Review Article

Progress in Microbes and Molecular Biology

HH PUBLISHER

Microbes from Peat Swamp Forest — The Hidden Reservoir for Secondary Metabolites?

Kuan-Shion Ong[1,2]*, Vengadesh Letchumanan[3], Jodi Woan-Fei Law[3], Catherine M. Yule[2,4], Sui-Mae Lee[1,2]

[1]Tropical Medicine and Biology Multidisciplinary Platform, Monash University Malaysia, Jalan Lagoon Selatan, Bandar Sunway, 47500, Subang Jaya, Selangor.
[2]School of Science, Monash University Malaysia, Jalan Lagoon Selatan, Bandar Sunway, 47500, Subang Jaya, Selangor.
[3]Novel Bacteria and Drug Discovery (NBDD) Research Group, Microbiome and Bioresource Research Strength (MBRS), Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, 47500, Bandar Sunway, Selangor Darul Ehsan, Malaysia.
[4]School of Science and Engineering, University of the Sunshine Coast, Sippy Downs, Queensland, 4556, Australia.

Abstract: Antimicrobial resistance is a significant threat to the healthcare sector. For the past century, there has been a decline in the discovery of new antibiotics. This has urged researchers to bio-prospect for new bioactive agents from microbes originating from untapped environments, as well as to explore the potential of other microbial genera apart from the well-known *Streptomyces*. Tropical peat swamp forests are an example of such an environment. Two novel antimicrobial-producing bacteria from the genera *Burkholderia* and *Paenibacillus* have been identified to produce potent antimicrobials. These two genera of bacteria have recently gained tremendous interest due to their genome complexity. They are known as multifaceted organisms not only because of their genetic content, but also due to their positive interactions with the environment along with a plethora of organisms including plants and animals. The interactions observed are attributed to their genomes and to their production of secondary metabolites including antimicrobials. Hence, this review provides an overview of the nature of tropical peat swamp forests, taxonomy and production of secondary metabolites of both *Burkholderia* and *Paenibacillus*, as well as discussing the future perspective of isolating antimicrobial-producing microbes from tropical peat swamp forests.

Keywords: Antimicrobials; *Burkholderia*; *Paenibacillus*; resistance; secondary metabolite; tropical peat swamp forest

***Correspondence:** Kuan-Shion Ong, Tropical Medicine and Biology Multidisciplinary Platform, Monash University Malaysia, Jalan Lagoon Selatan, Bandar Sunway, 47500, Subang Jaya, Selangor. kuanshion@gmail.com

Received: 18th March 2020
Accepted: 20th April 2020
Published Online: 25th April 2020

***Citation*:** Ong K-S, Letchumanan V, Law JW-F, *et al.* Microbes from Peat Swamp Forest — The Hidden Reservoir for Secondary Metabolites?. Prog Mircobes Mol Bio1 2020; 3(1): a0000077. https://doi.org/10.3687/pmmb.a0000077

INTRODUCTION

Antimicrobials have been used for generations as prophylaxis to prevent initial or recurrence of infection, and as agents to destroy, inhibit or prevent pathogenic action of microbes[1]. Over time, use of antimicrobials has created an inevitable selective pressure leading to the evolution of microbes to resist the action of antimicrobials. Microbes can gain resistance towards antimicrobials intrinsically through mutations or by acquiring the ability via conjugation[2]. This phenomenon is further exacerbated by the extensive use of antimicrobials to control infections which has unprecedentedly accelerated the process and emergence of resistant microbes[3]. This is an alarming issue as the rapid emergence of antimicrobial-resistant pathogens limits treatment options and increases mortality. According to the Director General of the World Health Organization (WHO), we are heading towards a post-antibiotic era in which common infections and injuries could once again kill[4]. Therefore, there is an urgent need for alternative measures to tackle the crisis of antimicrobial resistance. One of the methods is by bioprospecting for new antimicrobials from untapped resources such as the tropical peat swamp forests where extreme conditions and low nutrients promote competition among microbes. The review will discuss the nature of tropical peat swamp forests, taxonomy and production of secondary metabolites of both *Burkholderia* and *Paenibacillus*, as well as discuss the future prospects of isolating antimicrobial-producing microbes from tropical peat swamp forests.

TROPICAL PEAT SWAMP FORESTS

Tropical peat swamp forests (TPSFs) are unique wetland ecosystems periodically flooded by fresh water

from rainfall[5]. Out of 30–45 million hectares of global wetlands in the world, about 18.1 million hectares are TPSFs widely distributed around Southeast Asia[6]. TPSFs contribute to almost 20% of the total global terrestrial organic carbon and form one of the largest terrestrial organic carbon sinks. Carbon is stored in the forest biomass with trees up to 70m tall, but most of it is sequestered peat layers up to 25m deep. Disturbance of TPSFs due to drainage and fire causes the release of greenhouse gases such as methane and carbon dioxide to the atmosphere. Burning of TPSFs results in about 25% of the total global greenhouse gas emissions from deforestation and forest degradation which result in an estimated 3% of total global anthropogenic greenhouse gas emissions. Furthermore, TPSFs hold a key role in regional hydrology (movement and distribution of water). This is because peat can hold 5–10 times its weight in water. This is important as the water stored can act as a buffer in reducing water velocity thus minimizing the impact of downstream flooding[5].

TPSFs grow on a substrate formed by the accumulation of layers of peat (partially decomposed organic matter) up to 25m deep. They are usually dome-shaped due to the buildup of peat, and are permanently waterlogged with a pH range of 2.9 to 4.5[8]. The leaching of tannic acids (20.2 ± 2.3 mg/l) from the leaves of endemic plants causes the dark brown, acidic water in TPSFs[9]. The dark brown water reduces light penetration and impedes photosynthesis by algae, which together with the slow flow rates and high temperatures create an anoxic environment, while toxic secondary compounds leach from the leaf litter which then reduces the microbial decomposition of organic matter (decay rates of 0.0006–0.0016 k day-1 for endemic plants), hindering nutrient recycling thus creating a highly concentrated carbon reservoir[5]. In addition, TPSFs are known to be ombrotrophic, receiving nutrients and water solely from rainfall and dust. The lack of nutrient input and slow decomposition rate results in a low nutrient environment in TPSFs[8].

BACTERIAL COMMUNITY IN TPSFS

It was previously thought that such extreme environmental conditions (acidic, waterlogged and low nutrient availability) meant low bacterial diversity. However, metagenomic studies have revealed the complexity of the genetic information of the bacterial community and high diversity[10]. Kanokratana *et al.* (2011)[10] deduced that bacteria constituted the most abundant microbial group in a Thailand TPSF. From the bacterial sequences identified, *Proteobacteria* was the largest species group (37.9% of total bacteria), which comprised mostly Alpha-proteobacteria, followed by *Acidobacteria* (35.0% of total bacteria). Other key minor bacterial phyla include *Verrumicrobia* (5.7%), *Planctomycetes* (9.6%), *Actinobacteria* (2.5%), *Bacteroidetes* (1.1%), *Nitrospirae* (1.8%), *Firmicutes* (0.4%) and others unclassified bacteria (6.0%). Moreover, the bacterial population (determined using next generation sequencing) in a Malaysian TPSF showed a similar pattern[11] as the Thailand TPSFs and was consistent with a previous study conducted by Jackson *et al.* (2009)[12] which showed that TPSFs are dominated by *Proteobacteria* and *Acidobacteria* (more than 50% of the total bacteria population).

Antimicrobial-producing bacteria from TPSFs

The slow degradation of organic matter in TPSF results in low levels of nutrients which creates a highly competitive environment[13]. Consequently, it is likely that bacteria would produce secondary metabolites such as antimicrobial compounds to secure their niche and resources. Such phenomena are consistent with the isolation of antimicrobial producing bacteria from two different TPSF: the southeast Pahang and Selangor TPSF. These antimicrobial producing isolates were identified via a polyphasic taxonomic approach to be novel species from the genus *Burkholderia* and *Paenibacillus*, namely *Burkholderia paludis* sp. nov. (from Pahang TPSF)[14] and *Paenibacillus tyrfis* sp. nov. (from Selangor TPSF)[15].

Burkholderia and their secondary metabolites

The *Burkholderia* genus consists of a group of ubiquitous bacteria that occur in aquatic environments, soil, plant rhizospheres and animals. *Burkholderia* are mesophilic Gram-negative rods, oxidase positive, motile microorganisms. *Burkholderia* can be characterized phenotypically by their pigmentation, presence of hydroxyl fatty acids of 14, 16 and 18 carbon atoms, possession of distinct polar lipids, and by having Q8 cellular respiratory quinones[14].

The genus can be divided into three groups: *Burkholderia* sensu stricto, *Paraburkholderia* and *Caballeronia*[16]. *Burkholderia* sensu stricto is a group of closely related *Burkholderia* species that share a high degree of 16S rRNA (98–100%) and recA (94–95%) gene sequence similarity which makes them difficult to be differentiated using conventional molecular techniques. To differentiate different species of *Burkholderia* sensu stricto, multilocus sequence analysis (MLSA) is usually adopted as the technique provides the discriminatory power needed for both identification and differentiation[17]. *Burkholderia* sensu stricto species have diverse ecological roles and have been used in biocontrol and bioremediation. Several *Burkholderia* sensu stricto species can be used for biocontrol agents as they can produce secondary metabolites to repress soil borne pathogens. Some *Burkholderia* sensu stricto species can act as plant growth promoters. They can also be used for bioremediation of recalcitrant xenobiotics, for instance, *Burkholderia xenovorans* can degrade chlorinated toxic phenolic compounds commonly found in pesticides and herbicides[18].

In contrast, nearly all *Paraburkholderia* species (e.g. *Paraburkholderia bryophila*, *Paraburkholderia tropica* and *Paraburkholderia nodosa*) and *Caballeronia* (e.g. *Caballeronia ginsengisoli*, *Caballeronia terrestris* and *Caballeronia humi*) are plant growth promoters as they are able to fix nitrogen and supply nutrients to their plant hosts[16, 19]. Many secondary metabolites with antimicrobial activity are produced by the *Burkholderia* species have been identified. They usually possess antifungal and/or antibacterial activity (Table 1).

Table 1. Antimicrobials produced by *Burkholderia* species.

Compounds	*Burkholderia* species	Bioactivity	References
2-pyrrolidone-5-carboxylic acid	*Burkholderia* sp. HD05	Antifungal	Zhang *et al.* (2019)[20]
Bis-(2-ethylhexyl) phthalate	*Burkholderia gladioli* OR1	Antibacterial	Bharti *et al.* (2015)[21]
Burkholdines	*Burkholderia ambifaria* 2.2N	Antifungal	Tawfik *et al.* (2010)[22]
Cepacidin A	*Burkholderia cepacia*	Antifungal	Lee *et al.* (1994)[23]
Cepacins A and B	*Burkholderia cepacia* SC 11	Antibacterial	Parker *et al.* (1984)[24]
Cepafungin	*Burkholderia* sp.	Antifungal	Shoji *et al.* (1990)[25]
Cepalycin	*Burkholderia cepacia*	Antifungal	Abe and Nakazawa (1994)[26]
Enacyloxins	*Burkholderia ambifaria AMMD*	Antibacterial	Mahenthiralingam *et al.* (2011)[27]
Gladiolin	*Burkholderia gladioli*	Anti-mycobacterium	Song *et al.* (2017)[28]
Icosalide	*Burkholderia gladioli*	Antibacterial	Dose *et al.* (2018)[29]
Iminopyrrolidines	*Burkholderia plantari* #9424 ICMP	Antibacterial	Mitchell and Teh (2005)[30]
Occidiofungin	*Burkholderia contaminans* MS14	Antifungal	Lu *et al.* (2009)[31]
Phencomycin	*Burkholderia glumae* 411gr-6	Antibacterial	Han *et al.* (2014)[32]
Pyochelin	*Burkholderia paludis*	Antibacterial	Ong *et al.* (2017)[33]
Pyrazoles derivatives	*Burkholderia glumae* #3729 ICMP	Antibacterial	Mitchell *et al.* (2008)[34]
Pyrrolnitrin	*Burkholderia cepacia*	Antifungal, antibacterial	El-Banna and Winkelmann (1998)[35]
Vietnamycin	*Burkholderia vietnamiensis*	Antibacterial	Rowe *et al.* (2016)[36]
Xylocandin	*Burkholderia cepacia*	Antifungal	Meyers *et al.* (1987)[37]

Paenibacillus and their secondary metabolites

The genus *Paenibacillus* comprises aerobic/facultative anaerobic and endospore-forming bacteria, with a majority of them typically showing Gram-positive cell wall structures[38,39]. This genus was initially included in the genus *Bacillus* based on morphological characteristics prior to reclassification. The genus *Paenibacillus* — which means "almost a *Bacillus*" was then proposed by Ash et. al (1993)[40] using phylogenetic classification[39]. The *Paenibacillus* spp. have MK-7 as major quinone, anteiso-$C_{15:0}$ as major cellular fatty acid, DNA G + C content which ranges from 39 to 59 mol%, and genome size ranges from 3.02 Mbp (eg. *Paenibacillus darwinianus*) to 8.82 Mbp (eg. *Paenibacillus mucilaginosus*)[38,39].

This group of bacteria can be isolated from a variety of environments, mainly from soil. They are often associated with humans, animals, and plants. The majority of the *Paenibacillus* spp. are producers of antimicrobial compounds and enzymes that are useful for bioremediation (Table 2). Furthermore, some of these compounds can be utilized as bio-fertilizers for plant growth promotion or bio-pesticides against root pathogens[39].

Table 2. Antimicrobials produced by *Paenibacillus* species.

Compounds	*Paenibacillus* species	Bioactivity	References
Paenibacillin	*Paenibacillus polymyxa* OSY-DF	Antibacterial	He *et al.* (2008)[41]
Paenicidin A	*Paenibacillus polymyxa* NRRL B-30509	Antibacterial	Lohans *et al.* (2012)[42]
Penisin	*Paenibacillus* sp. A3	Antibacterial	Baindara *et al.* (2016)[43]
Polymyxin	*Paenibacillus polymyxa*	Antibacterial	Nation and Li (2017)[44]
Colistin	*Paenibacillus polymyxa*	Antibacterial	Tambadou *et al.* (2015)[45]
Octapeptin	*Paenibacillus tianmuensis*	Antibacterial	Qian *et al.* (2012)[46]
Paenibacterin	*Paenibacillus tiaminolyticus* OSY-SE	Antibacterial	Huang *et al.* (2014)[47]
Pelgipeptin	*Paenibacillus elgii* B69	Antibacterial	Ding *et al.* (2011)[48]
Gavaserin	*Paenibacillus polymyxa*	Antibacterial	Pichard *et al.* (1995)[49]
Fusaricidins	*Paenibacillus polymyxa* KT-8	Antibacterial	Kajimura and Kaneda (1997)[50]

FUTURE PERSPECTIVES IN TPSF MICROBIAL CULTIVATION

Thus far, only two bacteria (*Burkholderia paludis* sp. nov and *Paenibacillus tyrfis* sp. nov) with antimicrobial-producing ability from TPSF have been successfully cultivated and identified. These bacteria such as *Burkholderia* from Proteobacteria and *Paenibacillus* from Firmicutes are common phyla of bacteria dominating the TPSFs. Hence, what needs to be improved in order to isolate the uncommon bacteria with antimicrobial-producing ability from TPSF? The possible reasons for isolating those common bacteria are the suitability of media used and the incubation period.

The use of alternative culture media

The failure in cultivating peat-inhabiting bacteria using culture dependent techniques is often due to the usage of conventional media such as nutrient and tryptone soy media. Such media contain near-neutral pH with high mineral salt content that do not simulate the acidic, low nutrient conditions of TPSFs[8]. Besides that, it favors fast growing bacteria and these fast-growing bacteria will outgrow the other slow growing bacteria[51]. Therefore, there is a need to use diluted acidic media with low salt content such as MM1, Medium M1, Medium M2, Medium M31, nitrate mineral salt media, peat extract medium and R2A in order to cultivate various peat-inhabiting bacteria at the same time suppressing the fast-growing bacteria (Table 3).

Table 3. Examples of media with low salt content.

Type of Media	Media Compositions	References
MM1	100 mM NaCl, 10 mM $(NH_4)_2SO_4$, 5 mM $MgSO_4$, 1 mM $CaCl_2$, 8mM KH_2PO_4, 16 mM K_2HPO_4 and micronutrient	Mehta and Rosato (2005)[52]; Schulte and Bonas (1992)[53]
Medium M1	0.25 g/L KNO_3, 0.1 g/L KH_2PO_4, 0.1 g/L $MgSO_4$, 0.02 g/L $CaCl_2.2H_2O$, 0.1 g/L yeast extract, 0.005 g/L Na_2MoO_4 and 0.05% (w/v) carbon source	Dedysh *et al.* (2006)[54]
Medium M2	0.1 g/L $(NH_4)_2SO_4$, 0.1 g/L $MgSO_4$, 0.02 g/L $CaCl_2.2H_2O$ and 0.05% (w/v) carbon source	Dedysh *et al.* (2006)[54]
Medium M31	0.1 g/L KH_2PO_4, 20 mL Hutner's basal salt, 1 g/L *N*-acetylglucosamine, 0.1 g/L peptone and 0.1 g/L yeast extract	Kulichevskaya *et al.* (2012b)[55]
Nitrate mineral salt media	1 g/L KNO_3, 1 g/L $MgSO_4.7H_2O$, 0.717 g/L $Na_2HPO_4.12H_2O$, 0.272 g/L KH_2PO_4, 0.2 g/L $CaCl_2.6H_2O$ and 0.005 g/L ferric ammonium EDTA	Dedysh and Dunfield (2011)[56]
Peat extract medium	500 ml of supernatant (400 g of wet peat mixed with 200 ml of distilled water) and 500 ml of base Medium M2	Dedysh *et al.* (2006)[54]
R2A	0.5 g/L yeast extract, 0.5 g/L proteose peptone, 0.5 g/L casamino acid, 0.5 g/L dextrose, 0.5 g/L soluble starch, 0.3 g/L sodium pyruvate, 0.3 g/L KH_2PO_4 and 0.05 g/L $MgCl_2$	Dedysh *et al.* (2006)[54]; Edenborn and Sexstone (2007)[57]; Taylor *et al.* (2002)[58]

Based on other studies on northern wetlands, several types of bacteria were isolated using the minimal media shown in Table 3. For example, an acidophilic methane-oxidizing bacterium was isolated using minimal mineral medium containing vitamin mixture with methane as sole carbon source. In another study conducted by Dedysh *et al.* (2006)[54], Alpha-proteobacteria, Beta-proteobacteria, Gamma-proteobacteria, *Actinobacteria*, *Firmicutes* and *Bacteroidetes* were isolated using Medium M1, Medium M2 and diluted R2A media. However, acidobacteria and planctomycetes were not found in the same study which might due to the reason that some Acidobacteria such as *Granulicella* species are inhibited by the presence of phosphates found in most minimal media[59]. Therefore, agar selection is one of the main criteria leading to successful cultivation of peat-inhabiting bacteria.

Prolonged incubation time

Most peat inhabiting bacteria are slow growing even under optimal growth conditions. These bacteria are usually fastidious facultative anaerobes such as methanotrophs, acidobacteria and planctomycetes. In a study conducted by Kulichevskaya *et al.* (2012a)[60], colonies of *Telmatocola sphagniphila* (planctomycetes) were developed after 4 weeks of incubation using modified Medium M2 supplemented with trace element and vitamins under 5% CO2 (v/v) condition. *Telmatobacter bradus* which is a facultative anaerobe belonging to the phylum Acidobacteria requires 4 weeks to grow using Medium M2[59]. In another example, *Telmatospirillum sibiriense* which is an acidotolerant facultative anaerobic, only had observable colonies after 5 months of incubation on N-free minimal media supplemented with a reducing agent[61]. This also indicates that the presence of reducing agents might promote the growth of fastidious facultative anaerobes. However, there is no published result on the successful isolation of strict anaerobes from either the northern wetlands or TPSFs, which suggest the need for other reducing agents to be included in the culture media[51]. Furthermore, a more stringent method should be applied during sampling collection where peat samples are to be placed immediately in anaerobic conditions prior to sample transportation. This reduces the exposure of oxygen to the anaerobic bacteria at the same time simulating the actual anoxic conditions in the TPSF. To sum up, there is a need to incubate the peat culture for a prolonged duration with anoxic conditions, minimal nutrients, and with appropriate supplements in order to isolate anaerobes from TPSF.

GENOMIC APPROACH TO DISCOVER BIOACTIVE SECONDARY METABOLITES PRODUCTION

Whole genome sequencing of bacteria has become increasingly common for routine use in microbiological

laboratories. Subsequently, a large quantity of DNA sequence data from different microorganisms is currently available in public databases. As a result, this creates a path for uncovering novel natural products from microbes by utilizing new bioinformatics tools[62]. For instance, many recent studies have been performing whole genome sequencing of drug-prolific producers such as the *Streptomyces* spp.[63–69] for further investigation of their secondary metabolite production ability This could also be useful for the prediction of novel products of non-ribosomal peptide synthetases (NRPSs) and polyketides synthases (PKSs) through application of various sequence analysis tools[62]. Similarly, this strategy has been applied for *Burkholderia* and *Paenibacillus*[70,71,72]. By taking the genus *Burkholderia* as an example, the determination of genome sequences of these bacteria has essentially created a route for in silico structural prediction, wet lab experimental design, and execution. Genome-guided approaches, which are made possible through accessibility of extensive genome sequence data coupled with genome-mining technologies, have warrant the discovery of structurally and functionally diverse natural products from numerous *Burkholderia* strains[71, 73,74].

CONCLUSION

Tropical peat swamp forests are indeed a promising environment to source for secondary metabolites. However, culture-dependent methodologies should be scrutinized to ensure cultivation of rare bacterial species with important ecological and commercial roles which have never been captured before. Besides, whole genome sequencing of the bacteria in the near future may allow further understanding of the antimicrobial synthesizing capability of these bacteria. Nevertheless, efforts should be made to culture microbes from different genera with similar potential to discover new bioactive secondary metabolites.

Conflict of Interest

The authors declare that there is no conflict of interest in this work.

Author Contributions

K-SO performed the literature search, critical data analysis and performed the writing of this review. Technical support and proofreading were contributed by JW-FL and VL. K-SO, CMY and S-ML founded the review writing project.

Acknowledgments

The authors would like to thank School of Science and Tropical Medicine and Biology Multidisciplinary Platform, Monash University Malaysia for their support.

References

1. Banin, E, Hughes, D, and Kuipers, OP. Bacterial pathogens, antibiotics and antibiotic resistance. FEMS Microbiol Rev 2017; 41(3): 450–452.
2. Munita, JM and Arias, CA. Mechanisms of antibiotic resistance. Microbiol Spect 2016; 4(2): 1–37.
3. Holmes, AH, Moore, LS, Sundsfjord, A, *et al.* Understanding the mechanisms and drivers of antimicrobial resistance. The Lancet 2016; 387(10014): 176–187.
4. WHO. *Antimicrobial resistance in the European Union and the world.* . 2012.
5. Yule, CM. Loss of biodiversity and ecosystem functioning in Indo-Malayan peat swamp forests. Biodivers Conserv 2010; 19(2): 393–409.
6. Page, S, Rieley, J, Shotyk, Ø, *et al.* Interdependence of peat and vegetation in a tropical peat swamp forest. Philosophical Transactions of the Royal Society London B 1999; 354: 1885–1897.
7. Jauhiainen, J, Takahashi, H, Heikkinen, JE, *et al.* Carbon fluxes from a tropical peat swamp forest floor. Glob Chang Biol 2005; 11(10): 1788–1797.
8. Yule, CM and Gomez, LN. Leaf litter decomposition in a tropical peat swamp forest in Peninsular Malaysia. Wetl Ecol Manag 2009; 17(3): 231–241.
9. Beamish, FWH, Beamish, RB, and Lim, SL-H. Fish assemblages and habitat in a Malaysian blackwater peat swamp. Environ Biol Fishes 2003; 68(1): 1–13.
10. Kanokratana, P, Uengwetwanit, T, Rattanachomsri, U, *et al.* Insights into the phylogeny and metabolic potential of a primary tropical peat swamp forest microbial community by metagenomic analysis. Microb Ecol 2011; 61(3): 518–528.
11. Too, CC, Keller, A, Sickel, W, *et al.* Microbial community structure in a Malaysian tropical peat swamp forest: the influence of tree species and depth. Front Microbiol 2018; 9: 2859.
12. Jackson, CR, Liew, KC, and Yule, CM. Structural and functional changes with depth in microbial communities in a tropical Malaysian peat swamp forest. Microb Ecol 2009; 57(3): 402.
13. Ong, CS, Juan, JC, and Yule, CM. Litterfall production and chemistry of *Koompassia malaccensis* and *Shorea uliginosa* in a tropical peat swamp forest: plant nutrient regulation and climate relationships. Trees 2015; 29(2): 527–537.
14. Ong, KS, Aw, YK, Lee, LH, *et al. Burkholderia paludis* sp. nov., an antibiotic-siderophore producing novel Burkholderia cepacia complex species, isolated from Malaysian tropical peat swamp soil. Front Microbiol 2016; 7: 2046.
15. Aw, Y-K, Ong, K-S, Lee, L-H, *et al.* Newly isolated *Paenibacillus tyrfis* sp. nov., from Malaysian tropical peat swamp soil with broad spectrum antimicrobial activity. Front Microbiol 2016; 7: 219.
16. Dobritsa, AP and Samadpour, M. Transfer of eleven species of the genus *Burkholderia* to the genus *Paraburkholderia* and proposal of *Caballeronia* gen. nov. to accommodate twelve species of the genera *Burkholderia* and *Paraburkholderia*. Int J Syst Evol Microbiol 2016; 66(8): 2836–2846.
17. Eberl, L and Vandamme, P. Members of the genus *Burkholderia*: good and bad guys. F1000Research 2016; 5: 1–10.
18. Kunakom, S and Eustáquio, AS. *Burkholderia* as a source of natural products. J Nat Prod 2019; 82(7): 2018–2037.
19. Sawana, A, Adeolu, M, and Gupta, RS. Molecular signatures and phylogenomic analysis of the genus *Burkholderia*: proposal for division of this genus into the emended genus Burkholderia containing pathogenic organisms and a new genus *Paraburkholderia* gen. nov. harboring environmental species. Front Genet 2014; 5: 429.
20. Zhang, L, Xu, D, Wang, F, *et al.* Antifungal activity of *Burkholderia* sp. HD05 against *Saprolegnia* sp. by 2-pyrrolidone-5-carboxylic acid. Aquac 2019; 511: 634198.
21. Bharti, P and Tewari, R. Purification and structural characterization of a phthalate antibiotic from *Burkholderia gladioli* OR1 effective against multi-drug resistant *Staphylococcus aureus*. J Microbiol Biotechnol Food Sci 2015; 5(3): 207–211.
22. Tawfik, KA, Jeffs, P, Bray, B, *et al.* Burkholdines 1097 and 1229, potent antifungal peptides from *Burkholderia ambifaria* 2.2 N. Org Lett 2010; 12(4): 664–666.
23. Lee, C-h, Kim, S, Hyun, B, *et al.* Cepacidine A, a novel antifungal antibiotic produced by *Pseudomonas cepacia*. J Antibiot 1994; 47(12): 1402–1405.
24. Parker, WL, Rathnum, ML, Seiner, V, *et al.* Cepacin A and cepacin B, two new antibiotics produced by *Pseudomonas cepacia*. J Antibiot 1984; 37(5): 431–440.
25. Shoji, Ji, Hinoo, H, Kato, T, *et al.* Isolation of cepafungins I, II and III from *Pseudomonas* species. J Antibiot, 1990; 43(7): 783–787.
26. Abe, M and Nakazawa, T. Characterization of hemolytic and antifungal substance, cepalycin, from *Pseudomonas cepacia*. Microbiol Immunol 1994; 38(1): 1–9.
27. Mahenthiralingam, E, Song, L, Sass, A, *et al.* Enacyloxins are products of an unusual hybrid modular polyketide synthase encoded by a cryptic *Burkholderia ambifaria* genomic island. Chem Biol 2011; 18(5): 665–677.
28. Song, L, Jenner, M, Masschelein, J, *et al.* Discovery and biosynthesis of gladiolin: a *Burkholderia gladioli* antibiotic with promising activity against *Mycobacterium tuberculosis*. J Am Chem Soc 2017; 139(23): 7974–7981.
29. Dose, B, Niehs, SP, Scherlach, K, *et al.* Unexpected bacterial origin

of the antibiotic icosalide: two-tailed depsipeptide assembly in multifarious *Burkholderia* symbionts. ACS Chem Biol 2018; 13(9): 2414–2420.
30. Mitchell, RE and Teh, KL. Antibacterial iminopyrrolidines from *Burkholderia plantarii*, a bacterial pathogen of rice. Org Biomol Chem 2005; 3(19): 3540–3543.
31. Lu, S-E, Novak, J, Austin, FW*, et al.* Occidiofungin, a unique antifungal glycopeptide produced by a strain of *Burkholderia contaminans*. Biochemistry 2009; 48(35): 8312–8321.
32. Han, J-W, Kim, J-D, Lee, J-M*, et al.* Structural elucidation and antimicrobial activity of new phencomycin derivatives isolated from *Burkholderia glumae* strain 411gr-6. J Antibiot 2014; 67(10): 721–723.
33. Ong, KS, Cheow, YL and Lee, SM. The role of reactive oxygen species in the antimicrobial activity of pyochelin. J Adv Res 2017; 8(4), 393–398.
34. Mitchell, RE, Greenwood, DR, and Sarojini, V. An antibacterial pyrazole derivative from *Burkholderia glumae*, a bacterial pathogen of rice. Phytochem 2008; 69(15): 2704–2707.
35. El-Banna, N and Winkelmann, G. Pyrrolnitrin from *Burkholderia cepacia*: antibiotic activity against fungi and novel activities against streptomycetes. J Appl Microbiol 1998; 85(1): 69–78.
36. Rowe, R, Jones, C, Bull, M*, et al.* Characterisation of vietnamycin: a novel *Burkholderia* antibiotic targeting mupirocin-resistant methicillin-resistant *Staphylococcus aureus* (MRSA). Planta Med 2016; 82(S 01): P630.
37. Meyers, E, Bisacchi, G, Dean, L*, et al.* Xylocandin: a new complex of antifungal peptides. J Antibiot 1987; 40(11): 1515-1519.
38. Baek, S-H, Yi, T-H, Lee, S-T*, et al. Paenibacillus pocheonensis* sp. nov., a facultative anaerobe isolated from soil of a ginseng field. Int J Syst Evol Microbiol 2010; 60(5): 1163–1167.
39. Grady, EN, MacDonald, J, Liu, L*, et al.* Current knowledge and perspectives of *Paenibacillus*: a review. Microbial Cell Factories 2016; 15(1): 203.
40. Ash, C, Priest, FG, and Collins, MD. Molecular identification of rRNA group 3 bacilli (Ash, Farrow, Wallbanks and Collins) using a PCR probe test. Antonie Van Leeuwenhoek 1993; 64(3-4): 253–260.
41. He, Z, Yuan, C, Zhang, L*, et al.* N□terminal acetylation in paenibacillin, a novel lantibiotic. FEBS Lett 2008; 582(18): 2787–2792.
42. Lohans, CT, Huang, Z, van Belkum, MJ*, et al.* Structural characterization of the highly cyclized lantibiotic paenicidin A via a partial desulfurization/reduction strategy. J Am Chem Soc 2012; 134(48): 19540–19543.
43. Baindara, P, Chaudhry, V, Mittal, G*, et al.* Characterization of the antimicrobial peptide penisin, a class Ia novel lantibiotic from *Paenibacillus* sp. strain A3. Antimicrob Agents Chemother 2016; 60(1): 580–591.
44. Nation, RL and Li, J. Polymyxins. In: Kucers the Use of Antibiotics: A Clinical Review of Antibacterial, Antifungal, Antiparasitic, and Antiviral Drugs. CRC Press; 2017: 1420–1449.
45. Tambadou, F, Caradec, T, Gagez, A-L*, et al.* Characterization of the colistin (polymyxin E1 and E2) biosynthetic gene cluster. Arch Microbiol 2015; 197(4): 521–532.
46. Qian, C-D, Wu, X-C, Teng, Y*, et al.* Battacin (Octapeptin B5), a new cyclic lipopeptide antibiotic from *Paenibacillus tianmuensis* active against multidrug-resistant Gram-negative bacteria. Antimicrob Agents Chemother 2012; 56(3): 1458–1465.
47. Huang, E, Guo, Y, and Yousef, AE. Biosynthesis of the new broad-spectrum lipopeptide antibiotic paenibacterin in *Paenibacillus thiaminolyticus* OSY-SE. Res Microbiol 2014; 165(3): 243–251.
48. Ding, R, Wu, X-C, Qian, C-D*, et al.* Isolation and identification of lipopeptide antibiotics from *Paenibacillus elgii* B69 with inhibitory activity against methicillin-resistant *Staphylococcus aureus*. J Microbiol 2011; 49(6): 942–949.
49. Pichard, B, Larue, J-P, and Thouvenot, D. Gavaserin and saltavalin, new peptide antibiotics produced by *Bacillus polymyxa*. FEMS Microbiol Lett 1995; 133(3): 215–218.
50. Kajimura, Y and Kaneda, M. Fusaricidins B, C and D, new depsipeptide antibiotics produced by *Bacillus polymyxa* KT-8: isolation, structure elucidation and biological activity. J Antibiot 1997; 50(3): 220–228.
51. Dedysh, SN. Cultivating uncultured bacteria from northern wetlands: knowledge gained and remaining gaps. Front Microbiol 2011; 2: 184.
52. Mehta, A and Rosato, YB. Identification of differentially expressed genes of *Xanthomonas axonopodis* pv. citri by representational difference analysis of cDNA. Genet Mol Biol 2005; 28(1): 140–149.
53. Schulte, R and Bonas, U. A *Xanthomonas* pathogenicity locus is induced by sucrose and sulfur-containing amino acids. Plant Cell 1992; 4(1): 79–86.
54. Dedysh, SN, Pankratov, TA, Belova, SE *et al.* Phylogenetic analysis and in situ identification of bacteria community composition in an acidic Sphagnum peat bog. Appl Environ Microbiol 2006; 72(3): 2110–2117.
55. Kulichevskaya, IS, Serkebaeva, YM, Kim, Y*, et al. Telmatocola sphagniphila* gen. nov., sp. nov., a novel dendriform planctomycete from northern wetlands. Front Microbiol 2012; 3: 146.
56. Dedysh, SN and Dunfield, PF. *Facultative and obligate methanotrophs: how to identify and differentiate them*. In: *Methods Enzymol*Elsevier; 2011: 31–44.
57. Edenborn, SL and Sexstone, A. DGGE fingerprinting of culturable soil bacterial communities complements culture-independent analyses. Soil Biol Biochem 2007; 39(7): 1570–1579.
58. Taylor, J, Wilson, B, Mills, MS*, et al.* Comparison of microbial numbers and enzymatic activities in surface soils and subsoils using various techniques. Soil Biol Biochem 2002; 34(3): 387–401.
59. Pankratov, TA and Dedysh, SN. *Granulicella paludicola* gen. nov., sp. nov., *Granulicella pectinivorans* sp. nov., *Granulicella aggregans* sp. nov. and *Granulicella rosea* sp. nov., acidophilic, polymer-degrading acidobacteria from Sphagnum peat bogs. Int J Syst Evol Microbiol 2010; 60(12): 2951–2959.
60. Kulichevskaya, IS, Detkova, EN, Bodelier, PL*, et al. Singulisphaera rosea* sp. nov., a planctomycete from acidic Sphagnum peat, and emended description of the genus *Singulisphaera*. Int J Syst Evol Microbiol 2012; 62(1): 118–123.
61. Sizova, MV, Panikov, NS, Spiridonova, EM*, et al.* Novel facultative anaerobic acidotolerant *Telmatospirillum siberiense* gen. nov. sp. nov. isolated from mesotrophic fen. Syst Appl Microbiol 2007; 30(3): 213–220.
62. Zerikly, M and Challis, GL. Strategies for the discovery of new natural products by genome mining. Chembiochem 2009; 10(4): 625–633.
63. Ser, H-L, Tan, W-S, Yin, W-F*, et al.* Whole genome sequence of *Streptomyces humi* strain MUSC 119^T isolated from intertidal soil. Prog Drug Discov Biomed Sci 2019; 2(1): a0000020.
64. Ser, H-L, Tan, W-S, Mutalib, N-SA*, et al.* Genome sequence of *Streptomyces gilvigriseus* MUSC 26^T isolated from mangrove forest. Braz J Microbiol 2018; 49(2): 207–209.
65. Ser, H-L, Chan, K-G, Tan, W-S*, et al.* Complete genome of mangrove-derived anti-MRSA streptomycete, *Streptomyces pluripotens* MUSC 135^T. Prog Micobes Mol Biol 2018; 1(1): a0000004.
66. Ser, H-L, Tan, W-S, Ab Mutalib, N-S*, et al.* Draft genome sequence of mangrove-derived *Streptomyces* sp. MUSC 125 with antioxidant potential. Front Microbiol 2016; 7: 1470.
67. Ser, H-L, Tan, W-S, Ab Mutalib, N-S*, et al.* Genome sequence of *Streptomyces mangrovisoli* MUSC 149^T isolated from intertidal sediments. Braz J Microbiol 2018; 49(1): 13–15.
68. Law, JW-F, Ser, H-L, Duangjai, A*, et al. Streptomyces colonosanans* sp. nov., a novel actinobacterium isolated from Malaysia mangrove soil exhibiting antioxidative activity and cytotoxic potential against human colon cancer cell lines. Front Microbiol 2017; 8: 877.
69. Law, JW-F, Ser, H-L, Ab Mutalib, N-S*, et al. Streptomyces monashensis* sp. nov., a novel mangrove soil actinobacterium from East Malaysia with antioxidative potential. Sci Rep 2019; 9(1): 1–18.
70. Ma, M, Wang, C, Ding, Y*, et al.* Complete genome sequence of *Paenibacillus polymyxa* SC2, a strain of plant growth-promoting rhizobacterium with broad-spectrum antimicrobial activity. J Bacteriol 2011; 193(1): 311–312.
71. Aw, YK, Ong, KS, Yule, CM, *et al.* Draft genome sequence of *Paenibacillus* sp. strain MSt1 with broad antimicrobial activity, isolated from Malaysian tropical peat swamp soil. Genome Announc 2014; 2(5), e01024–14.
72. Esmaeel, Q, Pupin, M, Kieu, NP*, et al.* Burkholderia genome mining for nonribosomal peptide synthetases reveals a great potential for novel siderophores and lipopeptides synthesis. MicrobiologyOpen 2016; 5(3): 512–526.
73. Liu, X and Cheng, Y-Q. Genome-guided discovery of diverse natural products from *Burkholderia* sp. J Ind Microbiol Biotechnol 2014; 41(2): 275–284.
74. Ong, KS, Aw, YK, Gan, HM, *et al.* Draft genome sequences of two antimicrobial-producing *Burkholderia* sp. strains, MSh1 and MSh2, isolated from Malaysian tropical peat swamp forest soil. Genome Announc 2014; 2(5), e01032–14.