipilih dalam kajian ini. Di setiap kawasan, tiga lokasi dipilih, iaitu kawasan Hutan Paya Gambut Sungai Karang 1 (SKPSF-1), Hutan Paya Gambut Raja Musa (RMPSF) dan Hutan Paya Gambut Sungai Karang 2 (SKPSF-2) untuk kawasan yang tidak terganggu, manakala untuk kawasan yang terganggu, kawasan sawah padi (PF), kebakaran hutan (FF) dan penanaman kelapa sawit (OP) telah dipilih.

Pembolehubah persekitaran oleh aktiviti antropogenik, pencirian hutan dan parameter fizikokimia air di kawasan yang tidak terganggu dan terganggu telah ditentukan. Selepas itu, teknik metagenomik telah digunakan untuk menilai komposisi, diversiti, taksonomi penanda bio dan gen berfungsi bakteria kawasan tidak terganggu (U) dan terganggu (D) dari sampel kandungan usus ikan (UF dan DF), air (UW dan DW) dan tanah (US dan DS) di kawasan kajian, dan juga mengaitkan penemuan metagenomik ini dengan pembolehubah persekitaran yang telah ditentukan.

Hasil kajian ke atas aktiviti antropogenik mendapati kawasan yang terganggu mempunyai skor pencemaran air (WP), tanah (LP) dan kebisingan (NP) dan aktiviti pertanian (AA) yang lebih tinggi. Aktiviti antropogenik lain yang juga dicatatkan di kawasan terganggu adalah jarak dari penempatan manusia (DHS), tahap akses (SA) dan penebangan hutan (DL), dan merupakan aktiviti antropogenik utama di kawasan terganggu. Manakala aktiviti pembinaan (CR) merangkumi semua kawasan kajian. Semakin tinggi peratusan anak pokok (PS) dalam OP dan sebaliknya telah dicatatkan, manakala peratusan pokok (PT) dan jumlah pokok tumbang (FT) adalah lebih tinggi dalam SKPSF-1. PF di kawasan terganggu dicirikan oleh intensiti cahaya relatif (RLI) yang tinggi. Sebaliknya, RLI secara relatif adalah lebih rendah di kawasan yang tidak terganggu. Kawasan yang tidak terganggu menunjukkan nilai oksigen larut yang lebih rendah (DO) dan ketara meningkat dari kawasan yang tidak terganggu ke kawasan yang terganggu, terutamanya di PF dan OP. FF adalah pengecualian, yang dilihat memiliki kepekatan DO yang secara relatif lebih rendah. Beberapa aktiviti antropogenik seperti DHS, SA, DL dan AA berkorelasi rapat dengan NH_3-N dan Fe di kawasan yang terganggu, manakala pencemaran udara (AP) di kawasan yang tidak terganggu berkait dengan NO_3^-.

Analisis metagenomik di kawasan tidak terganggu dan terganggu menunjukkan kekayaan dan kepelbagaian komuniti bakteria pada 18 sampel kandungan usus ikan, air dan tanah. Tambahan pula, indeks alpha menunjukkan perbezaan yang signifikan ($p < 0.05$) di antara kawasan terganggu dan tidak terganggu untuk setiap sampel. Penipisan di antara sampel menunjukkan lekukan pada titik di mana bilangan organisma meningkat, tetapi jumlah spesies tetap sama di kawasan kajian. Proteobacteria merupakan filum yang paling mendominasi, diikuti oleh taksa *unassigned*, Firmicutes dan Actinobacteria, di mana mereka menunjukkan relatif kepentingan di kawasan terganggu pada sampel DF dan DS. Penemuan ini menunjukkan perbezaan yang signifikan dalam kelimpahan relatif beberapa filum di antara kawasan yang tidak terganggu dan terganggu. Kelimpahan relatif beberapa taksa seperti *Novosphingobium* dalam UW, *Desulfobacter* dalam DS menunjukkan kehadiran bahan pencemar di kawasan yang tidak terganggu dan terganggu. Begitu juga, filum Acidobacteria nampaknya hadir di seluruh sampel kawasan tidak terganggu dan merupakan kumpulan bakteria yang paling biasa dikesan di kawasan yang tidak terganggu. Pseudomonadales dan Desulfobacteraceae adalah taksa penanda bio yang lazim terdapat pada sampel yang tidak terganggu, manakala, penanda bio taksa yang dikenalpasti di kawasan terganggu adalah *Methylobacterium*, *Ralstonia* dan *Bacillus*.

Di samping itu, di antara ketiga sampel iaitu tanah, air dan kandungan usus ikan, sampel tanah merekodkan perbezaan OTU yang tinggi di antara kawasan tidak terganggu and terganggu. Demikian, perbezaan ciri komuniti bakteria di dalam sampel tanah telah diramalkan. Ciri metagenomik taksa di dalam sampel tanah menunjukkan ACK_M1, Hydrogenophilaceae dan *Thiobacillus* adalah antara taksa penanda bio yang lazim dijumpai di kawasan tidak terganggu, manakala taksa penanda bio di kawasan terganggu adalah p_WPS_2, Planctomycetaia and Gemmatales. Perbezaan ciri metagenomik mengesan penanda bio KO melalui LEfSe, dimana ia menunjukkan ciri yang tinggi di dalam sampel DS, dan kebanyakan daripada KO tersebut adalah berkaitan dengan kemotaksis dan pemindahan elektron. Kebanyakan penanda bio KO di sampel US adalah berkaitan dengan pemindahan, lekatan protein dan besi. Penanda bio fungsi yang hadir di dalam sampel DS menunjukkan hubungkait dengan protein sintesis dan enzim berkaitan denga asid amino, seperti replikasi DNA, faktor translasi, polimeras RNA dan aminoacyl_tRNAbiosintesis. Sebaliknya, kebanyakan penanda bio fungsi yang ditunjukkan di dalam sampel US adalah berkaitan dengan metabolisma dan degradasi kimia seperti metabolisma askorbat dan alderat, *C5_branched dibasic* metabolisma asid, biosintesis dan biodegradasi metabolit sekunder dan degradasi dioxin. Sumbangan metagenom oleh keluarga gene menunjukkan Enterobacteriaceae dan Aeromonadaceae adalah berkait rapat dengan K03088. Namun demikian, hanya Moraxellaceae yang diramal berkait rapat dengan K03406. Bilangan penanda bio taksa dan sumbangan metagenom oleh keluarga gen adalah antara yang tertinggi direkodkan di dalam sampel DS. Oleh yang demikian, ia menunjukkan bahawa bakteria konsortium hadir dengan sinergi atau aksi antagonistik di kawasan yang terganggu. Ini boleh menjadi salah satu sumber yang mendorong kepada perbezaan ekologi di antara kawasan terganggu dan kawasan tidak terganggu di NSPSF.

Analisis berlebihan telah digunakan untuk menganalisis dan meringkaskan hubungan di antara aktiviti antropogenik, pencirian hutan dan fizikokimia air dengan taksa penanda bio bakteria pada sampel tanah di kawasan tidak terganggu dan terganggu. Penanda bio taksa menghubungkan lima aktiviti antropogenik iaitu SA, AA, CR, DL dan DHA dengan c_TK17, *Legionella*, p__WPS_2, *Spirochaeta* and *Acinetobacter* di dalam sampel DS. Menariknya, penanda bio taksa yang sama seperti C__TK17, g__*Legionella*, p__WPS_2, g__*Spirochaeta* dan g__*Acinetobacter* menunjukkan hubungan yang kuat denga dua ciri hutan iaitu RLI dan PS yang dijumpai di dalam sampel DS. Selain itu, Hydrogenophilaceae, *Thiobacillus*, *Candidatus Rhodoluna* dan f__ACK_M1 merupakan antara penanda bio yang terdapat di dalam sampel US yang berhubung kait rapat dengan NO_3^-, kekeruhan dan kedalaman air.

Di dalam kajian ini, beberapa cadangan telah dikemukakan, termasuklah untuk mengatur urus pembinaan terusan, jalan raya dan bangunan lain di kawasan yang tidak terganggu dan terganggu. Oleh itu, penilaian terhadap kesan persekitaran harus dilakukan dan cadangan ini perlu dipatuhi sebelum sebarang projek dijalankan di dalam dan sekitar NSPSF. Di bawah kategori ciri hutan, pembenihan boleh dilakukan melalui nurseri tiruan di kawasan yang tidak terganggu dimana ia merekodkan PS yang rendah. Walaupun terdapat perbezaan di antara faktor alam sekitar di antara kawasan terganggu dan kawasan tidak terganggu, tiada perbezaan yang ketara ditunjukkan di kedua-dua kawasan tersbut dari segi diversiti dan komposisi bakteria. Menariknya, NO_3^-, kekeruhan dan kedalam air menunjukkan kesatuan yang kuat dengan penanda bio taksa di kawasan tidak terganggu. Dengan itu, ia menunjukkan bahawa perbuhan diantara tiga faktor tersebut akan memberi kesan kepada distribusi dan kebanyakan spesis di dalam penanda bio bakteria yang boleh dikesan di kawasan NSPSF. Tambahan pula, kajian lebih lanjut mengenai analisis metagenomik ke atas faktor biotik dan abiotik perlu dilakukan untuk mengeksploitasi pengaruh variasi musim terhadap keadaan persekitaran NSPSF. Tambahan itu, komuniti bakteria berstatus *unassigned* atau taksa yang tidak dapat diklasifikasi di NSPSF juga perlu disiasat untuk mencari ciri taksonomi dan fungsinya. Informasi dari kajian ini akan menambah nilai terhadap pengkalan data komuniti bakteria sedia ada di NSPSF. Tambahan pula, kajian ini berpotensi untuk memberi garis panduan untuk pengenalpastian, remediasi dan mengembalikan hutan paya gambut yang merosot dengan lebih efektif, di samping memberikan gambaran mengenai isu kesihatan umum, pemantauan ekologi dan konservasi NSPSF dan alam sekitarnya.

ACKNOWLEDGEMENTS

I want to express my profound gratitude to almighty Allah S.W.T for the successful completion of my PhD programme within the stipulated time frame. Foremost, my sincere gratitude goes to the chairman of my supervisory committee, Assoc. Prof. Dr. Mohammad Noor Amal Azmai for not only funding the research work, but also for his guidance, patience and constructive criticism during the conduct of this study. Besides that, I would like to thank the rest of my supervisory committee, Prof. Dr. Ahmad Ismail, Dr. Syaizwan Zahmir Zulkifli and Dr. Amalia Mohd Hashim, for their encouragement, insightful comments, and mentorship which guided me throughout the period of the research.

I would like to thank the effort of Federal College of Education Katsina, Nigeria, most especially the provost and deputy provost; Dr. Aliyu Idris Maikaji and Dr. Sam Ohanado respectively, for giving me the opportunity to further my study under the Tertiary Education Trust Fund staff training and development programme. I must salute Alhaji Danjuma Muhammad, Dr. Maharazu Mamman, Dr. Sabiru Dahiru Yusuf, Alhaji Badamasi Lurwan Gafai, and the entire staffs of School of Science, Federal College of Education, Katsina, Nigeria for all the support and encouragement.

I am grateful to all the participants of this research work, especially my fellow postgraduate students for their kind support and of course friendship particularly Jumria Sutra, Saba Abdulwakil and Dr. Nurliyana Mohamad who assisted me throughout this study. I must thank you all for the encouragement and support received. It really helped me to get the results of better quality. Similarly, thanks also to all staffs at the Department of Biology, Faculty of Science, and Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, who have directly or indirectly contributed to the success of this work.

Last but not the least, I would also like to thank my father, Malam Saadu and my mother, Hajia Saratu, brothers and sisters for all the encouragement received throughout this most challenging time in my academic career. Kudos to my children, Fatima, Ummi-salma, Muhammad, Aliyu, Alhassan, Khadija, Aminatu, Alhusain, Zainab, Amira and Abdallah for being so tolerant even when being ‘without dad’ was tough and coupled with their willingness to engage with the struggle and ensuing discomfort during my absence throughout the period of this study. A very special thanks to my wives, Nafisa and Fatima for their practical and emotional support, and for being not only dedicated, but also a loyal partner.

This thesis was submitted to the Senate of the Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

Mohammad Noor Amal Azmai, PhD
Associate Professor
Faculty of Science
Universiti Putra Malaysia
(Chairman)

Ahmad Ismail, PhD
Professor
Faculty of Science
Universiti Putra Malaysia
(Member)

Syaizwan Zahmir Zulkifli, PhD
Senior Lecturer
Faculty of Science
Universiti Putra Malaysia
(Member)

Amalia Mohd Hashim, PhD
Senior Lecturer
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Member)

ZALILAH MOHD SHARIFF, PhD
Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date: 10 June 2021

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

NSPSF	North Selangor Peat Swamp Forest
PSF	Peat swamp forests
NGS	next-generation sequencing
DNA	deoxyribonucleic acid
RNA	ribonucleic acid
DNA-Seq	deoxyribonucleic acid- Sequencing
16S rRNA	16 Svedberg unit/16 Subunit of ribosomal RNA
MGE	mobile genetic elements
PPFM	pink-pigmented facultative methylotrophic
ACC	aminocyclopropane-1-carboxylic acid
PAH	Polycyclic Aromatic Hydrocarbon
HTS	high throughput sequencing
PCR	polymerase chain reaction
O_2	oxygen
CO_2	carbon dioxide
CH_4	methane
NO_2	nitrite
NO_3	nitrate
Fe	iron
TDS	total dissolved solids
PO_4	phosphate oxide
SO_4	sulphate oxide
NH_3	ammonia
DO	dissolved oxygen
DOC	dissolved organic carbon
HCH	hexachlorocyclohexane
T	temperature

TU	turbidity
WD	water depth
ha	hectare
mm	millimeter
km^2	Kilometer square
km^2/year	Kilometer square per year
Mha	million hectare
m	meters’ square
mL	millilitre
$^{\circ}$C	degree centigrade
pH	presence of hydrogen ion concentration
Gt	Giga tonne
$<$	less than
$>$	greater than
$\leq$	less than or equal to
$\geq$	greater than or equal to
μ	micro
μL	microlitre
μm	micrometer
$	American Dollar
RM	Malaysian Ringgit
SE	standard error
SD	standard deviation
p	p- value/probability value
ANOVA	analysis of variance
PCA	Principal Component Analysis
CCA	Canonical Component Analysis
RDA	Redundancy Analysis

PERMANOVA	permutational multivariate ANOVA
ANOSIM	analysis of similarity
PAST	PAleontological STatistics
STAMP	statistical analysis of metagenomic profiles
SPPS	Statistical Package for Social Science
IBM SPSS	International Bussiness Machine Statistical Package for Social Science
NMDS	Non-Parametric Dimensional Scaling
n	Population size
H*o*	Null hypothesis
H*a*	Alternate hypothesis
IUCN	International Union for Conservation of Nature
ESA	Endangered Species Act
GEC	Global Environmental Conservation
NOS	National Ocean Service
UNDP	United Nations Development Programme
CDDEP	Center for Disease Dynamics Economics Policy
SERAS	Scientific Engineering Response and Analytical Servives
LULUCF	Land Use, Land-Use Change and Forest
GHG	greenhouse gas
FAO	Food Agricultural Organisation
BBFRE	Bukit Belata Forest Reserve Extension
SDFWR	Sungai Dusun Forest/Wildlife Reserve
RMPSF	Raja Musa Peat Swamp Forest
SKPSF	Sungai Karang Peat Swamp Forest
BLAST	Basic Local Alignment Search Tool
QIIME	Quantitative Insights Into Microbial Ecology
GG	GreenGenes
OTU	operational taxonomic unit

PICRUSt	Phylogenetic Investigation of Communities by Reconstruction of Unobserved States
NSTI	Nearest Sequenced Taxon Index
RDP	Ribosomal Database project
COG	Clusters of Orthologous Grou
LEfSe	Linear Discriminant Analysis (LDA) Effective Size
KEGG	Kyoto Encyclopedia of Genes and Genomes
KO	KEGG Ortholog
SRA	Sequence Read Archive
NCBI	National Center for Biotechnology Information
MS-222	(tricaine)methanesulfonate
EDTA	ethylenediaminetetraacetic acid
GH	glycoside hydrolase
H	actual tree height
h_1	eye height
h_2	height of tree above researcher's eye level
DBH	diameter at breast height
tan θ	tan theta
x	distance between the tree and researcher observing position
FC	Foot-Candle
LIC	Light intensity net under canopy
LIO	Light intensity net open space
CRD	Complete randomized design

CHAPTER 1

INTRODUCTION

1.1 Background of the study

North Selangor Peat Swamp Forest (NSPSF), like all other peatland ecosystems is subjected to various threats such as forest fire, expansion of area for industrial and agricultural activities, canal construction, deforestation, and air, water and land pollution (Elliott et al., 2015). Muda et al. (2012) reported that between the periods of 1997-1998, about 630 hectares (ha) of forest reserve was destroyed. Altogether, the landmass has been estimated to be about 6,500 ha is subjected to repeated forest fires (Turetsky et al., 2015). Thus, proactive actions should be taken to conserve and protect the area, in order to maintain the remaining endangered and endemic species of flora and fauna there (Muda et al., 2012).

Population growth leads to increasing agricultural activities in NSPSF (Adila et al., 2017). Other human related activity such deforestation and land clearing for agricultural activity might have been the cause of fire incidence in NSPSF, which lead to subsequently habitat degradation (Muda, et al, 2012). In this way, peat swamp forest (PSF), including the NSPSF, that use to be pristine is gradually being loss for good. In conjunction with canal excavation and other related of drainage, it initiates peat decomposition which subsequently lead to carbon emissions in PSF of South East Asia (Lampela et al., 2017). Following drainage and related human activity, an estimated of 600 tetragrams of carbon is being loss annually, while burning of peat due to fire incidence had also led to the emission of 640 tetragrams of carbon annually (Hooijer et al., 2006). As such, ecological and conservational management is important, and this require monitoring as core activity in biodiversity conservation (Marsh and Trenham, 2008).

The characterization of anthropogenic factors and microbial communities of polluted and degraded PSF could potentially provide guidelines for effective identification, remediation and restoration of such environments. The research findings could form the basis for library construction and the study of bacterial composition and abundance and its relationships between anthropogenic, forest and physicochemical factors of NSPSF.

1.2 Research problems

Peat swamp forest is an important ecosystem which serve many significance purposes, but it is constantly being disturbed, degraded and sometimes loss completely. Anthropogenic activities and other environmental related agents such as flooding (Hugron et al., 2013), fire and climate change (Xu et al., 2018) leading to contamination and destruction of such habitat are the major issues especially in countries of southeast Asia such as Vietnam, Thailand, Indonesia and Malaysia (Fitzherbert et al., 2008; Simpson, 2014; Lampela et al., 2017; Xu et al., 2018). Mining, logging, construction of buildings, roads, canals, agriculture and other related activities that could alter or lead to addition of substances consider to be harmful to the peat swamp ecosystem. As water pollution was observed along Tengi River of NSPSF following mining of tin, sand and clay (Irvine et al., 2013; GEC 2014a), pollution from manure and waste application in paddy field and oil palm plantation were also reported in NSPSF (Sule et al., 2019). Appropriate technologies and strategies are being devised toward remediation, rehabilitation and restoration of these polluted and degraded environments. The fact that the majority of the technologies developed and in use for the correction of the environmental abnormality in question exploit the potential of biological systems, in particular microbial systems (Mukherjee et al., 2017). Microbes is often grown on pollutants produced by anthropogenic related agents and much of the research conducted on bioremediation has concentrated on the capabilities of a single or couple of microbes exhibiting robust and effective growth on such pollutants (Mukherjee et al., 2017). Peat accumulates following inhibition of the microbial activities due to waterlogged anaerobic conditions and the recalcitrant plant detritus, resulting in an acidic, toxic and phenol-rich peat substrate (Too et al., 2018). However, anthropogenic activity may likely lead to change in bacterial community, thereby affecting the accumulated peat of NSPSF. For instance, construction and excavation are processes which requires both removal of the primary vegetation and soil drainage, the latter resulting in peat shrinkage through a combination of water loss, enhanced aerobic decomposition as the diversity and composition of bacterial community in PSF is altered. As at 2010, 233 million tonnes of CO_2 have been produced and loss through decomposition (CO_2 production) of organic matter losses resulting from subsidence of drained and cultivated peat in Malaysia (Page and Rieley, 2006). This imply that maintaining the status quo of the bacterial community in NSPSF means protecting it against degradation and destruction.

The forest vegetation is an important component of the PSF as it covers and protect the forest floor against excessive temperature (GEC, 2014b). This could adversely affect the functioning of bacteria. And bearing in mind the ecological roles of bacteria as an agent of disintegration, decomposition of dead organisms and subsequently recycling organic nutrients (De Boer, 2017). Notably, the nutrient deficient condition of PSF is evident by the low elemental content of the peat, while forest growth is dependent upon the supply of nutrients (Page and Rieley, 2006). Thus, it’s prompted the need for better understanding of bacterial community which recycle the existing nutrient pool within the NSPSF ecosystem.

Additionally, bioremediation could be employed as alternative solution in converting degraded and polluted environment (Mukherjee et al., 2017). Environmental bioremediation is usually a complex process involving co-metabolism, cross-induction, inhibition and non-interaction among microbes. The synergistic and sometimes antagonistic actions of microbes is possibly due to nature of the pollutants, which come from a mixture of different substances and therefore are used differently by different microbes. Thus, bioremediation is necessary. Bioremediation is a conversation of pollutants to less harmful substances through a process mediated by living organisms including consortium of microbes rather than a few, and hence, characterization of microbial communities of NSPSF could potentially provide guidelines for effective remediation and restoration of such environments (Mukherjee et al., 2017). Furthermore, available research and knowledge of the bacteria in NSPSF is often confined to traditional culture methods (Yooseph et al., 2013). Moreover, there is limited literature on the metagenomic study of bacterial community particularly in relation to environmental characteristics of NSPSF.

Until recently, microbes were studied traditionally by using a few numbers of microorganisms of interest, where it will be isolated from source materials (such as blood, soil, water or air), given the restrictions of the composition of culture media which cannot reflect and mimic the dynamic nutrient fluxes of the source environment. Indeed, only 1% of microorganisms were found to be cultivable using a set of media from the highly characterized soil rhizosphere (Mukherjee et al., 2017). Therefore, using traditional culture methods will only capture minute representation of those microbes in their habitats (Vieira and Nahas, 2005).

Another vital role play by peat swamp forest is housing of rare, threaten and endangered fish species (Ismail, 2015). There are many distinctive fish species collected and use as food, and ornamental and other recreational purposes (Song et al., 2013). The bacteria may be a cheap source of pathogens causing infectious diseases to fish living in the wild (Sudheesh, et al., 2012). The disease outbreaks against aquatic animal have increased in an alarming rate (Chen et al., 2018). The bacterial related infections from such outbreak could result in massive fish deaths. Since ecosystem is an interconnected process, which linked biotic elements among themselves and connects them with abiotic components hence, the degradation which affects one or more organisms could invariably affect all the dwelling organisms in the ecotone. Notably, increasing residential and agricultural activities could directly affect the flowing water thereby increase in potential water pollutant which most likely ends in NSPSF (Adila et al., 2017). Moreover, some bacteria in the fish gut help maintain metabolic homeostasis in the fish (Li et al., 2020). While some bacteria are source of fish feeds as they may provide vital nutritional sources of diet to fish. Thus, many bacteria activate beneficial biological activities and promote healthy growth of the host (Banerjee et al., 2000; Wang et al., 2019). Having said that, then it’s vital to study the environmental factors, the bacterial community in the soil, water as well as host organism in the NSPSF. Study of bacterial community in the host organism such as fish gut contents could give information and better picture of beneficial and harmful bacteria. The intruding and threatening bacteria which could subsequently endangered fish host. Therefore, this research will enhance knowledge of fish gut microbiota in the study area.

The next-generation sequencing methods (NGS) include a variety of procedures to study any biological system such as amplicon sequencing (for various identification and phylogenetic surveys), whole genome shotgun sequencing (for single organism genome and metagenomes) and DNA-Seq. This technique allowed us to investigate the entire complement of organisms inhabiting a certain environment. The availability of bioinformatics tools for prediction of functions i.e. metagenomes, from 16S DNA gene sequences is particularly attractive to microbial ecologists, as it allows them to study the metabolomes of complex microbial communities with reasonable precision and confidence at a high taxonomic resolution, while being able to construct robust hypotheses for further works. It has been reported that soil microbial communities respond to environmental change by changing their taxonomic and functional composition, and any functional shift means alteration in the physiological responses of the bacteria which can be detected using metagenomics signatures of the study area (Pold, 2019). The identification of the environmental parameters influencing the composition and functions of bacteria in NSPSF will give insight toward a better understanding of bacterially mediated processes.

Unfortunately, despite the large amount of work done on microbial community composition, no attempt has been made to find differential metagenomics signatures through DNA sequencing in soil, water and fishes of NSPSF. The aim of the present study is to assess the profile of bacterial community using metagenomic analysis and characterize environmental factors in and nearby NSPSF, as well as to evaluate the relationship between the significant environmental factors and functional genes of the bacterial community.

1.3 Objectives of the study

The specific objectives include:

1. To identify the environmental characteristics of undisturbed NSPSF and its adjacent disturbed area.
2. To determine the composition and diversity of bacterial communities in fish gut contents, water and soil of undisturbed NSPSF and its adjacent disturbed area, Selangor, Malaysia.
3. To determine the differential features and core bacterial communities in soil samples from undisturbed NSPSF and its adjacent disturbed area.
4. To evaluate the relationships between the environmental variables with bacterial taxa biomarker in soil samples from undisturbed NSPSF and its adjacent disturbed area.

1.4 Limitation of the study

Metagenomics sequencing used to be expensive, which can be a limiting factor for microbial ecology research in limited funded projects. Analysis of metagenomics sequencing datasets is manifold computationally intensive and gene analyses will require many advanced software. It thereby escalates further the operational costs. Moreover, pooling the fish gut content of all fish’s species for determination of bacterial diversity and composition may alter the fish gut metagenomic data as different fish species could have different microbiome diversity.

REFERENCES

Abanda-Nkpwatt, D., Musch, M., Tschiersch, J., Boettner, M., & Schwab, W. (2006). Molecular interaction between Methylobacterium extorquens and seedlings: growth promotion, methanol consumption, and localization of the methanol emission site. Journal of Experimental Botany, 57(15):4025–4032.

Abazari, M., Owlia, P., Zarrini, G. and Aghdasinia, H. (2020). Isolation of Methylococcus Strain Resistant to Abnormal Climate Change to Reduce Methane Emissions from the Iranian Salt Lake. Geomicrobiology Journal, 37(7): 610-617.

Adila, N., Sasidhran, S., Kamarudin, N., Puan, C.L., Azhar, B. and Lindenmayer, D.B. (2017). Effects of peat swamp logging and agricultural expansion on species richness of native mammals in Peninsular Malaysia. Basic and Applied Ecology, 22: 1-10.

Aguirre, M., Abad, D., Albaina, A., Cralle, L., Goñi-Urriza, M.S., Estonba, A. and Zarraonaindia, I. (2017). Unraveling the environmental and anthropogenic drivers of bacterial community changes in the Estuary of Bilbao and its tributaries. PLOS One, 12(6): e0178755.

Ahmad, M.F. and Samat, A. (2015). Species composition and abundance of peat swamp fishes in selected areas of Selangor, Malaysia. Malaysian Applied Biology, 44(1): 139-146.

Ahmed, W., Staley, C., Hamilton, K.A., Beale, D.J., Sadowsky, M.J., Toze, S. and Haas, C.N. (2017). Amplicon-based taxonomic characterization of bacteria in urban and peri-urban roof-harvested rainwater stored in tanks. Science of the Total Environment, 576: 326-334.

Ainuddin, N.A. and Goh, K. (2010). Effect of forest fire on stand structure in Raja Musa Peat Swamp Forest Reserve, Selangor, Malaysia. Journal of Environmental Science and Technology, 3(1): 56-62.

Alexandrino, D.A.M., Mucha, A.P., Almeida, C.M., Gao, W., Jia, Z. and Carvalho, M.F. (2017). Biodegradation of the veterinary antibiotics enrofloxacin and ceftiofur and associated microbial community dynamics. Science of the Total Environment, 581-582: 359-368.

Allan L. Truant, Rajeev Gulati, Olarae Giger, Vilas Satishchandran, James G. Caya, (1998). Methylobacterium species: an increasingly important opportunistic pathogen. Laboratory Medicine, 29(11): 1-7.

Anamulai S, Sanusi R, Zubaid A, Lechner A.M, Ashton-Butt A. and Azhar B. (2019). Land use conversion from peat swamp forest to oil palm agriculture greatly modifies microclimate and soil conditions. Peer J, 7: e7656.

Anders, J.M. (2012). Forests-their influence upon climate and rainfall. American Society of Naturalists, 16(1): 19-30.

Armstrong, A.H., Shugart, H.H. and Fatoyinbo, T.E. (2011). Characterization of community composition and forest structure in a Madagascar lowland rainforest. Tropical Conservation Science, 4(4): 428-444.

Arcand, M.M., Levy-Booth, D.J. and Helgason, B.L. (2017). Resource legacies of organic and conventional management differentiate soil microbial carbon use. Frontiers in Microbiology, 8: 1-17.

Aw, Y.K., Ong, K.S., Lee, L.H., Cheow, Y.L., Yule, C.M. and Lee, S.M. (2016). Newly isolated *Paenibacillus tyrfis* sp. nov., from Malaysian tropical peat swamp soil with broad spectrum antimicrobial activity. Frontiers in Microbiology, 7:1-9.

Azhar, B., Lindenmayer, D.B., Wood, J., Fischer, J., Manning, A., McElhinny, C. and Zakaria, M. (2011). The conservation value of oil palm plantation estates, smallholdings and logged peat swamp forest for birds. Forest Ecology and Management, 262 (12): 2306-2315.

Bacosa, H. P., Erdner, D. L., Rosenheim, B. E., Shetty, P., Seitz, K. W., Baker, B. J. and Liu, Z. (2018). Hydrocarbon degradation and response of seafloor sediment bacterial community in the northern Gulf of Mexico to light Louisiana sweet crude oil. The ISME Journal, 12(10):2532-2543.

Baillie, J. E. M., Hilton-taylor, C. & Stuart, S. N. (2004). 2004 IUCN Red List of Threatened Species A Global Species Assessment. World Conservation Union, pp. 217.

Baldani, J.I., Rouws, L., Cruz, L.M., Olivares, F.L., Schmid, M. and Hartmann, A. (2014). The Family Oxalobacteraceae. In: Rosenberg, E., DeLong, E.F., Lory, S., Stackebrandt, E., Thompson F. (eds) The Prokaryotes. Springer, Berlin, Heidelberg, pp. 919-974.

Baldrian, P. (2017). Forest microbiome: Diversity, complexity and dynamics. FEMS Microbiology Reviews*, 41*(2):109-130.

Balkwill, D.L., Drake, G.R., Reeves, R.H., Fredrickson, J.K., White, D.C., Ringelberg, D.B. and Spadoni, C.M. (1997). Taxonomic study of aromatic-degrading bacteria from deep-terrestrial-subsurface sediments and description of *Sphingomonas aromaticivorans* sp. nov., *Sphingomonas subterranea* sp. nov., and *Sphingomonas stygia* sp. nov. International Journal of Systematic Bacteriology, 47(1): 191-201.

Balkwill, D.L., Fredrickson, J.K. and Romine, M.F. (2006). Sphingomonas and related genera. The Prokaryotes, 7:605-629.

Banerjee, S., Azad, S.A., Vikineswary, S., Selvaraj, O.S. and Mukherjee, T.K. (2000). Phototrophic bacteria as fish feed supplement. Asian-Australian Journal of Animal Science. 13(7): 991-994.

Bao, K., Wang, G., Jia, L. and Xing, W. (2019). Anthropogenic impacts in the Changbai Mountain region of NE China over the last 150 years: geochemical records of peat and altitude effects. Environmental Science and Pollution Research, 26:7512-7524

Bashir, M.J.K., Aziz, H.A., Amr, S.S.A., Sethupathi, S.A.P., Ng, C.A. and Lim, J.W. (2014). The competency of various applied strategies in treating tropical municipal landfill leachate. Desalination and Water Treatment, 54(9): 1-14.

Beamisha, F.W.H., Beamish, R.B and Lim, SL-H. (2003). Fish assemblages and habitat in a Malaysian blackwater peat swamp, Environmental Biology of Fishes 68(2003): 1–13.

Beare, P.A., Samuel, J.E., Howe, D., Virtaneva, K., Porcella, S.F. and Heinzen, R.A. (2006). Genetic diversity of the Q fever agent, *Coxiella burnetii*, assessed by microarray-based whole-genome comparisons. Journal of Bacteriology, 188(7): 2309-2324.

Bengtson, P., Sterngren, A.E. and Rousk, J. (2012). Archaeal abundance across a pH gradient in an arable soil and its relationship to bacterial and fungal growth rates. Applied and Environmental Microbiology, 78(16): 5906-5911.

Bezuijen, MR., Webb, G.J.W., Hartoyo, P. and Samedi, R. (2001). Peat swamp forest and the false gharial *Tomistoma schlegelii* (Crocodilia, reptilia) in the Merang River, Eastern Sumatra, Indonesia. Oryx, 35(4): 301-307.

Biagioni, S., Krashevska, V., Achnopha, Y., Saad, A., Sabiham, S. and Behling, H. (2015). 8000 years of vegetation dynamics and environmental changes of a unique inland peat ecosystem of the Jambi Province in Central Sumatra, Indonesia. Palaeogeography, Palaeoclimatology, Palaeoecology, 440: 813-829.

Bigot, C., Meile, J.C., Remize, F. and Strub, C. (2015). Applications of metagenomics to fermented foods. Fermented foods. Part I, Biochemistry and Biotechnology, CRC Press.

Blagodatskaya, E. and Kuzyakov, Y. (2013). Soil biology and biochemistry active microorganisms in soil: critical review of estimation criteria and approaches. Soil Biology and Biochemistry, 67: 192-211.

Boden, R., Hutt, L.P. and Rae, A.W. (2017). Reclassification of *Thiobacillus aquaesulis* (Wood and Kelly, 1995) as *Annwoodia aquaesulisgen*. nov., comb. nov., transfer of *Thiobacillus* (Beijerinck, 1904) from the Hydrogenophilales to the Nitrosomonadales, proposal of Hydrogenophilalia class. nov. within the 'Proteobacteria', and four new families within the orders Nitrosomonadales and Rhodocyclales. International Journal Systematic Evolution Microbiology, 67: 4205-4209.

Bojko, J., Dunn, A.M., Stebbing, P.D., van Aerle, R., Bacela-Spychalska, K., Bean, T.P. and Stentiford, G.D. (2018). "*Candidatus aquirickettsiella gammari*" (Gammaproteobacteria: Legionellales: Coxiellaceae): A bacterial pathogen of the freshwater crustacean *Gammarus fossarum* (Malacostraca: Amphipoda). Journal of Invertebrate Pathology, 156: 41-53.

Bouhajja, E., Agathos, S.N. and George, I.F. (2016). Metagenomics: probing pollutant fate in natural and engineered ecosystems. Biotechnology Advances, 34(8): 1413-1426.

Brower, J.E., Zar, J.H. and Ende., C. von. (1998). Field and laboratory methods for general ecology. Retrieved from http://www.sisal.unam.mx/labeco/LabB_Ecologicia /Ecologia_de_Poblaciones_y_Comunidades_files/GeneralEcology.pdf

Campbell, B.J. (2014). The family Acidobacteriaceae. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E. and Thompson F. (eds). The Prokaryotes. Springer, Berlin, Heidelberg.

Cano, R. and Borucki, M. (1995). Revival and identification of bacterial spores in 25- to 40-million-year-old Dominican amber. Science, 268(5213): 1060-1064.

Cao, X., Liu, J., Chen, J., Zheng, G., Kuntner, M. and Agnarsson, I. (2016). Rapid dissemination of taxonomic discoveries based on DNA barcoding and morphology. Scientific Reports, 6: 1-13.

Caporaso, JG., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F.D., Costello, E.K. and Knight, R. (2010). QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 7(5): 335-336.

Carpousis, A.J. (2007). The RNA degradosome of *Escherichia coli*: An mRNA-degrading machine assembled on RNase E. Annual Review of Microbiology, 61(1): 71-87.

Casati, S., Conza, L., Bruin, J., and Gaia, V. (2010). Compost facilities as a reservoir of Legionella pneumophila and other Legionella species. Clinical Microbiology and Infection, 16(7): 945–947.

Catão, E.C.P., Lopes, F.A.C., Araújo, J.F., de Castro, A.P., Barreto, C.C., Bustamante, M.M.C. and Krüger, R.H. (2014). Soil acidobacterial 16S rRNA gene sequences reveal subgroup level differences between Savanna-like Cerrado and Atlantic forest Brazilian biomes. International Journal of Microbiology, 2014: 1-12.

Chávez-Romero, Y., Navarro-Noya, Y.E., Reynoso-Martínez, S.C., Sarria-Guzmán, Y., Govaerts, B., Verhulst, N. and Luna-Guido, M. (2016). 16s metagenomics reveals changes in the soil bacterial community driven by soil organic C, Nfertilizer and tillage-crop residue management. Soil and Tillage Research, 159: 1-8.

Chen, Y., Shi, M., Cheng, Y., Zhang, W., Tang, Q. and Xia, X. Q. (2018). FVD: The fish-associated virus database. *Infection, Genetics and Evolution*, 58(August 2017):23–26.

Chimner, R.A. and Ewel, K.C. (2005). A tropical freshwater wetland: II. Production, decomposition, and peat formation. Wetlands Ecology and Management, 13(6): 671-684.

Chowdhury, S.P., Hartmann, A., Gao, X. and Borriss, R. (2015). Biocontrol mechanism by root-associated *Bacillus amyloliquefaciens* FZB42 - a review. Frontiers in Microbiology, 6: 1-11.

Chroňáková, A., Schloter-Hai, B., Radl, V., Endesfelder, D., Quince, C., Elhottová, D. and Schloter, M. (2015). Response of archaeal and bacterial soil communities to changes associated with outdoor cattle overwintering. PLOS One, 10(8): e0135627.

Cleary, DFR, Becking L.E, Voogd N.J, Pires A.C.C, Polónia ARM, Egas, C. and Gomes, N.C.M. (2013). Habitat-and host-related variation in sponge bacterial symbiont communities in Indonesian waters. FEMS Microbial Ecology, 85: 465-482.

Clemons, W.M., May, J.L. C., Wimberly, B.T., McCutcheon, J.P., Capel, M.S. and Ramakrishnan, V. (1999). Structure of a bacterial 30S ribosomal subunit at 5.5 Å resolution. Nature, 400(6747): 833-840.

Collins-Fairclough, A.M., Co, R., Ellis, M.C. and Hug, L. A. (2018). Widespread antibiotic, biocide, and metal resistance in microbial communities inhabiting a municipal waste environment and anthropogenically impacted river. Applied and Environmental Science, 3(5): 1-17.

Crib, T., Arms, C., Sy, S., Asia, S.E., Kay, G., Ball, J. and See, L.S. (2008). President: Chair: Technical Director: Treasurer: Independent examiner: Special Issue: REDD and the Evolution of an International Forest Regime Europe.

Cui, J., Zhao, J., Wang, Z., Cao, W., Zhang, S., Liu, J. and Bao, Z. (2020). Diversity of active root-associated methanotrophs of three emergent plants in a eutrophic wetland in northern China. AMB Expr 10(48):1-9.

Czekalski, N., Berthold, T., Caucci, S., Egli, A. and Bürgmann, H. (2012). Increased levels of multiresistant bacteria and resistance genes after wastewater treatment and their dissemination into Lake Geneva, Switzerland. Frontiers in Microbiology, 3: 1-18.

De Boer, W. (2017). Upscaling of fungal–bacterial interactions: from the lab to the field. Current Opinion in Microbiology, 37(2017): 35–41.

Dedysh, S.N. and Knief, C. (2018). Diversity and phylogeny of described aerobic methanotrophs. Methane biocatalysis: paving the way to sustainability. Springer International Publishing.

Denny, T. (2006). Plant pathogenic *Ralstonia* species. Gnanamanickam, S (ed.) Plant-associated bacteria. Springer Publishing, Dordrecht, Netherlands.

Derr, P., Boder, E., & Goulian, M. (2006). Changing the Specificity of a Bacterial Chemoreceptor. Journal of Molecular Biology, 355(5): 923–932.

Deris, Z.Z., Akter, J., Sivanesan, S., Roberts, K.D., Thompson, P.E., Nation, R.L. and Velkov, T. (2013). A secondary mode of action of polymyxins against Gram-negative bacteria involves the inhibition of NADH-quinone oxidoreductase activity. The Journal of Antibiotics, 67(2): 147-151.

Devarapalli, P. and Kumavath, R.N. (2015). Metagenomics a technological drift in bioremediation. Advances in bioremediation of wastewater and polluted soil. Intech Open, London.

Diemont, H., Hillegers, P.JM., Joosten, H. and Wosten, H. (2002). Fire and peat forests, what are the solutions? Conference: Workshop on prevention and control of fire in peatlands, 19-21 March 2002, Kuala Lumpur, Malaysia.

Díaz-Flores, Á., Montero, J.C., Castro, F.J., Alejandres, E.M., Bayón, C., Solís, I. and Rodríguez, G. (2015). Comparing methods of determining *Legionella* spp. in complex water matrices. BMC Microbiology, 15(1): 1-11.

Dogra, C., Raina, V., Pal, R., Suar, M., Lal, S., Gartemann, K.H. and Lal, R. (2004). Organization of lin genes and IS6100 among different strains of hexachlorocyclohexane-degrading *Sphingomonas paucimobilis*: evidence for horizontal gene transfer. Journal of Bacteriology, 186(8): 2225-2235.

Dolan, R., Buckingham, H., Jones, P., Astbury, S. and Evans, C.D. (2017). Historical peat loss explains limited short-term response of drained blanket bogs to rewetting. Journal of Environmental Management, 188: 278-286.

Dominguez-Bello, M.G., De Jesus-Laboy, K. M., Shen, N., Cox, L.M., Amir, A., Gonzalez, A. and Clemente, J. C. (2016). Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. Nature Medicine, 22(3): 250-253.

Doughari, H.J., Ndakidemi, P.A., Human, I.S. and Benade, S. (2011). The ecology, biology and pathogenesis of *Acinetobacter* spp.: an overview. Microbes and Environments, 26(2): 101-112.

Dourado, M.N., Aparecida, C.N.A., Santos, D.S. and Araújo, W.L. (2015). Biotechnological and agronomic potential of endophytic pink-pigmented methylotrophic *Methylobacterium* spp. BioMed Research International, 2015: 1-19.

Edgar, R.C. (2010). Search and clustering orders of magnitude faster than BLAST. Bioinformatics, 26(19): 2460-2461.

Edgar, R.C., Haas, B.J., Clemente, J.C., Quince, C. and Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection. Bioinformatics, 27(16): 2194-2200.

Elliott, D.R., Caporn, S.J.M., Nwaishi, F., Nilsson, R.H. and Sen, R. (2015). Bacterial and fungal communities in a degraded ombrotrophic peat land undergoing natural and managed re-vegetation. PLOS One, 10(5): 1-20.

Elzinga, C.L., Salzer D.W. and Willoughby, J.W. (1998). Measuring and monitoring plant populations. U.S. Bureau of Land Management Papers. Bureau of Land Management National Business Center, Denver.

Fanning, S., Proos, S., Jordan, K. and Srikumar, S. (2017). A review on the applications of next generation sequencing technologies as applied to food-related microbiome studies. Frontiers in Microbiology, 8: 1-16.

FAO (2012). Global forest land-use change 1990-2005. FAO Forestry Paper 169. Food and Agriculture Organization of the United Nations, Rome.

FAO (2007). State of the world’s forests. Food and Agriculture Organization of the United Nations, Rome.

FAO (2006). The State of Food and Agriculture. Food aid for food security? Food and Agriculture Organization of the United Nations, Rome.

FAO (2020). Red palm weevil: guidelines on management practices. Food and Agriculture Organization of the United Nations, Rome.

Fatimawali, Kepel, B. J., Gani, M. A., & Tallei, T. E. (2020). Comparison of Bacterial Community Structure and Diversity in Traditional Gold Mining Waste Disposal Site and Rice Field by Using a Metabarcoding Approach. International Journal of Microbiology, 2020: 1–8.

Felipe, H.C., João V R., Ferreira, A.S.S., Ida, C.N.D., Denise, M.M.P. and Alexander, M.C. (2014). Metagenomic profiling for assessing environmental healthy. In Camilla, B. (ed). Microbiology research advances metagenomics methods, applications and perspectives. Nova Science Publishers, New York.

Ferrández, A., Miñambres, B., García, B., Olivera, E. R., Luengo, J. M., García, J. L. and Díaz, E. (1998). Catabolism of phenylacetic acid in *Escherichia coli*. Journal of Biological Chemistry, 273(40): 25974–25986.

Flower, A.M. (2007). The SecY translocation complex: convergence of genetics and structure. Trends in Microbiology, 15(5): 203-210.

Fiałkiewicz-Kozieł, B., Kołaczek, P., Piotrowska, N., Michczyński, A., Łokas, E., Wachniew, P. and Sensuła, B. (2014). High-resolution age-depth model of a peat bog in Poland as an important basis for paleoenvironmental studies. Radiocarbon, 56(1): 109-125.

Fiałkiewicz-Kozieł, B., De Vleeschouwer, F., Mattielli, N., Fagel, N., Palowski, B., Pazdur, A. and Smieja-Król, B. (2018). Record of anthropocene pollution sources of lead in disturbed peatlands from Southern Poland. Atmospheric Environment, 179: 61-68.

Fisher, J.C., Levican, A., Figueras, M.J. and McLellan, S.L. (2014). Population dynamics and ecology of *Arcobacter* in sewage. Frontiers in Microbiology, 5: 525.

Fitzherbert, E., Struebig, M., Morel, A., Danielsen, F., Bruhl, C., Donald, P. and Phalan, B. (2008). How will oil palm expansion affect biodiversity? Trends in Ecology and Evolution, 23(10): 538-545.

Forsberg, K.J., Reyes, A., Wang, B., Selleck, EM., Sommer, M.O.A. and Dantas, G. (2012). The shared antibiotic resistome of soil bacteria and human pathogens. Science, 337(6098): 1107-1111.

Foysal, M.J., Momtaz, F., Kawser, A.Q.M.R., Chaklader, M.R., Siddik, M.A.B., Lamichhane, B. and Fotedar, R. (2019). Microbiome patterns reveal the transmission of pathogenic bacteria in hilsa fish (*Tenualosa ilisha*) marketed for human consumption in Bangladesh. Journal of Applied Microbiology, 126(6): 1879-1890.

Gao, S., Pan, L., Huang, F., Song, M., Tian, C. and Zhang, M. (2018). Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp (*Litopenaeus vannamei*). Aquaculture, 499: 109-118.

Gao, W., Hodgkinson, L., Jin, K., Watts, C.W., Ashton, R.W., Shen, J. and Whalley, W.R. (2016). Deep roots and soil structure. Plant Cell and Environment, 39(8): 1662-1668.

Garrido-Sanz, D., Redondo-Nieto, M., Guirado, M., Pindado Jiménez, O., Millán, R., Martin, M. and Rivilla, R. (2019). Metagenomic insights into the bacterial functions of a diesel-degrading consortium for the rhizoremediation of diesel-polluted soil. Genes, 10(6): 456.

Gasim, M.B., Ismail, B.S., Toriman, E., Mir, S.I. and Chek, T.C. (2007). A physico-chemical assessment of the Bebar River, Pahang, Malaysia. Journal of Biological Sciences, 9: 730-737.

Gastauer, M., Caldeira, C.F., Ramos, S.J., Silva, D.F. and Siqueira, J. (2019). Active rehabilitation of Amazonian sand mines converges soils, plant communities and environmental status to their predisturbance levels. Land Degradation and Development, 31(5): 607-618.

Garrity, G.M., Bell, J.A. and Lilburn, T. (2015). Oxalobacteraceae fam. nov. Bergey's Manual of Systematics of Archaea and Bacteria, Springer, New York.

Gene S. Helfman, Bruce B. Collette, D. E. F. (2009). *The diversity of fishes: Biology, Evolution, and Ecology*. Southern Gate, Chichester: Blackwell Publishing. Pp1-737.

Gerard, V. A. (1984). The light environment in a giant kelp forest: influence of *Macrocystis pyrifera* on spatial and temporal variability. Marine Biology, 84(2): 189-195.

Ghosh, R., Barman, S. and Mandal, N.C. (2019). Phosphate deficiency induced biofilm formation of *Burkholderia* on insoluble phosphate granules plays a pivotal role for maximum release of soluble phosphate. Scientific Reports, 9(1): 5477.

Giesen, W. and Macdonald, E.M. (2016). Project report for master plan for the conservation and guidelines for the rehabilitation of degraded peat swamp forests in Central Kalimantan master plan for the conservation and development of the ex-mega rice project area. Jakarta, Indonesia.

Global Environment Centre. (2014a). Integrated management plan for North Selangor Peat Swamp Forest 2014-2023. Selangor State Forestry Department, Volume 1. pp. 185.

Global Environment Centre. (2014b). Integrated management plan for North Selangor Peat Swamp Forest 2014-2023. Selangor State Forestry Department, Volume 2. pp 217.

Goh, K.J., Teo, C.B., Chew, P.S. and Chiu, S.B. (1999). Fertiliser management in oil palm: agronomic principles and field practices. In: Fertiliser management for oil palm plantations. 20-21 September 1999. ISP North-East Branch, Sandakan, Malaysia.

Goldford, J.E., Lu, N., Bajić, D., Estrela, S., Tikhonov, M., Sanchez-Gorostiaga, A. and Sanchez, A. (2018). Emergent simplicity in microbial community assembly. Science, 361(6401): 469-474.

Gupta, S. and Pandey, S. (2019). ACC Deaminase producing bacteria with multifarious plant growth promoting traits alleviates salinity stress in French bean (*Phaseolus vulgaris*) Plants. Frontiers in Microbiology, 10: 1-17.

Grady, E.N., MacDonald, J., Liu, L., Richman, A., and Yuan, Z.C. (2016). Current knowledge and perspectives of *Paenibacillus*: a review. Microbial Cell Factories, 15(2016): 203.

Greninger, A.L. (2018). The challenge of diagnostic metagenomics. Expert Review of Molecular Diagnostics, 18(7): 605-615.

Green, P.N. (2006). Methylobacterium. The Prokaryotes. In: Dworkin M., Falkow S., Rosenberg E., Schleifer KH. And Stackebrandt E. (eds). The Prokaryotes. Springer, New York.

Grossi, C.E.M, Fantino, E., Serral, F., Zawoznik, M.S., Fernandez, D.D.A. and Ulloa, R.M. (2020). *Methylobacterium* sp. 2A is a plant growth-promoting rhizobacteria that has the potential to improve potato crop yield under adverse conditions. Frontiers in Plant Science, 11: 71.

Grützke, J., Malorny, B., Hammerl, J.A., Busch, A., Tausch, S.H., Tomaso, H. and Deneke, C. (2019). Fishing in the soup - pathogen detection in food safety using metabarcoding and metagenomic sequencing. Frontiers in Microbiology, 10: 1-15.

Haas, B.J., Gevers, D., Earl, A.M., Feldgarden, M., Ward, D.V. and Giannoukos, G. (2011). Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. Genome Research, 21: 494-504.

Hakan, R. and Jeglum, J.K. (2013). The biology of peat lands (Second). Oxford: Oxford University Press.

Harms, W.R., Schreuder, H.T., Hook, D.D. and Brown, C.L. (1980). The effects of flooding on the swamp forest in Lake Ocklawaha, Florida. Ecology, 61(6), 1412-1421.

Hausmann, B., Knorr, K.H., Schreck, K., Tringe, S.G., Glavina del Rio, T., Loy, A. and Pester, M. (2016). Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. The ISME Journal, 10(10): 2365-2375.

Hausmann, B., Pelikan, C., Herbold, C.W., Köstlbacher, S., Albertsen, M., Eichorst, S.A. and Loy, A. (2018). Peatland *Acidobacteria* with a dissimilatory sulfur metabolism. The ISME Journal, 12(7): 1729-1742.

Hergoualc'h, K., Gutiérrez-Vélez, V.H., Menton, M. and Verchot, L.V. (2017). Characterizing degradation of palm swamp peat lands from space and on the ground: an exploratory study in the Peruvian Amazon. Forest Ecology and Management, 393: 63-73.

Hirano, T., Segah, H., Harada, T., Limin, S., June, T., Hirata, R. and Osaki, M. (2007). Carbon dioxide balance of a tropical peat swamp forest in Kalimantan, Indonesia. Global Change Biology, 13(2): 412-425.

Hobbie, S. N., Li, X., Basen, M., Stingl, U. and Brune, A. (2012). Humic substance-mediated Fe(III) reduction by a fermenting Bacillus strain from the alkaline gut of a humus-feeding scarab beetle larva. Systematic and Applied Microbiology, 35(4): 226–232.

Holden, J., Chapman, P.J., Lane, S.N. and Brookes, C. (2006). Impacts of artificial drainage of peat lands on runoff production and water quality. Developments in Earth Surface Processes, 9: 501-528.

Hooker, O. E., Barry, J., Van Leeuwen, T. E., Lyle, A., Newton, J., Cunningham, P., and Adams, C. E. (2016). Morphological, ecological and behavioural differentiation of sympatric profundal and pelagic Arctic charr (Salvelinus alpinus) in Loch Dughaill Scotland. Hydrobiologia, 783(1), 209–221.

Hooijer, A., Page, S., Jauhiainen, J., Lee, W.A., Lu, X.X., Idris, A. and Anshari, G. (2012). Subsidence and carbon loss in drained tropical peatlands. Biogeosciences, 9(3): 1053- 1071.

Hoojier, A., Silvius, M., Wosten, H. and Page, S. (2006). Assessment of CO_2 emissions from drained peat lands in SE Asia. Delft Hydraulics report Q3943. Retrieved from file:///C:/Users/user/Downloads/PEAT-CO2_SE_Asia_assessment_2006.pdf

Hornschuh, M., Grotha, R., & Kutschera, U. (2002). Epiphytic bacteria associated with the bryophyte *Funaria hygrometrica*: Effects of *Methylobacterium* strains on protonema development. Plant Biology, 4(6):682-687.

Hossain, M.A., Akamine, H., Ishimine, Y., Teruya, R., Aniya, Y., Yamawaki, K. and Yamawaki, K. (2015). Effects of relative light intensity on the growth, yield and curcumin content of turmeric (*Curcuma longa* L.) in Okinawa, Japan. Plant Production Science, 9: 12-29.

Huber, K.J. and Overmann, J. (2018). Taxonomic description: Vicinamibacteraceae fam. nov., the first described family within the subdivision Acidobacteria. International Journal of Systematic and Evolutionary Microbiology, 68: 2331-2334

Hugron, S., Bussières, J. and Rochefort, L. (2013). Tree plantations within the context of ecological restoration of peat lands: practical guide. Retrieved from http://www.gret-perg.ulaval.ca/uploads/tx_centrerecherche/Tree_Plantation_guide.pdf.

Huss, A., Derks, L. A. N., Heederik, D. J. J. and Wouters, I. M. (2020). Green waste compost as potential reservoirs of Legionella in the Netherlands. Clinical Microbiology and Infection. 26(9): 1259.e1-1259.e3.

Ibrahim, K.N., Yet, Z.R., Som, A.M., Razali, N., Rahaizah, N.M., Othman, E.N., Burok, N., Yunos, Y.M., Othman, R. and Yahya, T.F.T. (2015). The heavy metal concentration (Pb, Cu, Fe, Zn, Ni) in plant parts of *Zea mays* L. cultivated in agricultural area near Alor Gajah, Melaka, Malaysia. American Journal of Environmental Engineering, 53: 8-12.

Illie, J. (1982). Tasek Bera: The ecology of a freshwater swamp, Dr W. Junk Publishers. The Hague-Boston-London pp1-417.

Insausti, M., Timmis, R., Kinnersley, R. and Rufino, M.C. (2019). Advances in sensing ammonia from agricultural sources. Science of the Total Environment, 135124: 1-48.

Irvine, K., Vermette, S. and Mustafa, F.B. (2013). The "black waters" of Malaysia: Tracking water quality from the peat swamp forest to the sea. Sains Malaysiana, 42(11): 1539-1548.

Ismail, A., Amal, M.N.A. and Hussein, A.S. (2015). Fish diversity of North Selangor Peat Swamp. Seminar Ekologi Malaysia 2015, 19 October 2015, Putrajaya International Convention Centre, Putrajaya.

Ismail, P. and Shamsudin, I. (2001). Raising planting materials of peat swamp forest species. Journal of Tropical Forest Science, 15(1): 237-240.

Ivanova, A.A., Wegner, C.E., Kim, Y., Liesack, W. and Dedysh, S.N. (2016). Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. Molecular Ecology, 25(19): 4818-4835.

Izard, A. and Maria, O. (2015). Metagenomics for microbiology. New York: Elsevier.

Jack, D. L., Paulsen, I. T. and Saier, M. H. (2000). The amino acid/polyamine/organocation (APC) superfamily of transporters specific for amino acids, polyamines and organocations. Microbiology, 146(8):1797–1814.

Jackson, C.R., Liew, K.C., and Yule, C.M. (2008). Structural and functional changes with depth in microbial communities in a tropical Malaysian peat swamp forest. Microbial Ecology, 57(3): 402-412.

Jackson, C.R. and Raub, S. (2010). The microbial ecology of peat swamp forest (Chapter 7). In: Horizons in Earth Science Research. Volume 2. Veress, B. and Szigethy, J. (eds.). Nova Science Publishers Inc.

Jaiswal, S., Singh, D.K. and Shukla, P. (2019). Gene editing and systems biology tools for pesticide bioremediation. Review Frontiers in Microbiology, 10: 1-87.

Jauhiainen, J., Idenori, H., TAakahas, H.I., Juhae, W., He, P. Nen, I.K.K. En, I., Pertti, Z., P. J. M.Z. and H. I.V.S. (2005). Carbon fluxes from a tropical peat swamp forest floor. Global Change Biology, 11: 1788-1797.

Jezberová, J., Jezbera, J., Znachor, P., Nedoma, J., Kasalický, V., and Šimek, K. (2017). The *Limnohabitans* genus harbors generalistic and opportunistic subtypes: evidence from spatiotemporal succession in a canyon-shaped reservoir. Applied and Environmental Microbiology, 83(21): e01530.

Johannes, F.I., Don, J.B., Noel, R.K. and James, T.S. (2005). Bergey's Manual of Systematic Bacteriology. Second Edition, Volume 2. The Proteobacteria Part B: The Gammaproteobacteria. Springer New York.

Jonsson, V., Österlund, T., Nerman, O. and Kristiansson, E. (2016). Statistical evaluation of methods for identification of differentially abundant genes in comparative metagenomics. BMC Genomics, 17(1): 1-12.

Joosten, H.M. and Clarke, D. (2002). Wise use of mires and peat lands and including framework for decision making. International Mire Conservation Group and International Peat Society. Retrieved from http://www.imcg.net/media/download_gallery/books/wump_wise_use_of_mires_and_peatlands_book.pdf.

Ju, F. and Zhang, T. (2015). 16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. Applied Microbiology and Biotechnology, 99(10): 4119-4129.

Juhas, M. (2013). Horizontal gene transfer in human pathogens. Critical Reviews in Microbiology, 41(1): 101-108.

Kanehisa, M. and Sato, Y. (2019) KEGG Mapper for inferring cellular functions from protein sequences. Protein Science, 29(1): 28-35.

Kanokratana, P., Uengwetwanit, T., Rattanachomsri, U., Bunterngsook, B., Nimchua, T., Tangphatsornruang, S., Plengvidhya,V., Champreda, V. and Eurwilaichitr, L. (2010). Insights into the phylogeny and metabolic potential of a primary tropical peat swamp forest microbial community by metagenomic analysis. Microbial Ecology 61: 518-528.

Kasalický, V., Jezbera, J., Hahn, M. W. and Šimek, K. (2013). The diversity of the *Limnohabitans* genus, an important group of freshwater bacterioplankton, by characterization of 35 isolated strains. PLOS One, 8(3): e58209.

Kasalický, V., Zeng, Y., Piwosz, K., Šimek, K., Kratochvilová, H. and Koblížek, M. (2017). Aerobic anoxygenic photosynthesis is commonly present within the genus *Limnohabitans*. Applied and Environmental Microbiology, 84(1): e02116-17.

Katoh, H., Hagino, N., Grossman, A. R. and Ogawa, T. (2001). Genes Essential to Iron Transport in the Cyanobacterium Synechocystis sp. Strain PCC 6803. Journal of Bacteriology, 183(9):2779–2784.

Keegan, K.P., Glass, E.M. and Meyer, F. (2016). Microbial environmental genomics (MEG). Microbial Environmental Genomics, 1399: 207-233.

Keddy, P.A. (2010). Wetland ecology. Cambridge: Cambridge University Press.

Kelly, D.P., McDonald, I.R. and Wood, A.P. (2014). The Family Methylobacteriaceae. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E. and Thompson F. (eds). The Prokaryotes. Springer, Berlin, Heidelberg.

Kits, K.D., Campbell, D.J., Rosana, A.R. and Stein, L.Y. (2015). Diverse electron sources support denitrification under hypoxia in the obligate methanotroph *Methylomicrobium album* strain BG8. Frontiers in Microbiology, 6: 11.

Kiyasu Y., Hitomia, S., Funayamab, Y., Saitoc, K., and Ishikawa, H. (2019). Characteristics of invasive *Acinetobacter* infection: A multicenter investigation with molecular identification of causative organisms. Journal of Infection Chemotherapy, 26(5): 475-482.

Klann, J., McHenry, A., Montelongo, C. and Goffredi, S.K. (2016). Decomposition of plant-sourced carbon compounds by heterotrophic betaproteobacteria isolated from a tropical Costa Rican bromeliad. Microbiology Open, 5(3): 479-489.

Kottelat, M., Britz, R., Tan, H.H. and Witte, K.E. (2006). *Paedocypris*, a new genus of Southeast Asian cyprinid fish with a remarkable sexual dimorphism, comprises the world's smallest vertebrate. Proceedings of the Royal Society B: Biological Sciences, 273(1589): 895-899.

Kox, M.A.R., Aalto, S.L., Penttilä, T., Ettwig, K.F., Jetten, M.S.M. and van Kessel, M.A.H.J. (2018). The influence of oxygen and methane on nitrogen fixation in subarctic *Sphagnum mosses*. AMB Express, 8(1): 19.

Krieg, D.J.B.N.R. and Staley, J.T. (2005). Systematic Bacteriology. The Alpha-, Beta-, Delta-, and Epsilonproteobacteria. Volume 2, Second Edition. Springer.

Krohn, C., Jin, J., Wood, J.L., Hayden, H.L., Kitching, M., Ryan, J., Fabijański, P., Franks, A.E and Tang, C. (2020). Highly decomposed organic carbon mediates the assembly of soilcommunities with traits for the biodegradation of chlorinated pollutants, *Journal of Hazardous Materials*, (2020): 124077.

Kuroda, T. Masuda, M. Ito, Y. Naoi, Y.H. Doan, K. Haga, S. Tsuchiaka, M. Kishimoto, K. Sano, T. Omatsu, Y. Katayama, M. Oba, H. Aoki, T. Ichimaru, F. Sunaga, I. Mukono, H. Yamasato, J. Shirai, K. Katayama, T. Mizutani, T. Oka, M. Nagai Genetic diversity and intergenogroup recombination events of sapoviruses detected from feces of pigs in Japan Infect. Genet. Evol., 55 (2017): 209-217.

Lai, C.C., Cheng, A., Liu, W.L., Tan, C.K., Huang, Y.T., Chung, K.P. and Hsueh, P.R. (2011). Infections caused by unusual *Methylobacterium* species. Journal of Clinical Microbiology, 49(9): 3329-3331.

Lampela, M., Jauhiainen, J., Sarkkola, S. and Vasander, H. (2017). Promising native tree species for reforestation of degraded tropical peat lands. Forest Ecology and Management, 394: 52-63.

Lampela, M., Jauhiainen, J. and Vasander, H. (2014). Surface peat structure and chemistry in a tropical peat swamp forest. Plant and Soil, 382(1-2): 329-347.

Langille, M.G.I., Zaneveld, J., Caporaso, J.G., McDonald, D., Knights, D. and Huttenhower, C. (2013). Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 31: 814-821.

Larjavaara, M. and Muller-Landau, H.C. (2013). Measuring tree height: a quantitative comparison of two common field methods in a moist tropical forest. Methods in Ecology and Evolution, 4(9): 793-801.

Lawrence, R., Rutherfurd, I., Ghadirian, P., White, M., Coates, F. and Thomas, I. (2009). The geography and hydrology of high-country peat lands in Victoria. Geography and Classification. Victorian Department of Sustainability and Environment Arthur Rylah Institute for Environmental Research Technical Report Series No. 173.

Lee, H., Ko, S., Lee, I., Lee, C., Ahn, C., Oh, H. and Jin, L. (2017). *Blastomonas fulva* sp. nov., aerobic photosynthetic bacteria isolated from a *Microcystis* culture taxonomic description. International Journal of Systematic and Evolutionary Microbiology, 67: 3071-3076.

Legendre, P. and Legendre, L. (1998). Numerical Ecology. Elsevier Science, Amsterdam.

Lerner, A. O., Abu-Hanna, J., Carmeli, Y., & Schechner, V. (2019). Environmental contamination by carbapenem-resistant Acinetobacter baumannii: The effects of room type and cleaning methods. Infection Control & Hospital Epidemiology, 1–6.

Lew, S., Glińska-Lewczuk, K. and Lew, M. (2019). The effects of environmental parameters on the microbial activity in peat-bog lakes. PLOS One, 14(10): e0224441.

Li, Y., Zhao, M., Motesharrei, S., Mu, Q., Kalnay, E. and Li, S. (2015). Local cooling and warming effects of forests based on satellite observations. Nature Communications, 6: 1-8.

Li, Z., Dong, L., Zhao, C. and Zhu, Y. (2019). Metagenomic insights into the changes in microbial community and antimicrobial resistance genes associated with different salt content of red pepper (*Capsicum annuum* L.) sauce. Food Microbiology, 103295: 1-10.

Lipson, D.A., Haggerty, J.M., Srinivas, A., Raab, T.K., Sathe, S. and Dinsdale, E.A. (2013). Metagenomic insights into anaerobic metabolism along an arctic peat soil profile. PLOS One, 8(5): e64659.

Liu, Z.P. (2005). *Novosphingobium taihuense* sp. nov., a novel aromatic-compound-degrading bacterium isolated from Taihu Lake, China. International Journal of Systematic and Evolutionary Microbiology, 55(3): 1229-1232.

Maczulak, A. (2010). Biodiversity conserving endangered species. New York: Library of Congress Cataloging-in-Publication Data Maczulak.

Madigan, M.T., Martinko, J.M., Stahl, D. and Clark, D.P. (2012). Brock biology of microorganisms. Upper Saddle River, NJ: Pearson Prentice Hall.

Mancinelli, R.L. (1996). The nature of nitrogen: an overview. Life Support Biosphere Science, 3(1-2): 17-24.

Mansor, M. and Mansor, A. (2014). Swamp forest. Universiti Sains Malaysia Malaysia, pp. 1-6.

Margulis, L., Ashen, J.B., Sole, M. and Guerrero, R. (1993). Composite, large spirochetes from microbial mats: spirochete structure review. Proceedings of the National Academy of Sciences, 90(15): 6966-6970.

Marsh, D.M. and Trenham, P.C. (2008). Current trends in plant and animal population monitoring. Conservation Biology, 22(3): 647-655.

Marsid, E.A., Sugiura, N., Zakaria, Z., Othman, N., Utsumi, M., Iwamoto, K., Goto, M. and Hara, H. (2015). Microbial diversity in disturbed and undisturbed peat swamp forest and isolation of cyanobacteria. International Conference on Sustainable Initiatives (ICSI 2015) in conjunction with 8th ASEAN Environmental Engineering Conference (AEEC), UTM Kuala Lumpur, Malaysia.

Megonigal, J.P., Edgewater, M.D. and Visscher, P.T. (2004). Anaerobic metabolism: linkages to trace gases and aerobic processes. Retrieved from: https://repository.si.edu/.../Megonigal_Hines_Visscher_2004.pdf

Michałowicz, J. and Duda, W. (2007). Phenols - sources and toxicity. Polish Journal of Environmental Studies, 16: 347-362.

Miller, L. D., Russell, M. H. and Alexandre, G. (2009). Chapter 3 Diversity in Bacterial Chemotactic Responses and Niche Adaptation. Advances in Applied Microbiology, 66 (2009): 53–75.

Mitsch, W.J., Bernal, B., Nahlik, A. M., Mander, Ü., Zhang, L., Anderson, C.J. and Brix, H. (2013). Wetlands, carbon, and climate change. Landscape Ecology, 28(4): 583-597.

Mishra, S., Lee, W.A., Hooijer, A., Reuben, S., Sudiana, I.M., Idris, A. and Swarup, S. (2014) Microbial and metabolic profiling reveal strong influence of water table and land-use patterns on classification of degraded tropical peatlands. Biogeosciences, 11: 1727-1741.

Muda Y., Abdul, B.H.R. and Md.Yusof, M. (2012). Rehabilition of peat swamp forest report: Selangor experience. Selangor State Forestry Department, Selangor, Malaysia.

Mukherjee, A., Chettri, B., Langpoklakpam, J.S., Basak, P., Prasad, A. Mukherjee, A.K., Bhattacharyya, M., Singh, A.K. and Chattopadhyay, D. (2017). Bioinformatics approaches including predictive metagenomics profiling reveal characteristics of bacterial response to petroleum hydrocarbon contamination in diverse environments. Journal of Scientific Reports, 7(1108): 1-22.

Mutert, E., Fairhurst, T.H.H. and von Uexküll, H.R.R. (1999). Agronomic management of oil palms on deep peat. Better Crops International. Retrieved from https://tinyurl.com/y5cfod39.

Munoz-Price, L. S., & Weinstein, R. A. (2008). Acinetobacter Infection. New England Journal of Medicine, 358(12):1271–1281.

Nadia, A., Mohamad, N., Wasli, M. E., Perumal, M., Lat, J. and Sani, H. (2018). Effects of soil compaction and relative light intensity on survival and growth performance of planted S*horea macrophylla* in riparian forest along Kayan Ulu River, Sarawak, Malaysia. International Journal of Forestry Research, 2018: 1-12.

Nannipeir, P. and Ascher, J. (2003). Microbial diversity and soil functions. Journal of Musculoskeletal Neuronal Interactions, 54: 655-670.

National Ocean Service (NOS) (2008). An introduction to NOAA's National Ocean Service, 10 National Ocean Service National Oceanic and Atmospheric Administration U.S. Department of Commerce.

Nguyen, K.T., Wu, J.C., Boylan, J.A. and Gherardini, F.C., and Pei, D. (2007). Zinc is the metal cofactor of *Borrelia burgdorferi* peptide deformylase. Archives of Biochemistry and Biophysics, 468(2): 217-225.

Nguyen, N.L., Yu, W.J., Yang, H.Y., Kim, J.G., Jung, M.Y., Park, S.J. and Rhee, S.K. (2017). A novel methanotroph in the genus *Methylomonas* that contains a distinct clade of soluble methane monooxygenase. Journal of Microbiology, 55(10): 775-782.

Nguyen, N.L., Yu, W.J., Gwak, J.H., Kim, S.J., Park, S.J., Herbold, C.W. and Rhee, S.K. (2018). Genomic insights into the acid adaptation of novel methanotrophs enriched from acidic forest soils. Frontiers in Microbiology, 9: 1-15.

Nguyen, N.-L., Yu, W.-J., Yang, H.-Y., Kim, J.-G., Jung, M.-Y., Park, S.-J. and Rhee, S.-K. (2017). A novel methanotroph in the genus Methylomonas that contains a distinct clade of soluble methane monooxygenase. Journal of Microbiology, 55(10): 775–782.

Noma, A., Sakaguchi, Y. and Suzuki, T. (2009). Mechanistic characterization of the sulfur-relay system for eukaryotic 2-thiouridine biogenesis at tRNA wobble positions. Nucleic Acids Research, 37(4): 1335-1352.

Ogiso, T.,Ueno, C., Dianou, D., Huy, T.V., Katayama, A., Kimura, M. and Asakawa, S. (2011). *Methylomonas koyamae* sp. nov., a type i methane-oxidizing bacterium from floodwater of a rice paddy field. International Journal of Systematic and Evolutionary Microbiology, 62: 1832-1837.

Oliveira, R.V., Oliveira, M.C. and Pelli, A. (2017). Disease infection by Enterobacteriaceae family in fishes: a review. Journal of Experimental and Clinical Microbiology, 4(5): 128.

Oshkin, I.Y., Kulichevskaya, I.S., Rijpstra, W.I.C., Damste, J.S.S., Rakitin, A.L., Ravin, N.V. and Dedysh, S.N. (2019a). *Granulicella sibirica* sp. nov., a psychrotolerant acidobacterium isolated from an organic soil layer in forested tundra, West Siberia. International Journal of Systematic and Evolutionary Microbiology, 69(4): 1195-1201.

Oshkin, I.Y., Miroshnikov, K.K. and Dedysh, S.N. (2019b). Draft genome sequence of *Methylocystis heyeri* H2T, a methanotroph with habitat-specific adaptations, isolated from a peatland ecosystem. Microbiology Resource Announcements, 8(29): 1-2.

Orlygsson, J., and Kristjansson, J. K. (2014). The Family Hydrogenophilaceae. In: The Prokaryotes-Alphaproteobacteria and Betaproteobacteria. Rosenberg E., DeLong E. F., Lory S., Stackebrandt E. and Thompson F. (eds.). Berlin: Springer.

Page, S.E., Rieley, J.O. and Wüst, R. (2006). Lowland tropical peat lands of Southeast Asia. Evolution and Records of Environmental and Climate Changes, 9: 145-172.

Page, S.E., Siegert, F., Rieley, J.O., Boehm, H.V, Jaya, A. and Limin, S. (2002). The amount of carbon released from peat and forest fires in Indonesia during 1997. Nature, 1999(1): 61-65.

Pandey, G. and Jain, R.K. (2002). Bacterial chemotaxis toward environmental pollutants: role in bioremediation, Minireviews, Applied and Environmental Microbiology, 68(12): 5789–5795.

Pankratov, T.A., Ivanova, A.O., Dedysh, S.N. and Liesack, W. (2011). Bacterial populations and environmental factors controlling cellulose degradation in an acidic sphagnum peat. Environmental Microbiology 13: 1800-1814.

Parish, F., & Madgwick, J. (2008). Assessment on Peatlands, Biodiversity and Climate change: Main Report. United Nations Environment Programme/Global Environment Facility (UNEP/GEF) with assistance from the Asia Pacific Network for Global Change Research (APN), Global Environment Centre, Kuala Lumpur.

Pawłowski, D., Okupny, D., Włodarski, W. and Zieliński, T. (2014). Spatial variability of selected physicochemical parameters within peat deposits in small valley mire: a geostatistical approach. Geologos, 20(4): 269-288.

Pereira, S.I.A. and Castro, P.M.L. (2014). Phosphate-solubilizing *Rhizobacteria* enhance *Zea mays* growth in agricultural P-deficient soils. Ecological Engineering, 73: 526-535.

Phukan, T., Kabyashree, K., Singh, R., Sharma, P. L., Singh, N., Barman, A. and Ray, S. K. (2019). Ralstonia solanacearum virulence in eggplant seedlings by the leaf-clip inoculation. Phytopathology Research, 1(1):1-1.

Pold, G. (2019). Drivers and consequences of carbon use efficiency - and its measurement in soil" (2019). Doctoral Dissertations. 1744. University of Massachusetts Amherst. Pp1-233.

Posa, M.R.C., Wijedasa, L.S. and Corlett, R.T. (2011). Biodiversity and conservation of tropical peat swamp forests. BioScience, 61(1): 49-57.

Prakash, T. and Taylor, T.D. (2012). Functional assignment of metagenomic data: challenges and applications. Briefings in Bioinformatics, 13(6): 711-727.

Quinten, M.C., Waltert, M., Syamsuri, F., and Hodges, J.K. (2010). Peat swamp forest supports high primate densities on Siberut Island, Sumatra, Indonesia. Oryx, 44(1): 147-151.

Rag. R. van der Werf, D.C. Morton, R.S. DeFries, J.G.J. Olivier, P.S. Kasibhatla, R.B. Jackson, G.J.C. and J.T.R. (2009). CO_2 emissions from forest loss. Nature Geoscience 2(11): 9-11.

Ramage, M.H., Burridge, H., Busse-wicher, M., Fereday, G., Reynolds, T., Shah, D.U. and Scherman, O. (2017). The wood from the trees: the use of timber in construction. Renewable and Sustainable Energy Reviews Journal, 68: 333-359.

Ramette, A. (2007). Multivariate analyses in microbial ecology. FEMS Microbial Ecology, 62(2): 142-160.

Ranjan, K.P. and Ranjan, N. (2013). *Citrobacter*: an emerging health care associated urinary pathogen. Urology Annal 5(4): 313-314.

Rao, C.S., Indoria, A.K. and Sharma, K.L. (2017). Effective management practices for improving soil organic matter for increasing crop productivity in rainfed agroecology of India. Current Science, 112(7): 1-8.

Remaut, H., Tang, C., Henderson, N. S., Pinkner, J. S., Wang, T., Hultgren, S. J. and Li, H. (2008). Fiber Formation across the Bacterial Outer Membrane by the Chaperone/Usher Pathway. Cell, 133(4):640–652.

Rhodius, V. A., Suh, W. C., Nonaka, G., West, J. and Gross, C. A. (2005). Conserved and Variable Functions of the σE Stress Response in Related Genomes. PLoS Biology, 4(1):1-18.

Riesenfeld, C.S., Goodman, R.M. and Handelsman. J. (2004). Uncultured soil bacteria are a reservoir of new antibiotic resistance genes. Environmental Microbiology, 6(9): 981-989.

Rodionova, A.B. and Grenaderova, A.V. (2018). Peat land development and paleoclimate records from the Holocene peat archive in the foothills of the Eastern Sayan Mountains. Earth and Environmental Science, 138(1): 1-8.

Ruppé, E., Baud, D., Schicklin, S., Guigon, G. and Schrenzel, J. (2016). Clinical metagenomics for the management of hospital- and healthcare-acquired pneumonia. Future Microbiology, 11(3): 427-439.

Rydin, H. and Jeglum, J.K. (2013). The biology of peat land. 2nd Edition. Oxford University Press.

Ryan, M. P., & Adley, C. C. (2013). Ralstonia spp.: emerging global opportunistic pathogens. European Journal of Clinical Microbiology & Infectious Diseases, 33(3): 291–304.

Schmidt, T. S. B., Matias Rodrigues, J. F., & von Mering, C. (2014a). Ecological Consistency of SSU rRNA-Based Operational Taxonomic Units at a Global Scale. PLoS Computational Biology, 10(4): e1003594.

Schmidt, O., Horn, M.A., Kolb, S. and Drake, H. L. (2014b). Temperature impacts differentially on the methanogenic food web of cellulose-supplemented peatland soil. Environmental Microbiology, 17(3): 720-734.

Schumann, M. and Joosten, H. (2008). Global Peat Land Restoration Manual, Institute of Botany and Landscape Ecology, Greifswald University, Germany.

Scientific Engineering Response and Analytical Servives (SERAS). (1994). Standard operating procedures: terrestrial plant community sampling. Retrieved from https://clu-in.org/download/ert/2037-R00.pdf.

Segata, N., Izard, J., Waldron, L., Gevers, D., Miropolsky, L., Garrett, W.S. and Huttenhower, C. (2011). Metagenomic biomarker discovery and explanation. Genome Biology, 12(6): 1-60.

Sheremet, A., Jones, G. M., Jarett, J., Bowers, R. M., Bedard, I., Culham, C., Dunfield, P. F. (2020). Ecological and genomic analyses of candidate phylum WPS -2 bacteria in an unvegetated soil. Environmental Microbiology, 22(8):3143-3157.

Shinagawa, E. (2011). Purification and Characterization of Fe (III)-EDTA Reductase from *Bacillus* sp. B-3. Bioscience, Biotechnology, and Biochemistry, 75(10):2063–2065.

Shuhada, S.N., Salim, S., Nobilly, F., Zubaid, A. and Azhar, B. (2017). Logged peat swamp forest supports greater macrofungal biodiversity than large-scale oil palm plantations and smallholdings. Ecology and Evolution, 7(18), 7187-7200.

Sierra, R. (2001). The role of domestic timber markets in tropical deforestation and forest degradation in Ecuador: implications for conservation planning and policy. Ecological Economics, 36: 327-340.

Simpson, B.K. (2014). Status assessment of *Tomistoma* in Peninsular Malaysia: peat swamp forests of Selangor and Pahang. *Tomistoma* Task Force of the IUCN/SSC Crocodile Specialist Group, Selangor.

Singh, B.K., Nunan, N. and Millard, P. (2009) Response of fungal, bacterial and ureolytic communities to synthetic sheep urine deposition in a grassland soil. FEMS Microbial Ecology, 70: 109-117.

Singh, D.P., Prabha, R., Gupta, V.K. and Verma, M.K. (2018). Metatranscriptome analysis deciphers multifunctional genes and enzymes linked with the degradation of aromatic compounds and pesticides in the wheat rhizosphere. Frontiers in Microbiology, 9: 1331.

Song, L.M., Munian, K., Abd Rashid, Z. and Bhassu, S. (2013). Characterisation of Asian snakehead murrel *Channa striata* (Channidae) in Malaysia: an insight into molecular data and morphological approach. The Scientific World Journal, 2013: 1-16.

Smirnoff, N. (2018). Ascorbic acid metabolism and functions: A comparison of plants and mammals. Free Radical Biology and Medicine, 122: 116-129.

Spahni, R., Joos, F., Stocker, B.D., Steinacher, M. and Yu, Z.C. (2013). Transient simulations of the carbon and nitrogen dynamics in northern peat lands: from the last glacial maximum to the 21st century. Climate of the Past, 9(3): 1287-1308.

Starke, R., Capek, P., Morais, D., Callister, S.J. and Jehmlich, N. (2019). The total microbiome functions in bacteria and fungi. Journal of Proteomics, 213(103623): 1-16.

Stillman, B. (1994). Smart machines at the DNA replication fork. Cell, 78(5): 725-728.

Spanggaard, B., Huber, I., Nielsen, J., Nielsen, T., Appel, K. and Gram, L. (2000). The microflora of rainbow trout intestine: a comparison of traditional and molecular identification. Aquaculture, 182(1-2): 1-15.

Sule, H.A. (2016a). Anthropogenic activities impact on water quality, fish community and bacteria presence in disturbed and undisturbed north Selangor peat swamp forest. MSc thesis. Department of Biology, Faculty of Science, Unversiti Putra Malaysia.

Sule, H.A., Ismail, A. and Amal, M.N.A. (2016b). A review of the ichthyofauna of Malaysian peat swamp forest. Pertanika Journal of Tropical Agricultural Science, 39(4): 421-458.

Sule, H.A., Ismail, A., Azmai Amal., M.N.A., Zulkifli, S.Z. and Roseli, M.A.M. (2019). Associations between the presence of bacteria and the physico-chemical parameters of water in peat swamp forest, paddy field and oil palm plantation in north Selangor, Malaysia, Pertanika Journal of Tropical Agricultural Science, 42(1): 185-207.

Sun, H., Terhonen, E., Kovalchuk, A., Tuovila, H., Chen, H., Oghenekaro, A.O. and Asiegbu, F.O. (2016). Dominant tree species and soil type affect the fungal community structure in a boreal peat land forest. Applied and Environmental Microbiology, 82(9): 2632-2643.

Subramanian, S. and Kearns, D.B. (2019). Functional regulators of bacterial flagella. Annual Review of Microbiology, 73: 225-246.

Surahman, A., Soni, P. and Shivakoti, G. P. (2018). Are peat land farming systems sustainable? Case study on assessing existing farming systems in the peat land of Central Kalimantan, Indonesia. Journal of Integrative Environmental Sciences, 15(1): 1-19.

Susan, T.B. (2015). Habitat Association of Klebsiella Species Published online by Cambridge University Press, 6(2): pp. 52-58.

Szurmant, H., Bunn, M. W., Cannistraro, V. J. and Ordal, G. W. (2003). Bacillus subtilisHydrolyzes CheY-P at the Location of Its Action, the Flagellar Switch. Journal of Biological Chemistry, 278(49), 48611–48616.

Tackmann, J., Arora, N., Schmidt, T. S. B., Rodrigues, J. F. M., & von Mering, C. (2018). Ecologically informed microbial biomarkers and accurate classification of mixed and unmixed samples in an extensive cross-study of human body sites. Microbiome, 6(1):1-16.

Techtmann, S. M. and Hazen, T. C. (2016). Metagenomic applications in environmental monitoring and bioremediation. Journal of Industrial Microbiology and Biotechnology, 43(10): 1345-1354.

Teixeira L.M. and Merquior V.L.C. (2014). The Family Moraxellaceae. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) *The Prokaryotes*. Springer, Berlin, Heidelberg. Pp 443–476.

Teufel, R., Mascaraque, V., Ismail, W., Voss, M., Perera, J., Eisenreich, W. and Fuchs, G. (2010). Bacterial phenylalanine and phenylacetate catabolic pathway revealed. Proceedings of the National Academy of Sciences, 107(32): 14390-14395.

Thavamani, P., Samkumar, R.A., Satheesh, V., Subashchandrabose, S.R., Ramadass, K., Naidu, R. and Megharaj, M. (2017). Microbes from mined sites: harnessing their potential for reclamation of derelict mine sites. Environmental Pollution, 230: 495-505.

Thiollay, J. and Thiollay, J. (2015). Response of avian community to rainforest degradation. Biodiversity and Conservation, 8: 513-534.

Tobin-Janzen, T., Shade, A., Marshall, L., Torres, K., Beblo, C., Janzen, C., Lenig, J., Martinez, A., Ressler, D. (2005). Nitrogen changes and domain bacteria ribotype diversity in soils overlying the Centralia, Pennsylvania underground coal mine fire, Soil Science: March 2005 - Volume 170 - Issue 3 - p 191-201

Too, C., Keller, A., Sickel, W., Lee, S. and Yule, C.M. (2018). Microbial community structure in a Malaysian tropical peat swamp forest: the influence of tree species and depth. Frontiers in Microbiology, 9: 2859.

Trevelline, B.K., Fontaine, S.S., Hartup, B.K. and Kohl, K.D. (2019). Conservation biology needs a microbial renaissance: a call for the consideration of host-associated microbiota in wildlife management practices. Proceedings of the Royal Society B: Biological Sciences, 286(1895): 20182448.

Truant, A.L., Gulati, R., Giger, O., Satishchandran, V. and Caya, J.G. (1998). *Methylobacterium* species: An increasingly important opportunistic pathogen. Laboratory Medicine, 29(11): 704-710.

Tsao, H.F., Scheikl, U., Volland, J.M., Köhsler, M., Bright, M., Walochnik, J. and Horn, M. (2017). "*Candidatus Cochliophilus cryoturris*" (Coxiellaceae), a symbiont of the testate amoeba *Cochliopodium minus*. Scientific Reports, 7(1): 1-8.

Turetsky, M.R., Benscoter, B., Page, S., Rein, G., Van Der Werf, G.R. and Watts, A. (2015). Global vulnerability of peatlands to fire and carbon loss. Nature Geoscience, 8(1): 11-14.

Udayangani, R.M.C., Dananjaya, S.H.S., Fronte, B., Kim, C.H., Lee, J. and De Zoysa, M. (2017). Feeding of nano scale oats β-glucan enhances the host resistance against *Edwardsiella tarda* and protective immune modulation in zebrafish larvae. Fish and Shellfish Immunology, 60: 72-77.

UNDP. (2006). Malaysia's peat swamp forest: conservation and sustainable use. International Journal of Integrated Engineering special Issue, 3(4): 33.

Urakawa, H. and Bernhard, A.E. (2017). Wetland management using microbial indicators. Ecological Engineering, 108: 456-476.

Vera, E., Taddei, S., Cavirani, S., Schiavi, J., Angelone, M., Cabassi, C.S. and Quintavalla, F. (2019). *Leptospira* seroprevalence in Bardigiano horses in Northern Italy. Animals, 10(1): 1-23.

Vieira, F.C.S. and Nahas, E. (2005). Comparison of microbial numbers in soils by using various culture media and temperatures. Microbiological Research, 160: 197-202.

Volodina, E. and Steinbüchel, A. (2014). (S)-3-hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase (FadB') from fatty acid degradation operon of *Ralstonia eutropha* H16. AMB Express, 4(1): 69.

Waldron, S., Vihermaa, L., Evers, S., Garnett, M.H., Newton, J. and Henderson, A. C. G. (2019). C mobilisation in disturbed tropical peat swamps: old DOC can fuel the fluvial efflux of old carbon dioxide, but site recovery can occur. Scientific Reports, 9(1): 12.

Wang, Q., Garrity, G. M., Tiedje, J.M. and Cole, J. R. (2017). Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. Applied and Environmental Microbiology, 73: 5261-5267.

Wang, Z., Duan, L., Liu, F., Hu, Y., Leng, C., Kan, Y., Yao, L. and Sh, H. (2020). First report of *Enterobacter hormaechei* with respiratory disease in calves, case report. BMC Veterinary Research, 16(1): 4.

Ward, N. L., Challacombe, J.F., Janssen, P.H., Henrissat, B., Coutinho, P.M., Wu, M. and Kuske, C. R. (2009). Three genomes from the phylum Acidobacteria provide insight into the lifestyles of these microorganisms in soils. Applied and Environmental Microbiology, 75(7): 2046-2056.

Ward, L. M., Cardona, T., & Holland-Moritz, H. (2019). Evolutionary implications of anoxygenic phototrophy in the bacterial Phylum *Candidatus Eremiobacterota (WPS-2).* Frontiers in Microbiology,10:1658.

Wendelin, W., Aleg, S., Andreas, H., Nina, T. and Vyacheslav, R.A.R. (2012). The 14th International Peat Congress. Using biomass as substitute for peat - examples for wet peat land management (paludiculture) in Belarus.

Wetlands International (2010). A quick scan of peatlands in Malaysia. Wetlands International-Malaysia: Petaling Jaya, Malaysia. pp91.

White, K.H., “Ralph” Marquez., R. B., Soward, L.R and Shankle, G. (2005) A guide freshwater ecology. Texas Commission on Environmental Quality, Austin, pp1-134.

Wich, S., Gaveau, D.L.A., Wich, S., Epting, J., Juhn, D., Kanninen, M. and Leader-williams, N. (2014). The future of forests and orangutans (Pongoabelii) in Sumatra: predicting impacts of oil palm plantations, road construction. Environmental Research Letters, 4(3): 12.

Widdel, F. (1987). New types of acetate-oxidizing, sulfate-reducing *Desulfobacter* species, *D. hydrogenophilus* sp. nov., *D. latus* sp. nov., and *D. curvatus* sp. nov. Archives of Microbiology, 148(4): 286-291.

Winsley, T., van Dorst, J.M., Brown, M.V. and Ferrari, B.C. (2012). Capturing greater 16S rRNA gene sequence diversity within the domain bacteria. Applied and Environmental Microbiology, 78(16): 5938-5941.

Wösten, J.H.M., Van Den Berg, J., Van Eijk, P., Gevers, G.J.M., Giesen, W.B.J.T., Hooijer, A. and Wibisono, I. T. (2006). Interrelationships between hydrology and ecology in fire degraded tropical peat swamp forests. International Journal of Water Resources Development, 22(1): 157-174.

Wowor, D., Muthu, V., Meier, R., Balke, M., Cai, Y. and Ng, P.K.L. (2009). Evolution of life history traits in Asian freshwater prawns of the genus *Macrobrachium* (Crustacea: Decapoda: Palaemonidae) based on multilocus molecular phylogenetic analysis. Molecular Phylogenetics and Evolution, 52(2): 340-350.

Wright, W. and Comas, X**.** (2016). Estimating methane gas production in peat soils of the Florida everglades using hydrogeophysical methods. *Journal of Geophysical Research* Biogeosciences, 121(4): 246.

Winkler, M. G., & Dewitt, C. B. (1985). Environmental Impacts of Peat Mining in the United States: Documentation for Wetland Conservation. Environmental Conservation, 12(4), 317–330

Xu, J., Morris, P.J., Liu, J. and Holden, J. (2018). Peatmap: Refining estimates of global peat land distribution based on a meta-analysis. Catena, 160: 134-140.

Xu, X., Zhang, R., Jiang, H. and Yang, F. (2020). Sulphur-based autotrophic denitrification of wastewater obtained following graphite production: Long-term performance, microbial communities involved, and functional gene analysis. Bioresource Technology, 306: 123117.

Yabuuchi, E. and Kosako, Y. (2015). *Sphingomonas*. Bergey's Manual of Systematics of Archaea and Bacteria. Pp. 39.

Yooseph, S., Andrews-Pfannkoch, C., Tenney, A., McQuaid, J., Williamson, S., Thiagarajan, M. and Venter, J. C. (2013). A Metagenomic Framework for the Study of Airborne Microbial Communities. PLoS ONE, 8(12): e81862.

Yule, C.M. (2010). Loss of biodiversity and ecosystem functioning in Indo-Malayan peat swamp forests. Biodiversity and Conservation, 19(2): 393-409.

Yule, C.M., Yule, C.M. and Gomez, Æ.L.N. (2008). Leaf litter decomposition in a tropical peat swamp forest in Peninsular Malaysia. Wetlands Ecology and Management, 17(3): 231-2411.

Yukgehnaish, K., Kumar, P., Sivachandran, P., Marimuthu, K., Arshad, A., Paray, B.A. and Arockiaraj, J. (2020). Gut microbiota metagenomics in aquaculture: factors influencing gut microbiome and its physiological role in fish. Reviews in Aquaculture. *In press*, https://doi.org/10.1111/raq.12416

Zarai, Y., Margaliot, M. and Tuller, T. (2016). On the ribosomal density that maximizes protein translation rate. PLOS One, 11(11): e0166481.

Zaura, E., Brandt, B.W., Teixeira de Mattos, M.J., Buijs, M.J., Caspers, M.P.M., Rashid, M.U. and Crielaard, W. (2015). Same exposure but two radically different responses to antibiotics: resilience of the salivary microbiome versus long-term microbial shifts in feces. mBio, 6(6): 11.

Zhang, J., Wang, X., Huo, D., Li, W., Hu, Q., Xu, C. and Li, C. (2014). Metagenomic approach reveals microbial diversity and predictive microbial metabolic pathways in Yucha, a traditional Li fermented food. Scientific Reports, 6(1): 9.

Zhang, T., Yang, C., Qu, H., Xia, Y., Wang, Y., Li, A.D. and Liu, R. (2016). Discovery of new cellulases from the metagenome by a metagenomics-guided strategy. Biotechnology for Biofuels, 9(1): 1-12.

Zhao, W., Wang, J., Liang, Y. and Huang, Z. (2017). Development of a 16S rRNA gene-based microarray for the detection of marine bacterioplankton community. Acta Oceanologica Sinica, 36(10): 106-114.

Zhao, Q., Yue, S., Bilal, M., Hu, H., Wang, W. and Zhang, X. (2017). Comparative genomic analysis of 26 *Sphingomonas* and *Sphingobium* strains: dissemination of bioremediation capabilities, biodegradation potential and horizontal gene transfer. Science of the Total Environment, 609: 1238-1247.