



***MICROBIAL COMMUNITY CHANGES DURING CO-COMPOSTING OF
OIL PALM EMPTY FRUIT BUNCH WITH PALM OIL MILL EFFLUENT
ANAEROBIC SLUDGE***

MOHD HUZAIRI BIN MOHD ZAINUDIN

FBSB 2015 27



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MOHD HUZAIRI BIN MOHD ZAINUDIN

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

February 2015

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in Fulfillment of the Requirement for the Degree of Doctor Philosophy

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February 2015

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The oil palm industry in Malaysia produces residues such as oil palm empty fruit bunch (OPEFB) and palm oil mill effluent (POME) anaerobic sludge which can be transformed into high value-added products. The utilization of these residues in the form of decomposed biomass for agricultural use create interest in improving the composting process to be more efficient and sustainable. During the composting process, organic materials including lignocellulose are broken down by the bacterial communities which develop in line with the symbiotic relationship among the species present. Recently, the enhanced co-composting of OPEFB and POME anaerobic sludge process has spurred increase attention into finding how microbial diversity influence the degradation process and what microbes are involved during the process. Hence, the overall objective of this study was to elucidate the bacterial communities participating in the enhanced composting process through isolation and characterization of cultivated microbes, polymerase chain reaction- denaturing gradient gel electrophoresis (PCR-DGGE), 16S rRNA clone library techniques and next generation sequencing (pyrosequencing). In the first study, 27 cellulolytic and hemicellulolytic bacteria strains were isolated at different stages of composting of which 23 strains were identified as closely related to *Bacillus subtilis*, *Bacillus firmus*, *Thermobifida fusca*, *Thermomonospora* sp. S22-23, *Cellulomonas* sp. ANA-WS2, *Ureibacillus thermosphaericus*, *Paenibacillus barengoltzii*, *Paenibacillus campinasensis* BL11, *Geobacillus thermodenitrificans* and *Pseudoxanthomonas byssovorax*. All of these were known to be commonly involved in lignocellulose degradation. Four strains related to *Exiguobacterium acetylicum* and *Rhizobium* sp which are previously not known as lignocellulosic degraders were found with cellulolytic and hemicellulolytic activities. Consequently, PCR-DGGE and 16s rRNA clone library methods were used to visualize the shift in microbial community and to identify the bacterial community species. PCR-DGGE showed that the bacterial community drastically shifted and the banding patterns correlate with the abundance of phyla *Actinobacteria* (high G+C content DNA bacterium) and *Firmicutes* (low G+C content DNA bacterium) during thermophilic, cooling and maturing stages as detected in the clone library. 16S rRNA clones belonging to the genera *Bacillus*, *Exiguobacterium*, *Desemzia*, and *Planococcus* were the dominant group with species closely related to *Solibacillus silvestris* was found to be major contributors to the changes in the lignocellulosic component throughout composting. Clones identified as *Thermobacillus xylanilyticus*, *Brachybact-*

erium faecium, *Cellulosimicrobium cellulans*, *Cellulomonas* sp., and *Thermobifida fusca*, which are known to be lignocellulosic-degrading bacteria, were also detected. The results were in line with identification of isolated cellulolytic and hemicellulolytic bacteria and revealed the presence of these bacteria types at different stages of composting. In depth analysis of the bacterial community structure and shift in microbial abundance using pyrosequencing showed that the largest bacterial communities were belonged to phyla *Firmicutes* and *Proteobacteria*, in which their species related to *Devosia yakushimensis* and *Planococcus rifietoensis* were found during thermophilic, cooling and maturing stages. It is of interest to report for the first time that sequence related to *Devosia yakushimensis* was found to be a dominant bacterial species during thermophilic stage which was not discovered in the analysis of clone library. The data obtained suggests that clone libraries can overlook important groups of bacteria, hindering the link between the microbial diversity to operational performance. The results of the present study clearly demonstrate the ensuing changes that take place in the microbial community during co-composting of oil palm empty fruit bunch with palm oil mill effluent anaerobic sludge.

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

PERUBAHAN KOMUNITI MIKROB SEMASA PENGKOMPOSAN TANDAN KOSONG KELAPA SAWIT DENGAN ENAPCEMAR ANAEROBIK EFFLUEN KELAPA SAWIT

Oleh

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Industri kelapa sawit di Malaysia menghasilkan sisa seperti tandan kosong kelapa sawit dan enapcemar anaerobik effluen kelapa sawit yang boleh diubah menjadi produk nilai tambah yang tinggi. Penggunaan sisa ini dalam bentuk biojisim terurai untuk kegunaan pertanian mewujudkan kepentingan dalam mempertingkatkan proses pengkomposan yang lebih cekap and mapan. Semasa proses pengkomposan, bahan-bahan organik seperti lignosellulosa diuraikan oleh komuniti bakteria yang berkembang selaras dengan hubungan simbiotik antara spesies yang hadir. Terkini, kecekapan proses pengkomposan OPEFB bersama enapcemar anaerobik POME telah mendorong meningkatkan perhatian dalam mencari pengaruh bagaimana kelpbagai mikroorganisma menjalankan proses penguraian dan mikroorganisma yang terlibat dalam proses tersebut. Oleh itu, objektif keseluruhan kajian ini adalah untuk menjelaskan komuniti bakteria yang terlibat dalam proses pengkomposan yang dipertingkatkan melalui pengasingan dan pencirian mikrob yang dihidupkan, tindak balas rantai polimerase-elektroforesis gel kecerunan nyahasli (PCR-DGGE) dan perpustakaan klon 16S rRNA gene dan penyusunan generasi akan datang (pyro-penyusunan. Di dalam kajian pertama, 27 bakteria pengurai selulosa dan hemiselulosa telah dipencilkan daripada peringkat proses pengkomposan yang berbeza di mana 23 bakteria telah dikenalpasti sebagai berkait rapat dengan *Bacillus subtilis*, *Bacillus firmus*, *Thermobifida fusca*, *Thermomonospora* sp. S22-23, *Cellulomonas* sp. ANA-WS2, *Ureibacillus thermosphaericus*, *Paenibacillus barengoltzii*, *Paenibacillus campinasensis* BL11, *Geobacillus thermodenitrificans* dan *Pseudoxanthomonas byssovorax*, semua yang telah diketahui umum terlibat dalam penguraian lignoselulosa. Empat bakteria yang berkaitan dengan *Exiguobacterium acetylicum* and *Rhizobium* sp yang sebelum ini tidak dikenali sebagai pengurai lignoselulosa telah ditemui dengan dan aktiviti selulose and hemiselulosa. Seterusnya, PCR-DGGE dan perpustakaan klon 16S rRNA gene telah digunakan untuk menggambarkan pangalihan komuniti mikoorganisma dan mengenalpasti spesis komuniti bakteria. PCR-DGGE menunjukkan bahawa komuniti bakteria beralih secara drastik dan keputusan corak jalur DGGE berhubung rapat dengan,banyaknya filum *Actinobacteria* (bakteria tinggi kandungan G+C DNA) dan *Firmicutes* (bakteria rendah kandungan G+ C DNA) pada peringkat termofilik serta penyejukan dan matang sebagaimana yang telah dikesan di dalam perpustakaan klon. Klon 16S rRNA kepunyaan genus *Bacillus*, *Exiguobacterium*, *Desemzia*, dan *Planococcus* ialah kumpulan dominan bersama dengan spesies yang

berkait rapat dengan *Solibacillus silvestris* didapati telah menjadi penyumbang utama kepada perubahan komponen lignoselulosa di sepanjang pengkomposan. Klon yang dikenal pasti sebagai *Thermobacillus xylanilyticus*, *Brachybacterium faecium*, *Cellulosimicrobium cellulans*, *Cellulomonas* sp., dan *Thermobifida fusca* yang dikenali sebagai bakteria pengurai lignoselulosa, juga telah dikesan. Keputusan yang diperolehi selaras dengan pemencilan bakteria pengurai selulosa dan hemiselulosa yang telah dikenalpasti dan seterusnya mendedahkan kehadiran bakteria jenis ini dipelbagai peringkat dalam proses pengkomposan. Analisis mendalam struktur komuniti bakteria dan peralihan lambakan mikrob dengan menggunakan pyro-penjujukan menunjukkan bahawa komuniti bakteria terbesar adalah kepunyaan filum *Firmicutes* dan *Proteobacteria* di mana spesies mereka yang berkaitan dengan *Devosia yakushimensis* dan *Planococcus rifietoensis* yang didapati semasa peringkat termofilik, penyejukan dan matang. Kajian ini buat pertama kalinya melaporkan bahawa jujukan berkait rapat dengan *Devosia yakushimensis*, telah didapati menjadi sebagai dominan spesies bakteria pada peringkat termofilik yang mana ianya tidak ditemui dalam analisis perpustakaan klon. Data yang diperolehi juga menunjukkan bahawa perpustakaan klon boleh mengabaikan beberapa kumpulan penting bakteria, menghalang kupayaan untuk menghubungkan kepelbagaian mikrob kepada prestasi operasi. Hasil kajian ini jelas menunjukkan perubahan yang berlaku dalam komuniti mikrob semasa pengkomposan tandan kosong kelapa sawit bersama enapcemar anaerobik effluen kelapa sawit.

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I certify that a Thesis examination committee has met on 27 February 2015 to conduct the final examination of Mohd Huzairi b. Mohd Zainudin on his thesis entitled “Microbial community changes during co-composting of oil palm empty fruit bunch with palm oil mill effluent anaerobic sludge” in accordance with Universities and University College Act and the Constitution of the Universiti Putra Malaysia [P.U. (A) 106] 15 March 1998. The committee recommends that the candidate be awarded the Doctor of Philosophy.

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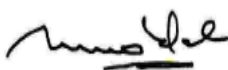
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LIST OF ABBREVIATIONS

Bp	Base pair
BLAST	Basic logical alignment search tool
BOD	Biological oxygen demand
CMC	Carboxymethylcellulose
COD	Chemical oxygen demand
CPO	Crude palm oil
DGGE	Denaturing gel gradient electrophoresis
DNA	Deoxyribonucleic acid
<i>E.coli</i>	<i>Escherichia coli</i>
dNTP	deoxynucleotide triphosphate
FFB	Fresh fruit bunch
IPTG	Isopropyl β -1-D-1-thiogalactopyranoside
MPOB	Malaysian Palm Oil Board
MPOC	Malaysian Palm Oil Congress
NCBI	National Center for Biotechnology Information
OPEFB	Oil palm empty fruit bunch
OTU	Operational Taxonomical unit
PCoA	Principal coordinates analysis
PCR	Polymerase chain reaction
POME	Palm oil mill effluent
Qiime	Quantitative insight into microbial ecology
RDP	Ribosomal database project
RSPO	Rountable on Sustainable of palm oil
RT-PCR	Real-time polymerase chain reaction
SREP	Small renewable energy program
rRNA	ribosomal ribonucleic acid
SEM	Scanning electron microscope

sp.

species

X-gal

5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside





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CHAPTER 1

INTRODUCTION

1.1 Background

With the high market price of palm oil, there is an increasing demand for increasing the supply by the industry. This leads to opening up lands where virgin forests are cleared for plantation purposes especially by major palm oil producers like Malaysia and Indonesia. As a result, the clearing of forest will not only destroy the biodiversity but also endanger the existing microflora and fauna. In addition, open burning; the most common practice that has been used to clear the forest would cause air pollution, haze and climate change. The open burning method has been claimed as one of major contributor to global warming due to the release of greenhouse gases. In order to achieve sustainability in oil palm production, several implementation guidelines have been proposed in the Roundtable on Palm Oil Production (RSPO) which was formed in August 2003 amongst which are conservation of biodiversity, land management, soil and water conservation, zero burning replanting technique, waste treatment and recycling of mill by products (Ooi and Subramaniam, 2008).

Currently, oil palm is a major plantation crop in Malaysia and the country has become the second largest producer of palm oil with a total of 16 million tones or 43% of the total world supply (Shuit *et al.*, 2009). In 2006, palm oil plantation area had been reported to be 4.2 million hectares and increased to 4.98 million hectares in 2011 (Shuit *et al.*, 2009; Ng *et al.*, 2012). The increase in palm oil plantation is due to the growing global demand of edible oil especially this oil. With the enhancement in palm oil production, the amount of residues generates from the industry also increases. The amount of residues produced in oil palm industry are mainly palm oil mill effluent (POME) followed by oil palm empty fruit bunch (OPEFB). POME contains high amount of organic matter with chemical oxygen demand (COD) of 30,000 – 100,000 mg/L and biological oxygen demand (BOD) of 11,000 – 44,000 mg/L and also considerable amounts of plant nutrients (Gobi and Vadivelu, 2013; Singh *et al.*, 2011). In common practice, anaerobic digestion is the method generally used to treat POME. Through this process, the organic matter is converted into methane biogas by a complex consortium of microorganism. POME anaerobic sludge, the by-product of anaerobic digestion consists of high amount of nutrients and has the potential to be used as a fertilizer for oil palm tree. OPEFB is the largest component of lignocellulosic waste materials produced in palm oil mill. The most common practice to eliminate this waste is through direct burning for energy generation and natural composting for production of organic fertilizer in the oil palm plantation. However the major drawback of this practice is that it releases greenhouse gases and takes a long period to decompose.

In order to encourage the sustainability of palm oil production, several approaches are developed through the utilization of plantation by-products (Shuit *et al.*, 2009; Singh *et al.*, 2011; Chin *et al.*, 2013; Gobi and Vadivellu, 2013). It has been reported by Schuchardt *et al.*, (2008) that co-composting is one the suitable methods to full-fill those guidelines implemented during the RSPO discussion which focused on reducing and recycling of waste, to reduce pollution and emission of greenhouse gases. As

reported by Yoshizaki *et al.*, (2013), the economic analysis of integrated biogas energy and compost production revealed that co-composting of EFB with POME anaerobic sludge is economically viable as compared to when the biogas energy and composting technology are installed individually. Therefore, co-composting could be one of the good solutions for sustainable management in oil palm production.

Production of compost from agro-industrial waste has currently been widely used by many researchers due the cheap and abundant resources. These wastes include organic matters which mainly consist of lignocellulose materials. One of the most common problems with agricultural waste composting is the decomposition of the recalcitrant compound such as lignocellulose complex structure which requires action of many different types of enzyme (Vargas-Garcia *et al.*, 2007). This obstacle may affect the compost productivity and thus, increase the cost of operation, energy and time in the compost production.

In order to overcome this problem, the application of the right microbes will ensure that efficient composting can be achieved and nurtured within the composting materials to trigger, accelerate and sustain the composting process. This strategy could be effectively viable for enhancing the compost productivity and may play an important role in the production of compost at pilot scale. Previous studies have reported that the compost productivity can be increased with the addition of inocula (Kanamam *et al.*, 2011; Yeoh *et al.*, 2011; Amira *et al.*, 2011; Kavitha *et al.*, 2013)

1.2 Problem statement

Although the inoculation of effective microorganisms has been used as a method to enhance the productivity of compost, but it is difficult to be proven commercially viable in large scale operation due to potential operating cost in preparation of inocula. Generally, microorganisms are added into the compost in order to increase the productivity by reducing the composting period. However, previous research has shown that the co-composting process can be enhanced without the addition of microorganism (Baharuddin *et al.*, 2010a). This system relies on the indigenous microbes present in POME anaerobic sludge which are assumed to be responsible for enhancing the compost productivity. In this technology, the use of POME anaerobic sludge as composting materials has also been proven to be economically viable through the integrated system.

As composting is a microbiologically-mediated process, the microbial communities have a large influence on the overall process and thus have a direct influence on the economic viability of the composting system. While numerous studies have examined the microbial communities in composting system (Mehta *et al.*, 2014; Nakasaki *et al.*, 2009; Ryckeboer *et al.*, 2003b), the microbial diversity and their activities in the present enhanced composting process system have not been well defined, due to the limitations in approaches including time, cost, and capability of each methods for determining the microbial diversity. Although various molecular analysis methods have been used to elucidate the microbial diversity (Baharuddin *et al.*, 2009; Guo *et al.*, 2007; Liew *et al.*, 2009; Lim *et al.*, 2009; Mehta *et al.*, 2014), the data set was often small and the sequences were less than 200 bp for each data set. In addition, the estimation of species richness for other composting systems is still less available or non-conclusive and the comparisons of the microbial diversity between previous results are always contradictory.

1.3 Scope of study

In this study, the prospect of microbial diversity of enhanced co-composting of OPEFB with POME anaerobic sludge was investigated. In order to initially examine the bacteria responsible for enhancing the production of compost, the first objective was performed based on the culture-dependent method through isolation and identification of cellulolytic and hemicellulolytic bacteria at different stages of the composting process. The goal of this study was to elucidate the cellulolytic and hemicellulolytic bacteria communities, which were assumed to be responsible for accelerating the production of compost.

The second objective was based on the examination of microbial communities through culture-independent approach. In this study, correlation between microbial community structure with the changes in the biochemical properties before, during and after composting process was determined. Polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) was used to visualize the changes in microbial community structure between the communities present at the start of compost operation to the community that ultimately established itself when the POME anaerobic sludge was continuously added throughout the composting process. In this study, microbiota analysis of 16S rRNA clone library was used to elucidate the bacterial communities during the composting process. The correlation of bacteria community succession and structure between the visualized PCR- DGGE banding pattern and the species identified through 16S rRNA clone library was determined.

The third objective was designed to take advantage of the recent advances in DNA sequencing to investigate bacterial diversity in depth and more thoroughly than previously achievable. The goal of this objective was to investigate in depth the bacterial community in order to clarify specific species involved and supported the enhanced co-composting process using 454 pyrosequencing methods. With this study, a deeper and more thorough investigation of bacterial communities and structure was carried out to explore and extend the results observed in the second objective.

1.4 Objectives

The primary objective of this research was to reveal the microbial communities participating in the co-composting process using culture-based and molecular -based methods. The specific objectives were:

1. To isolate and characterize indigenous cellulolytic and hemicellulolytic bacteria during enhanced co-composting of oil palm empty fruit bunch with palm oil mill effluent anaerobic sludge
2. To identify and characterize the bacterial community structure and biochemical changes associated with co-composting of lignocellulose oil palm empty fruit bunch by DGGE and clone library methods.
3. To assess in-depth the bacterial community succession during enhanced rapid co-composting of OPEFB and palm oil mill effluent anaerobic sludge by high-throughput pyrosequencing.

REFERENCES

- Abd-Rahman, R. Kalil, M. S. and Abu Zahrim, Y. 2003. Composting palm oil mill sludge—sawdust: effect of different amount of sawdust. In: Proceedings of national workshop in conjunction with ARRPET workshop on wastewater treatment and recycling 2: removal chloroorganics and heavy metals. ISBN 983-2982-04-9
- Abid, N., Chamkha, M., Godon, J.J. and Sayadi, S. 2007. Involvement of microbial populations during the composting of olive mill wastewater sludge. *Environmnetal Technology* 28: 751–60.
- Adams, J.D.W. and Frostick, L.E. 2009. Analysis of bacterial activity, biomass and diversity during windrow composting. *Waste Management* 29: 598–605.
- Ahmad, A. L., Ismail, S. and Bhatia, S. 2003. Water recycling from palm oil mill effluent (POME) using membrane technology. *Desalination* 157: 87–95.
- Ahmad, M. N., Mokhtar, M. N., Baharuddin, A. S, Lim, S. H., Ali, S. R. A., Abd-Aziz, S., Rahman, N. R. A, and Hassan M. A. 2011. Changes in physicochemical and microbial community during co-composting of oil palm frond with palm oil mill effluent anaerobic sludge. *BioResources* 6: 4762-4780.
- Al-Daher, R., Al-Awadhi, N. and El-Nawawy, A. 1998. Bioremediation of damaged desert environment using the windrow soil pile system in Kuwait. *Environment International*. 24: 175–180.
- Alfreider, A., Peters, S., Tebbe, C.C., Rangger, A. and Insam, H. 2002. Microbial Community Dynamics During Composting of Organic Matter as Determined by 16S Ribosomal DNA Analysis. *Compost Science & Utilization*. 10: 303–312.
- Alrawi, R.A., Ahmad, A., Ismail, N. and Kadir, M.O.A. 2011. Anaerobic co-digestion of palm oil mill effluent with rumen fluid as a co-substrate. *Desalination* 269: 50–57.
- Amira, R.D., Roshanida, A.R., Rosli, M.I., Zahrah, M.F.S.F., Anuar, J.M. and Adha, C.M.N. 2011. Bioconversion of empty fruit bunches (EFB) and palm oil mill effluent (POME) into compost using *Trichoderma virens*. *African Journal of Biotechnology* 10:18775-18780
- Amir, S., Hafidi, M., Merlina, G. and Revel, J.C. 2005. Sequential extraction of heavy metals during composting of sewage sludge. *Chemosphere* 59: 801–810.

- Amir, S., Merlina, G., Pinelli, E., Winterton, P., Revel, J.C. and Hafidi, M. 2008. Microbial community dynamics during composting of sewage sludge and straw studied through phospholipid and neutral lipid analysis. *Journal of Hazardous Material* 159: 593–601.
- Amore, A., Pepe, O., Ventrino, V., Birolo, L., Giangrande, C. and Faraco, V. 2013. Industrial waste based compost as a source of novel cellulolytic strains and enzymes. *FEMS Microbiology Letter* 339: 93–101.
- Ampe, F., Sirvent, A. and Zakhia, N. 2001. Dynamics of the microbial community responsible for traditional sour cassava starch fermentation studied by denaturing gradient gel electrophoresis and quantitative rRNA hybridization. *International Journal of Food Microbiology* 65: 45–54.
- An, D. S., Im, W. T., Yang, H. C., Kang, M. S., Kim, K. K., Jin, L., Kim, M. K., and Lee, S.T. 2005. *Cellulomonas terrae* sp. nov., a cellulolytic and xylanolytic bacterium isolated from soil. *International Journal of Systematic and Evolutionary Microbiology* 55: 1075-1079.
- Anastasi, A., Varese, G.C. and Filipello, M.V. 2005. Isolation and identification of fungal communities in compost and vermicompost. *Mycologia* 97: 33–44.
- Antizar-Ladislao, B., Lopez-Real, J. and Beck, A.J. 2005. Laboratory studies of the remediation of polycyclic aromatic hydrocarbon contaminated soil by in-vessel composting. *Waste Management* 25: 281–289.
- Araya, R., Tani, K., Takagi, T., Yamaguchi, N. and Nasu, M. 2003. Bacterial activity and community composition in stream water and biofilm from an urban river determined by fluorescent in situ hybridization and DGGE analysis. *FEMS Microbiology Ecology* 43: 111–119.
- Arya, M., Shergill, I.S., Williamson, M., Gommersall, L., Arya, N., Patel, H.R.H., 2005. Basic principles of real-time quantitative PCR. *Expert Review of Molecular Diagnostics* 5: 209–19.
- Arslan, E.I., Ünlü, A. and Topal, M. 2011. Determination of the Effect of Aeration Rate on Composting of Vegetable-Fruit Wastes. *CLEAN - Soil, Air, Water* 39: 1014–1021.
- Astimar, A.A. and Wahid, M.B. 2007. Supply outlook of oil palm biomass in Malaysia. Proceeding of the Seminar on Ecomat Research and Promotion: Towards Enrichment of the Environment pp. 13-26.
- Atif, A., Fakhrulrazi, A., Ngan, M., Morimoto, M., Iyuke, S. and Veziroglu, N. 2005. Fed batch production of hydrogen from palm oil mill effluent using anaerobic microflora. *International Journal of Hydrogen Energy* 30: 1393–1397.

- Bachman, S.L. and McCarthy, A.J. 1991. Purification and cooperative activity of enzymes constituting the xylan-degrading system of *Thermomonospora fusca*. *Applied and Environmental Biotechnology*. 57: 2121-2130
- Baharuddin, A. S., Kazunori, N., Abd-Aziz, S., Tabatabaei, M., Abdul Rahman, N. R., Hassan, M. A., Sakai, K. and Shirai, Y. 2009a. Characteristic and microbial succession in co-composting of oil palm empty fruit bunch and partially treated palm oil mill effluent. *The Open Biotechnology Journal* 3: 91-100.
- Baharuddin, A. S., Wakisaka, W., Shirai, Y., Abd Aziz, S., Abdul Rahman, N. A. and Hassan, M. A. 2009b. Co-composting of empty fruit bunch and partially treated palm oil mill effluent in pilot scale,” *International Journal of Agricultural Research*. 4: 69-78.
- Baharuddin, A. S., Lim, S. H., Md Yusof, M. Z., Rahman, N. A., Umikalsom, M. S., Hassan, M. A., Wakisaka, M., Sakai, K., and Shirai, Y. (2010a). “Effects of palm oil mill effluent (POME) anaerobic sludge from 500 m³ of closed anaerobic methane digested tank on pressed-shredded empty fruit bunch (EFB) composting process,” *African Journal of Biotechnology* 9: 2427-2436.
- Baharuddin, A.S., Razak, M.N.A., Hock, L.S., Ahmad, M.N., Abd-Aziz, S., Abdul Rahman, N.A., Md Shah, U.K., Hassan, M.A., Sakai, Kenji., and Shirai, Y. (2010b). Isolation and Characterization of Thermophilic Cellulase-Producing Bacteria from Empty Fruit Bunches-Palm Oil Mill Effluent. *American Journal of Applied Sciences* 7: 56–62.
- Baharuddin, A.S., Rahman, N.A.A., Umikalsom, M.D., Hassan, M.A, Wakisaka, M., Sakai, K. and Shirai, Y. 2011 Evaluation of pressed shredded empty fruit bunch (EFB)-palm oil mill effluent (POME) anaerobic sludge based compost using Fourier transform infrared (FTIR) and nuclear magnetic resonance (NMR) analysis. *African Journal of Biotechnology* 10: 2427-2436.
- Bhatia, A., Madan, S., Sahoo, J., Ali, M., Pathania, R. and Kazmi, A.A. 2013. Diversity of bacterial isolates during full scale of drum composting. *Waste Management* 33: 1595-1601.
- Barman, D., Habib, M. R., Islam, M. F., Hossain, K., and Yeasmin, T. 2011. Isolation of cellulolytic bacterial strain from soil for effective and efficient bioconversion of solid waste,” *Life Science and Medical Research* 25: 1-5.
- Barrington, S., 2002. Effect of carbon source on compost nitrogen and carbon losses. *Bioresource Technology* 83: 189–194.
- Bautista, V. V, Monsalud, R.G. and Yokota, A. 2010. *Devosia yakushimensis* sp. nov., isolated from root nodules of *Pueraria lobata* (Willd.) Ohwi. *International Journal of Systematic and Evolutionary Microbiology* 60: 627–32.

- Beffa T., Blanc M., Marilley L., Fischer J.L., Lyon P.F. and Aragno M. 1996. Taxonomic and metabolic microbial diversity during composting. In: De Bertoldi, M., Sequi, P., Lemmes, B., Papi, T. (Eds) *The Science of Composting*. Chapman and Hall, London pp. 149-161
- Béki, E., Nagy I., Vanderleyden, J., Jäger, S., Kiss, L., Fülöp, L., Hornok, L. and Kukolya, J. 2003. Cloning and heterologous expression of a β -D-mannosidase (EC 3.2.1.25)-Encoding gene from *Thermobifida Fusca* TM51. *Applied in Environmental Microbiology* 69: 1944-1952.
- Ben Omar, N. and Ampe, F. 2000. Microbial Community Dynamics during Production of the Mexican Fermented Maize Dough Pozol. *Applied Environmental Microbiology* 66: 3664–3673.
- Banegas, V., Moreno, J.L., Moreno, J.I., García, C., León, G. and Hernández, T. 2007. Composting anaerobic and aerobic sewage sludge using two proportions of sawdust. *Waste Management* 27: 1317-1327.
- Benito, M., Masaguer, A., De Antonio, R. and Moliner, A. 2005. Use of pruning waste compost as a component in soilless growing media. *Bioresource Technology* 96: 597–603.
- Bernal, M. P., Navarro A.F., Cegarra, A.R.J. and Gracia, D. 1996. Carbon and nitrogen transformation during composting of sweet shorghum baggase. *Biology and Fertility of Soils*. 22: 141-148
- Bernal, M.P., Navarro, A.F., Sánchez-Monedero, M.A., Roig, A. and Cegarra, J. 1998. Influence of sewage sludge compost stability and maturity on carbon and nitrogen mineralization in soil. *Soil Biology and Biochemistry* 30: 305–313.
- Bibby, K., Viau, E. and Peccia, J. 2010. Pyrosequencing of the 16S rRNA gene to reveal bacterial pathogen diversity in biosolids. *Water Research* 44: 4252–4260.
- Blanc, M., 1999. Thermophilic bacterial communities in hot composts as revealed by most probable number counts and molecular (16S rDNA) methods. *FEMS Microbiology Ecology* 28: 141–149.
- Bollmann, A., Palumbo, A. V, Lewis, K., Epstein, S.S., 2010. Isolation and physiology of bacteria from contaminated subsurface sediments. *Applied and Environmental Microbiology* 76: 7413–9.
- Borchert, N., Dieterich, C., Krug, K., Schutz, W., Jung, S., Nordheim, A., Sommer, R.J., Macek, B., 2010. Proteogenomics of *Pristionchus pacificus* reveals distinct proteome structure of nematode models. *Genome Research* 20: 837–846.

- Brewer, L.J., Sullivan, D.M., 2003. Maturity and Stability Evaluation of Composted Yard Trimmings. *Compost Science & Utilization* 11: 96-112.
- Buée, M., Reich, M., Murat, C., Morin, E., Nilsson, R.H., Uroz, S. and Martin, F. 2009. 454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. *The New Phytologist* 184: 449–56.
- Cahyani, V.R., Matsuya, K., Asakawa, S. and Kimura, M. 2003. Succession and phylogenetic composition of bacterial communities responsible for the composting process of rice straw estimated by PCR-DGGE analysis. *Soil Science and Plant Nutrition* 49: 619–630.
- Cahyani, V.R., Watanabe, A., Matsuya, K., Asakawa, S. and Kimura, M. 2002. Succession of microbiota estimated by phospholipid fatty acid analysis and changes in organic constituents during the composting process of rice straw. *Soil Science and Plant Nutrition* 48: 735–743.
- Carpenter-Boggs, L., Kennedy, A.C. and Reganold, J.P. 1998. Use of Phospholipid Fatty Acids and Carbon Source Utilization Patterns To Track Microbial Community Succession in Developing Compost. *Applied Environmental Microbiology* 64: 4062–4064.
- Casamayor, E.O., Schafer, H., Baneras, L., Pedros-Alio, C. and Muyzer, G. 2000. Identification of and Spatio-Temporal Differences between Microbial Assemblages from Two Neighboring Sulfurous Lakes: Comparison by Microscopy and Denaturing Gradient Gel Electrophoresis. *Applied Environmental Microbiology* 66: 499–508.
- Castaldi, P., Alberti, G., Merella, R. and Melis, P. 2005. Study of the organic matter evolution during municipal waste solid composting aimed at identifying suitable parameters for the evaluation of compost maturity. *Waste Management* 25: 209–213.
- Cayuela, M.L., Sánchez-Monedero, M.A. and Roig, A. 2006. Evaluation of two different aeration systems for composting two-phase olive mill wastes. *Process Biochemistry* 41: 616–623.
- Chandna, P., Nain, L., Singh, S. and Kuhad, R.C. 2013. Assessment of bacteria diversity during composting of agricultural by product. *BMC Microbiology* 13: 99.
- Chan, Y.J., Chong, M.F., and Law, C.L. 2012. Anintegrated anaerobic–aerobic bioreactor (IAAB) for the treatment of palm oil mill effluent (POME): Start-up and steady state performance. *Process Biochemistry* 47: 485–495.
- Chang, J.I., Tsai, J.J. and Wu, K.H. 2006. Thermophilic composting of food waste. *Bioresource Technology* 97: 116–122.

- Charbonneau, D. M., Moulelhi, F. M., Boissinot, M., Sirois, M. and Beauregard, M. 2012. Identification of thermophilic bacterial strains producing thermotolerant hydrolytic enzymes from manure compost. *Indian Journal of Microbiology* 52: 41-47.
- Chavalparit, O., Rulkens, W.H., Mol, A.P.J. and Khaodhair, S. 2006. Options for environmental sustainability of the crude palm oil industry in Thailand through enhancement of industrial ecosystems. *Environmental, Development and Sustainability* 8: 271-287
- Chiesa, S., Gnansounou, E., 2014. Use of Empty Fruit Bunches from the oil palm for bioethanol production: a thorough comparison between dilute acid and dilute alkali pretreatment. *Bioresource Technology* 159: 355–364.
- Chin, K. K., Lee, S.W. and Mohammad, H. H. 1996. A study of palm oil mill effluent treatment using a pond system. *Water Science and Technology* 34: 119–23.
- Chin, M. J., Eong, P. P., Ti T, B., Seng, C. E and Ling C.K. 2013. Biogas from palm oil mill effluent (POME) : opportunities and challenges from Malaysia's perspective. *Renewable and Sustainable Energy Reviews* 26:717:726
- Chong, M.L., Rahim, R.A., Shirai, Y. and Hassan, M.A. 2009. Biohydrogen production by *Clostridium butyricum* EB6 from palm oil mill effluent. *International Journal of Hydrogen Energy* 34:764-771
- Chroni, C., Kyriacou, A., Manios, T. and Lasaridi, K.E. 2009. Investigation of the microbial community structure and activity as indicators of compost stability and composting process evolution. *Bioresource Technology* 100: 3745–3750.
- Chu, F.J., Lin, C.W., I, Y.P., Wu, C.H. and Chen, D.H. 2012. Hydrolysis of bamboo cellulose and cellulase characteristics by *Streptomyces griseoaurantiacus* ZQBC691. *Journal of The Taiwan Institute Chemical Engineers* 43: 220–225.
- Clarridge, J.E., 2004. Impact of 16S rRNA gene sequence analysis for identification of bacteria on clinical microbiology and infectious diseases. *Clinical Microbiology Review* 17: 840–862,
- Cocolin, L., Manzano, M., Cantoni, C. and Comi, G. 2001. Denaturing gradient gel electrophoresis analysis of the 16S rRNA gene V1 region to monitor dynamic changes in the bacterial population during fermentation of Italian sausages. *Applied Environmental Microbiology* 67: 5113–5121.
- Connon, S.A., Giovannoni, S.J., 2002. High-Throughput Methods for Culturing Microorganisms in Very-Low-Nutrient Media Yield Diverse New Marine Isolates. *Applied and Environmental Microbiology* 68: 3878–3885.

- Contreras-Ramos, S.M., Alvarez-Bernal, D., Trujillo-Tapia, N. and Dendooven, L. 2004. Composting of tannery effluent with cow manure and wheat straw. *Bioresource Technology* 94: 223–228.
- Cuesta, G., García-de-la-Fuente, R., Abad, M. and Fornes, F. 2012. Isolation and identification of actinomycetes from a compost-amended soil with potential as biocontrol agents. *Journal of Environmental Management* 95: 280-284.
- Cukjati, N., Zupančić, G.D., Roš, M. and Grilc, V. 2012. Composting of anaerobic sludge: An economically feasible element of a sustainable sewage sludge management. *Journal of Environmental Management* 106: 48-55.
- Danon, M., Chen, Y. and Hadar Y. 2010. Ascomycete communities associated with suppression of *Sclerotium rolfsii* in compost. *Fungal Ecology* 3: 20-30
- Danon, M., Franke-Whittle, I.H., Insam, H., Chen, Y. and Hadar, Y. 2008. Molecular analysis of bacterial community succession during prolonged compost curing. *FEMS Microbiology Ecology* 65: 133–144.
- Davis, C.L., Donkin, C.J., Hinch, S.A. and Germishuizen, P. 1992. The microbiology of pine bark composting: An Electron-microscope and physiological study. *Bioresource Technology* 40: 195–204.
- Davis, J. B. and Reilly, P. J. A. 1980. Palm oil mill effluent-a summary of treatment methods. *Oleagineux* 35: 323-330.
- de Bertoldi, M., Vallini, G. and Pera A. 1983. The biology of composting: A review. *Waste Management Research* 1: 195-176
- de Gannes, V., Eudoxie, G. and Hickey, W.J. 2013. Prokaryotic successions and diversity in composts as revealed by 454-pyrosequencing. *Bioresource Technology* 133: 573–580.
- Dees, P.M. and Ghiorse, W.C. 2001. Microbial diversity in hot synthetic compost as revealed by PCR-amplified rRNA sequences from cultivated isolates and extracted DNA. *FEMS Microbiology Ecology* 35: 207–216.
- Eiland, F., Klamer, M., Lind, A.M., Leth, M. and Bååth, E. 2001a. Influence of initial C/N ratio on chemical and microbial composition during long term composting of straw. *Microbiology Ecology* 41: 272–280.
- Eiland, F., Leth, M., Klamer, M., Lind, A.M., Jensen, H.E.K. and Iversen, J.J.L. 2001b. C and N Turnover and Lignocellulose Degradation During Composting of Miscanthus Straw And Liquid Pig Manure. *Compost Science & Utilization* 9: 186–196.
- Fahma, F., Iwamoto, S., Hori, N., Iwata, T., Takemura, A., 2010. Isolation, preparation, and characterization of nanofibers from oil palm empty-fruit-bunch (OPEFB). *Cellulose* 17: 977–985.

- Fakruddin, M., Chowdhury, A., 2012. Pyrosequencing-An Alternative to Traditional Sanger Sequencing. *American Journal of Biochemistry Biotechnology* 8: 14–20.
- Fang, M. and Wong, J.W.C. 2000. Changes in Thermophilic Bacteria Population and Diversity during Composting of Coal Fly Ash and Sewage Sludge. *Water Air and Soil Pollution* 124: 333–343.
- Fierer, N., Nemergut, D., Knight, R. and Craine, J.M. 2010. Change through time: integrating microorganism into the study of succession. *Research Microbiology* 161: 635–642.
- Fontana, C., Vignolo, G. and Cocconcelli, P.S. 2005. PCR-DGGE analysis for the identification of microbial populations from Argentinean dry fermented sausages. *Journal of Microbiological Methods* 63: 254–263.
- Fracchia, L., Dohrmann, A.B., Martinotti, M.G. and Tebbe, C.C. 2006. Bacterial diversity in a finished compost and vermicompost: differences revealed by cultivation-independent analyses of PCR-amplified 16S rRNA genes. *Applied Microbiology and Biotechnology* 71: 942–952.
- Francou, C., Linères, M., Derenne, S., Villio-Poitrenaud, M.L. and Houot, S., 2008. Influence of green waste, biowaste and paper-cardboard initial ratios on organic matter transformations during composting. *Bioresource Technology* 99: 8926–8934.
- Fujio, Y., Kume, S., 1991. Isolation and identification of thermophilic bacteria from sewage sludge compost. *Journal of Fermentation and Bioengineering* 72, 334–337.
- Gao, M., Liang, F., Yu, A., Li, B. and Yang, L. 2010. Evaluation of stability and maturity during forced-aeration composting of chicken manure and sawdust at different C/N ratios. *Chemosphere* 78: 614–619.
- García-Fraile, P., Rivas, R., Willems, A., Peix, A., Martens, M., Martínez-Molina, E., Mateos, P.F. and Velázquez, E. 2007. *Rhizobium cellulosityticum* sp. nov., isolated from sawdust of *Populus alba*. *International Journal of Systematic and Evolutionary Microbiology* 57: 844–848.
- Gerasimova, J. and Kuisiene, N. 2012. Characterization of the novel xylanase from the thermophilic *Geobacillus thermodenitrificans* JK1. *Microbiology*. 81: 418–424.
- Ghabane, J., William, S.P.M.P., Bhidyadhar, R., Bhilawe, P., Anand, D., Vaidya, A.N. and Wate, S.R. 2012. Additives aided composting of green waste: effects on organic matter degradation, compost maturity and quality of the finished compost. *Bioresource Technology* 114: 382–388.

- Ghazifard, A., Kasra-Kermanshahi, R. and Far, Z.E. 2001. Identification of thermophilic and mesophilic bacteria and fungi in Esfahan (Iran) municipal solid waste compost. *Waste Management and Research* 19: 257–261.
- Glazunova, O. O., Raoult, D., and Roux, V. (2006). “*Bacillus massiliensis* sp. nov., isolated from cerebrospinal fluid,” *International Journal of Systematic and Evolutionary Microbiology* 56: 1485-1488.
- Gobi, K. and Vadivellu, V.M. 2013. By-product of palm oil mill effluent treatment plant – A step towards sustainability. *Renewable and Sustainable Energy Reviews* 28:788-803.
- Gobi, K., Mashitah, M.D. and Vadivelu, V.M. 2011 Adsorptive removal of Methylene Blue using novel adsorbent from palm oil mill effluent waste activated sludge: equilibrium, thermodynamics and kinetic studies. *Chemical Engineering Journal* 171: 1246–1252
- Goering, H. K. and Van Soest, P. J. 1970. *Forage Fiber Analysis (Apparatus, Reagents, Procedures and Application)*, USDA Handbook 379, U.S. Gov. Print. Office, Washington, DC, 20 p.
- Gontcharova, V., Youn, E., Wolcott, R.D., Hollister, E.B., Gentry, T.J. and Dowd, S.E. 2010. Black box chimera check (B2C2) a window-based software for batch depletion of chimeras from bacterial 16s rRNA gene dataset. *Open Microbiology Journal* 4:47-52
- Green, S. J., Michel Jr., F. C., Hadar, Y. and Minz. D. 2004. Similarity of bacterial community in sawdust- and straw-amended cow manure. *FEMS Microbiology Letter* 233: 115-123.
- Guo, R., Li, G., Jiang, T., Schuchardt, F., Chen, T., Zhao, Y. and Shen, Y. 2012. Effect of aeration rate, C/N ratio and moisture content on the stability and maturity of compost. *Bioresource Technology* 112: 171–178.
- Guo, Y., Zhu, N., Zhu, S. and Deng, C. 2007. Molecular phylogenetic diversity of bacteria and its spatial distribution in composts. *Journal of Applied Microbiology* 103: 1344–1354.
- Haminen, M. and Hänninen, K. . 2011. Composting of bio-waste, aerobic and anaerobic sludge – Effect of feedstock on the process and quality of compost. *Bioresource Technology* 102: 2842-2852.
- Hammes, W. P. and Hartel, C. 2006. The genera of *Lactobacillus* and *Carnobacterium*. *Prokaryotes* 4: 320-403.
- Hanajima, D., Fukumoto, Y., Yasuda, T., Suzuki, K., Maeda, K. and Morioka, R. 2011. Bacterial community dynamics in aerated cow manure slurry at different aeration intensities. *Journal of Applied Microbiology* 111: 1416-1425

- Hansgate, A.M., Schloss, P.D., Hay, A.G. and Walker, L.P. 2005. Molecular characterization of fungal community dynamics in the initial stages of composting. *FEMS Microbiology Ecology* 51: 209–214.
- Hassen, A., Belguith, K., Jedidi, N., Cherif, A., Cherif, M. and Boudabous, A. 2001. Microbial characterization during composting of municipal solid waste. *Bioresources Technology* 80: 217–225.
- He, M., Tian, G. and Liang, X. 2009. Phytotoxicity and speciation of copper, zinc and lead during the aerobic composting of sewage sludge. *Journal of Hazardous Materials* 163: 671–677.
- He, Y., Inamori, Y., Mizuochi, M., Kong, H., Iwami, N. and Sun, T. 2000. Measurement of N₂O and CH₄ from the aerated composting of food waste. *Science of The Total Environment* 254: 65–74.
- He, Y., Xie, K., Xu, P., Huang, X., Gu, W., Zhang, F. and Tang, S. 2013. Evolution of microbial community diversity and enzymatic activity during composting. *Research in Microbiology* 164: 189–198.
- Hellmann, B., Zelles, L., Palojarvi, A. and Bai, Q. 1997. Emission of Climate-Relevant Trace Gases and Succession of Microbial Communities during Open-Windrow Composting. *Applied Environmental Microbiology* 63: 1011–1018.
- Hermansson, A. and Lindgren, P.E. 2001. Quantification of ammonia-oxidizing bacteria in arable soil by real-time PCR. *Applied Environmental Microbiology* 67: 972–976.
- Hernández, T., Masciandaro, G., Moreno, J.I. and García, C. 2006. Changes in organic matter composition during composting of two digested sewage sludge. *Waste Management* 26: 1370–1376.
- Heylen, K., Vanparys, B., Wittebolle, L., Verstraete, W., Boon, N. and De Vos, P. 2006. Cultivation of denitrifying bacteria: optimization of isolation conditions and diversity study. *Applied in Environmental Microbiology* 72: 2637–2643
- Hill, G.T., Mitkowski, N.A., Aldrich-Wolfe, L., Emele, L.R., Jurkonie, D.D., Ficke, A., Maldonado-Ramirez, S., Lynch, S.T. and Nelson, E.B., 2000. Methods for assessing the composition and diversity of soil microbial communities. *Applied Soil Ecology* 15: 25–36.
- Hoitink, H.A.J. and Fahy, P.C. 1986. Basis for the control of soil borne plant pathogens with composts. *Annual Review of Phytopathology* 24: 93–114.
- Hong, J.H. and Park, K.J. 2005. Compost biofiltration of ammonia gas from bin composting. *Bioresource Technology* 96: 741–745.

- Hong, J.H., Keener, H.M. and Elwell, D.L. 1998. Preliminary Study of the Effect of Continuous and Intermittent Aeration on Composting Hog Manure Amended With Sawdust. *Compost Science & Utilization* 6: 74–88.
- Huang, D. L., Zeng, G. M., Feng, C. L., Hu, S., Lai, C., Zhao, M. H., Su, F. F., Tang, L. and Liu, H. L. 2010. Changes of microbial population structure related to lignin degradation during lignocellulosic waste composting *Bioresource Technology* 101: 4062-4067.
- Huang, G.F., Wong, J.W.C., Wu, Q.T. and Nagar, B.B. 2004. Effect of C/N on composting of pig manure with sawdust. *Waste Management* 24: 805–813.
- Hubbe, M.A., Mousa, N., Sanchez, C., 2010. Composting as a way to convert cellulosic biomass and waste organic into high-value soil amendments: a review *BioResources* 5: 2808–2854.
- Hugenholtz, P., Goebel, B.M. and Pace, N.R. 1998. Impact of culture-Independent studies on the emerging phylogenetic view of bacterial diversity. *Journal of Bacteriology* 180: 4765–4774.
- Humblot, C. and Guyot, J.P. 2009. Pyrosequencing of tagged 16S rRNA gene amplicons for rapid deciphering of the microbiomes of fermented foods such as pearl millet slurries. *Applied Environmental Microbiology* 75: 4354–4361.
- Ibrahim, M.N.M, Nadiyah, M.Y.N., Norliyana, M.S., Sipaut, C.S., Shuib, S., 2008. Separation of Vanillin from Oil Palm Empty Fruit Bunch Lignin. *CLEAN – Soil, Air, Water* 36: 287–291.
- Inceoglu, O., Hoogwout, E.F., Hill, P. and van Elsas, J.D. 2010. Effect of DNA extraction method on the apparent microbial diversity of soil. *Applied and Environmental Microbiology* 76: 3378–3382.
- Insam, H. and de Bertoldi M. 2007. Microbiology of the composting process. In: Diaz, L.F., de Bertoldi M., Bidlingmaier, w. and Stentiford, E. *Compost Science & Technology*, pp. 38
- Iqbal, M.K., Shafiq, T. and Ahmed, K. 2010. Characterization of bulking agents and its effects on physical properties of compost. *Bioresoure Technology* 101: 1913–1919.
- Irvan, I., Trisakti, B., Wongistani, V. and Tomiuchi, Y. 2012. Methane Emission from Digestion of Palm Oil Mill Effluent (POME) in a Thermophilic Anaerobic Reactor. *International Journal of Science and Engineering* 1: 32-35
- Ishii, K., Fukui, M. and Takii, S. 2000. Microbial succession during a composting process as evaluated by denaturing gradient gel electrophoresis analysis. *Journal of Applied Microbiology* 89: 768–777.

- Ismail, I., Hassan, M.A., Abdul Rahman, N.A. and Soon, C.S. 2010. Thermophilic biohydrogen production from palm oil mill effluent (POME) using suspended mixed culture. *Biomass and Bioenergy* 34: 42–47.
- Jiang, T., Schuchardt, F., Li, G., Guo, R. and Zhao, Y. 2011. Effect of C/N ratio, aeration rate and moisture content on ammonia and greenhouse gas emission during the composting. *Journal of Environmental Sciences* 23: 1754–1760.
- Jones, R.T., Robeson, M.S., Lauber, C.L., Hamady, M., Knight, R. and Fierer, N. 2009. A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. *The ISME Journal* 3: 442–453.
- Juvonen, R., Koivula, T. and Haikara, A. 2008. Group-specific PCR-RFLP and real-time PCR methods for detection and tentative discrimination of strictly anaerobic beer-spoilage bacteria of the class Clostridia. *International Journal of Food Microbiology* 125: 162–169.
- Kaeberlein, T., Lewis, K., Epstein, S.S., 2002. Isolating “uncultivable” microorganisms in pure culture in a simulated natural environment. *Science* 296: 1127–1129.
- Kala, D. R., Rosenani A. B., Fauziah C. I. and Thohirah L. A. 2009. Composting oil palm wastes and sludge sewage for use in potting media of ornamental plants *Malaysian Journal of Soil Sciences* 13: 77-91.
- Kananam, W., Suksaroj, T. T. and Suksaroj, C. 2011. Biochemical changes during oil palm (*Elaeis guineensis*) empty fruit bunch composting with decanter sludge and chicken manure *Science Asia* 37: 17-23.
- Kaplan, D.L. and Kaplan, A.M. 1982. Thermophilic biotransformations of 2,4,6-trinitrotoluene under simulated composting conditions. *Applied and Environmental Microbiology* 44: 757–760.
- Karadag, D., Özkaya, B., Ölmez, E., Nissilä, M.E., Çakmakçı, M., Yıldız, Ş. and Puhakka, J.A. 2013. Profiling of bacterial community in a full-scale aerobic composting plant. *International Biodeterioration & Biodegradation* 77: 85–90.
- Karpowicz, E., Novinscak, A., Bärlocher, F. and Filion, M. 2010. qPCR quantification and genetic characterization of *Clostridium perfringens* populations in biosolids composted for 2 years. *Journal of Applied Microbiology* 108: 571–581.
- Kato, K. and Miura, N. 2008. Effect of matured compost as a bulking and inoculating agent on the microbial community and maturity of cattle manure compost. *Bioresource Technology* 99: 3372–3380.
- Kavitha, B., Jothimani, P. and Rajannan, G. 2013. Empty fruit bunch – A potential organic manure for agriculture. *International Journal of Science, Environmental and Technology* 2:930-937

- Kavroulakis, N., Ntougias, S., Besi, M.I., Katsou, P., Damaskinou, A., Ehaliotis, C., Zervakis, G.I. and Papadopoulou, K.K. 2010. Antagonistic bacteria of composted agro-industrial residues exhibit antibiosis against soil-borne fungal plant pathogens and protection of tomato plants from *Fusarium oxysporum* f. sp. *radicis-lycopersici*. *Plant and Soil* 333: 233–247.
- Kementerian Tenaga, Teknologi Hijau dan Air (KeTTHA), 2012. Small Renewable Energy Power Programme. Available from: (accessed 27.01.12). www.kettha.gov.my/en/content/small-renewable-energy-power-programme-srep.
- Khan, M., Ueno, K., Horimoto, S., Komai, F., Tanaka, K. and Yoshitaka, O. 2009 Physicochemical, including spectroscopic and biological analyses during composting of green tea waste and rice bran. *Biology Fertility Soils* 45: 305–313
- Kiyohara, M., Koyanagi, T., Matsui, H., Yamamoto, K., Take, H., Katsuyama, Y., Tsuji, A., Miyamae, H., Kondo, T., Nakamura, S., Katayama, T. and Kumagai, H. 2012. Changes in Microbiota Population during Fermentation of Narezushi as Revealed by Pyrosequencing Analysis. *Bioscience, Biotechnology and Biochemistry* 76: 48–52.
- Klamer, M. and Baath, E. 1998. Microbial community dynamics during composting of straw material studied using phospholipid fatty acid analysis. *FEMS Microbiology Ecology* 27: 9–20.
- Klein, M., Brown, L., Ashbolt, N.J., Stuetz, R.M. and Roser, D.J. 2011. Inactivation of indicators and pathogens in cattle feedlot manures and compost as determined by molecular and culture assays. *FEMS Microbiology Ecology* 77: 200–210.
- Ko, C.H., Chen, W.L., Tsai, C.H., Jane, W.N., Liu, C.C. and Tu, J. 2007. *Paenibacillus campinasensis* BL11: a wood material-utilizing bacterial strain isolated from black liquor. *Bioresource Technology* 98: 2727–2733.
- Korniłowicz-Kowalska, T. and Bohacz, J. 2010. Dynamics of growth and succession of bacterial and fungal communities during composting of feather waste. *Bioresource Technology* 101: 1268–1276.
- Kuczynski, J., Stombaugh, J., Walters, W.A., González, A., Caporaso, G. and Knight, R. 2012. Using QIIME to analyze 16S rRNA gene sequences from Microbial Communities. *Current protocol in bioinformatics* CHAPTER: unit 10.7, pp. 1–26
- Kulcu, R., Yaldiz, O., 2004. Determination of aeration rate and kinetics of composting some agricultural wastes. *Bioresource Technology* 93: 49–57.

- Laine, M.M. and Jørgensen, K.S. 1997. Effective and Safe Composting of Chlorophenol-Contaminated Soil in Pilot Scale. *Environmental Science and Technology* 31: 371–378.
- LaMontagne, M.G., Michel, F.C., Holden, P.A. and Reddy, C.A. 2002. Evaluation of extraction and purification methods for obtaining PCR-amplifiable DNA from compost for microbial community analysis. *Journal Microbiological Methods* 49: 255–264.
- Langarica-Fuentes, A., Zafar, U., Heyworth, A., Brown, T., Fox, G. and Robson, G.D. 2014. Fungal succession in an in-vessel composting system characterized using 454 pyrosequencing. *FEMS Microbiology Ecology* 88: 296-308
- Lauber, C.L., Hamady, M., Knight, R. and Fierer, N. 2009. Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale. *Applied and Environmental Microbiology* 75: 5111–5120.
- Law, W.M., Lau, W.N., Lo, K.L., Wai, L.M. and Chiu, S.W. 2003. Removal of biocide pentachlorophenol in water system by the spent mushroom compost of *Pleurotus pulmonarius*. *Chemosphere* 52: 1531–1537.
- Lei, F. and Vander Gheynst, J. 2000. The effect of microbial inoculation and pH on microbial community structure changes during composting. *Process Biochemistry* 35: 923–929.
- Li, A., Chu, Y., Wang, X., Ren, L., Yu, J., Liu, X., Yan, J., Zhang, L., Wu, S., Li, S., 2013. A pyrosequencing-based metagenomic study of methane-producing microbial community in solid-state biogas reactor. *Biotechnology for Biofuels* 6, 3.
- Li, Q., Ng, W.T., Puah, S.M., Bhaskar, R.V., Soh, L.S., Macbeath, C., Parakattil, P., Green, P., Wu, J.C., 2014. Efficient production of fermentable sugars from oil palm empty fruit bunch by combined use of acid and whole cell culture-catalyzed hydrolyses. *Biotechnology and Applied Biochemistry* 61, 426-431.
- Li W.H., Yue, Q.Y., Gao, B.Y., Wang, X.J., Qi, Y.F., Zhao, Y.Q. and Li Y.J. 2011. Preparation of sludge based activated carbon made from paper mill sewage sludge by steam activation for dye waste water treatment. *Desalination* 278: 179–185.
- Li, X., Zhang, R. and Pang, Y. 2008. Characteristics of dairy manure composting with rice straw. *Bioresource Technology* 99: 359–367.
- Li, H., Xu, X., Chen, H., Zhang, Y., Xu, J., Wang, J. and Lu, X. 2013. Molecular analyses of the functional microbial community in composting by PCR–DGGE targeting the gene of the β -glucosidase. *Bioresource Technology* 134: 51–58.

- Liang, C., Das, K. and McClendon, R. 2003. The influence of temperature and moisture contents regimes on the aerobic microbial activity of a biosolids composting blend. *Bioresource Technology* 86: 131–137.
- Liew, P.W.Y., Jong, B.C., Goh, C.M. and Ahmad, M. 2009. Bacterial diversity associated with empty oil palm fruit bunch compost as revealed by cultivation-independent analyses of PCR-amplified 16S rRNA genes. *Journal of General Applied Microbiology* 55: 233–240.
- Lim, S. C., Baharuddin, A. S., Ahmad, M. N., Md Shah, U. K., Abd Rahman, N. A., Abd Aziz, S., Shirai, Y. and Hassan, M. A. 2009. Physicochemical changes in windrow co-composting process of oil palm mesocarp fiber and palm oil mill effluent anaerobic sludge *Australian Journal of Basic Applied Sciences* 3: 2809-2816.
- Lim, Y.W., Kim, B.K., Kim, C., Jung, H.S., Kim, B.S., Lee, J.H. and Chun J. 2010. Assessment of soil fungal communities using pyrosequencing. *Journal of Microbiology* 48: 284-289.
- Lin, Y., Du, D., Si, C., Zhao, Q., Li, Z. and Li P. 2014. Potential biocontrol *Bacillus* sp. strains isolated by an improved method from vinegar waste compost exhibit antibiosis against fungal pathogens and promote growth of cucumbers. *Biological control* 71: 7-5
- Liu, B.R., Jia, G.M., Chen, J. and Wang, G. 2006. A Review of Methods for Studying Microbial Diversity in Soils. *Pedosphere* 16: 18–24.
- Liu, L., Li, Y., Li, S., Hu, N., He, Y., Pong, R., Lin, D., Lu, L. and Law, M. 2012. Comparison of next-generation sequencing systems. *Journal of Biomedicine and Biotechnology* 2012: 11.
- Lo, Y.C., Saratale, G.D., Chen, W.M., Bai, M.D. and Chang, J.S. 2009. Isolation of cellulose-hydrolytic bacteria and applications of the cellulolytic enzymes for cellulosic biohydrogen production. *Enzyme and Microbial Technology* 44: 417–425.
- Lulakis, M.D., Petsas, S.I., 1995. Effect of humic substances from vine-canes mature compost on tomato seedling growth. *Bioresource Technology* 54: 179–182.
- Lydkis, A., Mavromatis, K., Ivanova, N., Anderson, I., Land, M., DiBartolo, G., Martinez, M., Lapidus, A., Lucas, S., Copeland, A., Richardson, P., Wilson, D.B. and Kyrpides, N. 2007. Genome sequence and analysis of the soil cellulolytic Actinomycete *Thermobifida fusca* YX. *Journal of Bacteriology*. 189: 2477-2486.
- Ma, A. N. (1999) Treatment of palm oil mill effluent. In: Singh G, Lim KH, Leng T, David LK (eds) Oil palm and the environment: a Malaysian perspective. Malaysia Oil Palm Growers' Council, Kuala Lumpur, pp. 113–126

- Maeda, K., Hanajima, D., Morioka, R. and Osada, T. 2010. Characterization and spatial distribution of bacterial communities within passively aerated cattle manure composting piles. *Bioresource Technology* 101: 9631–9637.
- Martin-Laurent, F., Philippot, L., Hallet, S., Chaussod, R., Germon, J.C., Soulas, G. and Catroux, G. 2001. DNA extraction from soils: old bias for new microbial diversity analysis methods. *Applied and Environmental Microbiology* 67: 2354–2359.
- Marttinen, S.K., Hänninen, K. and Rintala, J.A. 2004. Removal of DEHP in composting and aeration of sewage sludge. *Chemosphere* 54: 265–272.
- Matteau, Y. and Ramsay, B. 1997. Active compost biofiltration of toluene. *Biodegradation* 8: 135–141.
- McKinley, V.L. and Vestal, J.R. 1984. Biokinetic analyses of adaptation and succession: microbial activity in composting municipal sewage sludge. *Applied and Environmental Microbiology* 47: 933–941.
- McKinley, V.L. and Vestal, J.R. 1985. Physical and chemical correlates of microbial activity and biomass in composting municipal sewage sludge. *Applied and Environmental Microbiology* 50: 1395–403.
- Meesap, K., Boonapatcharoen, N., Techkarnjanaruk, S. and Chaiprasert, P. 2012. Microbial communities and their performance in anaerobic hybrid sludge bed-fixed film reactor for treatment of palm oil mill effluent under various organic pollutant concentrations. *Journal of Biomedicine and Biotechnology* 11
- Mehta, C.M., Palni, U., Franke-Whittle, I.H. and Sharma, A.K. 2014. Compost: its role, mechanism and impact on reducing soil-borne plant diseases. *Waste Management* 34: 607–22.
- Meunchang, S., Panichsapatana, S. and Weaver, R.W. 2005. Co-composting of filter cake and bagasse; by-products from a sugar mill. *Bioresource Technology* 96: 437–442.
- Miaomiao, H., Wenhong, L., Xinqiang, L., Donglei, W. and Guangming, T. 2009. Effect of composting process on phytotoxicity and speciation of copper, zinc and lead in sewage sludge and swine manure. *Waste Management* 29: 590–597.
- Miller, F.C. 1993. Ecological process control of composting. In: Metting F.B., Jr., Ed., *Soil microbiology ecology*. Marcel Dekker, New York, pp. 529-536
- Mirhendi, H., Dida, K., Rezaei, A., Hosseinpour, N. and Khodadadi, H. 2007. Colony-PCR is a rapid and sensitive method for DNA Amplification in Yeasts. *Iranian Journal of Public Health* 36: 40-41

- Moeller, J. and Reeh, U. 2003. Degradation of DEHP, PAHs and LAS in Source Separated MSW and Sewage Sludge During Composting. *Compost Science & Utilization* 11: 370–378.
- Mohd Yasin, N.H., Rahman, N.A., Man, H.C., Mohd Yusoff, M.Z. and Hassan, M.A. 2011. Microbial characterization of hydrogen-producing bacteria in fermented food waste at different pH values. *International Journal of Hydrogen Energy* 36: 9571–9580.
- Morohoshi, T., Tominaga, Y., Someya, N. and Ikeda, T. 2012. Complete genome sequence and characterization of the N-acylhomoserine lactone-degrading gene of the potato leaf-associated *Solibacillus silvestris*. *Journal of Bioscience and Bioengineering* 113: 20-25.
- MPOC, Malaysian Palm Oil Industry .Available: /<http://www.mpoc.org.my/> Malaysian _Palm_Oil_Industry. aspxS [accessed 31.3.2014].
- Najafpour, G. D., Zinatizadeh, A. A. L., Mohamed, A. R., Hasnain Isa M. and Nasrollahzadeh H. 2006 High-rate anaerobic digestion of palm oil mill effluent in an upflow anaerobic sludge-fixed film bioreactor. *Process Biochemistry* 41: 370–379.
- Nakasaki, K., Sasaki, M., Shoda, M. and Kubota, H. 1985a. Change in microbial numbers during thermophilic composting of sewage sludge with reference to CO₂ evolution rate. *Applied and Environmental Microbiology* 49: 37–41.
- Nakasaki, K., Sasaki, M., Shoda, M. and Kubota, H. 1985b.Characteristic of mesophilic bacteria isolates isolated during thermophilic composting of sewage sludge. *Applied and Environmental Microbiology* 49: 42-45.
- Nakasaki, K., Tran, L.T.H., Idemoto, H., Abe, M. and Rollon, A.P. 2009. Comparison of organic matter degradation and microbial community during thermophilic composting of two different types of anaerobic sludge. *Bioresource Technology* 100: 676-682.
- Nakasaki, K., Yaguchi, H., Sasaki, Y. and Kubota, H. 1992. Effects of ratio on thermophilic composting of garbage. *Journal of Fermentation and Bioengineering* 73: 43–45.
- Nakatsu, C.H., Torsvik, V., and Øvreås, L. 2000. Soil Community Analysis Using DGGE of 16S rDNA Polymerase Chain Reaction Products. *Soil Science Society of America Journal* 64: 1382.
- Nam, Y.D., Yi, S.H. and Lim, S.I. 2012. Bacterial diversity of cheonggukjang, a traditional Korean fermented food, analyzed by barcoded pyrosequencing. *Food Control* 28: 135–142.
- Neyla, S., Soulwene, K., Fadhel, M.H., Naceur, J., Meriam, M., Abdennaceur, H., Hadda, O., 2009. Microbiological parameters and maturity degree during composting of *Posidonia oceanica* residues mixed with vegetable wastes in

semi-arid pedo-climatic condition. *Journal of Environmental Science* 21: 1452–1458.

Ng, F.Y., Yew, F.K., Basiron, Y. and Sundram, K. 2011. A renewable future driven with Malaysian palm oil-based green technology. *Journal of Oil Palm and Environment* 2: 1-7.

Ng, W.P.Q., Lam, H.L., Ng, F.Y., Kamal, M. and Lim, J.H.E. 2012. Waste-to-wealth: green potential from palm biomass in Malaysia. *Journal of Cleaner Production* 34: 57–65.

Novinscak, A., Surette, C. and Filion, M. 2007. Quantification of *Salmonella* spp. in composted biosolids using a TaqMan qPCR assay. *Journal of Microbiological Methods* 70: 119–126.

Ntougias, S., Zervakis, G.I., Kavroulakis, N., Ehaliotis, C. and Papadopoulou, K.K. 2004. Bacterial diversity in spent mushroom compost assessed by amplified rDNA restriction analysis and sequencing of cultivated isolates. *Systematic and Applied Microbiology* 27: 746–754.

Ogunwande, G.A., Osunade, J.A., Adekalu, K.O. and Ogunjimi, L.A.O. 2008. Nitrogen loss in chicken litter compost as affected by carbon to nitrogen ratio and turning frequency. *Bioresource Technology* 99: 7495–7503.

Ohnishi, A., Nagano, A., Fujimoto, N. and Suzuki, M. 2011. Phylogenetic and physiological characterization of mesophilic and thermophilic bacteria from a sewage sludge composting process in Sapporo, Japan. *World Journal of Microbiology and Biotechnology* 27: 333-340.

Ooi, H. S. and Subramaniam, S.K. S. 2008. Co-composting for sustainable crude palm oil production in Malaysia. *JURUTERA* p. 22-26.

O-Thong, S., Boe, K. and Angelidaki, I. 2012. Thermophilic anaerobic co-digestion of oil palm empty fruit bunches with palm oil mill effluent for efficient biogas production. *Applied Energy* 93: 648–654.

Pace, N.R. 1997. A Molecular View of Microbial Diversity and the Biosphere. *Science* 276: 734–740.

Palatinszky, M., Nikolausz, M., Sváb, D. and Márialigeti, K. 2011. Preferential ligation during TA-cloning of multitemplate PCR products--a factor causing bias in microbial community structure analysis. *Journal of Microbiological Methods* 85: 131–136.

Papasotiriou, F.G., Varypatakis, K.G., Christofi, N., Tjamos, S. E. and Paplomatas, E.J. 2013. Olive mill wastes: A source of resistance for plants against *Verticillium dahliae* and a reservoir of biocontrol agents. *Biological control*. 67: 51-60

- Paredes, C., Bernal, M.P., Cegarra, J. and Roig, A. 2002. Biodegradation of olive mill wastewater sludge by its co-composting with agricultural wastes. *Bioresource Technology* 85:1-8
- Partanen, P., Hultman, J., Paulin, L., Auvinen, P. and Romantschuk, M. 2010. Bacterial diversity at different stages of the composting process. *BMC Microbiology* 10: 94.
- Pavel, A.B. and Vasile, C.L. 2012. PyElph – a software tool for gel images analysis and phylogenetics. *BMC Bioinformatics* 13: 9.
- Pearce, D.A. 2003. Bacterioplankton community structure in a maritime antarctic oligotrophic lake during a period of holomixis, as determined by denaturing gradient gel electrophoresis (DGGE) and fluorescence in situ hybridization (FISH). *Microbiology Ecology* 46: 92–105.
- Pedra, F., Polo, A., Ribeiro, A. and Domingues, H. 2007. Effects of municipal solid waste compost and sewage sludge on mineralization of soil organic matter. *Soil Biology and Biochemistry* 39: 1375–1382.
- Peters, S., Koschinsky, S., Schwieger, F. and Tebbe, C.C. 2000. Succession of Microbial Communities during Hot Composting as Detected by PCR-Single-Strand-Conformation Polymorphism-Based Genetic Profiles of Small-Subunit rRNA Genes. *Applied and Environmental Microbiology* 66: 930–936.
- Petrosino, J.F., Highlander, S., Luna, R.A., Gibbs, R.A., Versalovic, J., 2009. Metagenomic pyrosequencing and microbial identification. *Clinical Chemistry* 55: 856–66.
- Poh, P.E. and Chong, M.F. 2009 Development of anaerobic digestion methods for palm oil mill effluent (POME) treatment. *Bioresource Technology* 100: 1-9
- Poh, P.E. and Chong, M.F. 2010. Biomethanation of Palm Oil Mill Effluent (POME) with a thermophilic mixed culture cultivated using POME as a substrate. *Chemical Engineering Journal* 164: 146–154.
- Poh, P.E., Yong, W.J. and Chong, M.F. 2010. Palm Oil Mill Effluent (POME) Characteristic in High Crop Season and the Applicability of High-Rate Anaerobic Bioreactors for the Treatment of POME. *Industrial and Engineering Chemistry Research* 49: 11732–11740.
- Raj, D. and Antil, R.S. 2011. Evaluation of maturity and stability parameters of composts prepared from agro-industrial wastes. *Bioresource Technology* 102: 2868–2873.

- Randazzo, C.L., Torriani, S., Akkermans, A.D.L., de Vos, W.M. and Vaughan, E.E. 2002. Diversity, Dynamics, and Activity of Bacterial Communities during Production of an Artisanal Sicilian Cheese as Evaluated by 16S rRNA Analysis. *Applied and Environmental Microbiology* 68: 1882–1892.
- Ranjard, L., Poly, F. and Nazaret, S. 2000. Monitoring complex bacterial communities using culture-independent molecular techniques: application to soil environment. *Research in Microbiology* 151: 167–177.
- Rasapoor, M., Nasrabadi, T., Kamali, M. and Hoveidi, H. 2009. The effects of aeration rate on generated compost quality, using aerated static pile method. *Waste Management* 29: 570–573.
- Rasdi, Z., Mumtaz, T., Abdul Rahman, N. and Hassan, M.A. 2012. Kinetic analysis of biohydrogen production from anaerobically treated POME in bioreactor under optimized condition. *International Journal of Hydrogen Energy* 37: 17724–17730.
- Rastogi, G. and Sani, R.K. 2011. Molecular techniques to assess microbial community structure, function and dynamics in the environment. In: Ahmad, I., et al. (Eds) *Microbes and Microbial Technology: Agricultural and environmental applications* pp. 29–58.
- Rebollido, R., Stegmann, R., 2008. Microbial populations during composting process of organic fraction of municipal solid waste. *Applied Ecology and Environmental Research* 6: 61–67.
- Rheims, H., Fruhling, A., Schumann, P., Rohde, M. and Stackerand, E. 1999. *Bacillus silvestris* sp. nov., a new member of the genus *Bacillus* that contains lysine in its cell wall. *International Journal of Systematic Bacteriology* 49: 792-802.
- Rivas, R., Vela, E., Willems, A., Vizcaíno, N., Subba-rao, N.S., Mateos, P.F., Gillis, M., Dazzo, F.B. and Martínez-molina, E. 2002. A New Species of *Devosia* That Forms a Unique Nitrogen-Fixing Root-Nodule Symbiosis with the Aquatic Legume *Neptunia natans* (L.f.) Druce. *Applied and Environmental Microbiology* 68: 5217–5222.
- Rivas, R., Willems, A., Subba-Rao, N.S., Mateos, P.F., Dazzo, F.B., Kroppenstedt, R.M., Martínez-Molina, E., Gillis, M. and Velázquez, E. 2003. Description of *Devosia neptuniae* sp. nov. that nodulates and fixes nitrogen in symbiosis with *Neptunia natans*, an aquatic legume from India. *Systematic and Applied Microbiology* 26: 47–53.
- Roca-Pérez, L., Martínez, C., Marcilla, P. and Boluda, R. 2009. Composting rice straw with sewage sludge and compost effects on the soil-plant system. *Chemosphere* 75: 781–787.

- Roesch, L.F.W., Fulthorpe, R.R., Riva, A., Casella, G., Hadwin, A.K.M., Kent, A.D., Daroub, S.H., Camargo, F.A.O., Farmerie, W.G. and Triplett, E.W. 2007. Pyrosequencing enumerates and contrasts soil microbial diversity. *The ISME Journal* 1: 283–290.
- Roh, S.W., Kim, K.H., Nam, Y.D., Chang, H.W., Park, E.J. and Bae, J.W. 2010. Investigation of archaeal and bacterial diversity in fermented seafood using barcoded pyrosequencing. *The ISME Journal* 4: 1–16.
- Romano, I., Giordano, A., Lama, L., Nicolaus, B. and Gambacorta, A. 2003. *Planococcus rifietensis* sp. nov, isolated from algal mat collected from a sulfurous spring in Campania (Italy). *Systematic and Applied Microbiology* 26: 357–366.
- Rupani, P.F., Singh, R.P., Ibrahim, M., H. and Esa, N. 2010. Review of current palm oil mill effluent (POME) treatment methods: vermi-composting as a sustainable practice. *World Applied Sciences Journal* 11: 70–81.
- Ruppitsch, W., Stöger, A., Indra, A., Grif, K., Schabereiter-Gurtner, C., Hirschl, A., Allerberger, F., 2007. Suitability of partial 16S ribosomal RNA gene sequence analysis for the identification of dangerous bacterial pathogens. *Journal of Applied Microbiology* 102: 852–859.
- Ryckeboer, J., Mergaert, J., Coosemans, J., Deprins, K. and Swings, J. 2003a. Microbiological aspects of biowaste during composting in a monitored compost bin. *Journal of Applied Microbiology* 94: 127–137.
- Ryckeboer, J., Mergaert, J., Vaes, K. and Klammer, S. 2003b. A survey of bacteria and fungi occurring during composting and self-heating processes. *Annals of Microbiology* 53: 349–410.
- Sabrina, D.T., Hanafi, M.M., Mahmud, T.M.M. and Azwady, A.A.N. 2009. Vermicomposting of Oil Palm Empty Fruit Bunch And its Potential in Supplying of Nutrients For Crop Growth. *Compost Science & Utilization* 17: 61–67.
- Saidu, M., Yuzir, A., Salim, M.R., Salmiati, Azman, S. and Abdullah, N. 2013. Influence of palm oil mill effluent as inoculum on anaerobic digestion of cattle manure for biogas production. *Bioresource Technology* 141, 174–176.
- Salvador Pedro, M., Haruta, S., Hazaka, M., Shimada, R., Yoshida, C., Hiura, K., Ishii, M. and Igarashi, Y. 2001. Denaturing gradient gel electrophoresis analyses of microbial community from field-scale composter. *Journal of Bioscience and Bioengineering* 91: 159–165.

- Sánchez-Monedero, M.A., Roig, A., Paredes, C. and Bernal, M.P. 2001. Nitrogen transformation during organic waste composting by the Rutgers system and its effects on pH, EC and maturity of the composting mixtures. *Bioresource Technology* 78: 301–308.
- Sanz, J.L. and Köchling, T. 2007. Molecular biology techniques used in wastewater treatment: An overview. *Process Biochemistry* 42: 119–133.
- Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., Hartmann, M., Hollister, E.B., Lesniewski, R.A., Oakley, B.B., Parks, D.H., Robinson, C.J., Sahl, J.W., Stres, B., Thallinger, G.G., Van Horn, D.J., Weber, C.F., 2009. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and Environmental Microbiology* 75: 7537–41.
- Schuchardt, F., Wulfret, K. and Herawan, T. 2008. Protect the Environment and Make Profit from the Waste in Palm Oil Industry assessed on July 2014. Available in: http://www.utebremen.com/usefiles/file/pdf/Paper_POSE_2008.pdf
- Sekiguchi, H., Watanabe, M., Nakahara, T., Xu, B. and Uchiyama, H. 2002. Succession of Bacterial Community Structure along the Changjiang River Determined by Denaturing Gradient Gel Electrophoresis and Clone Library Analysis. *Applied Environmental Microbiology* 68: 5142–5150.
- Selvakumar, G., Joshi, P., Nazim, S., Mishra, P.K., Kundu, S. and Gupta, H.S. 2008. *Exiguobacterium acetylicum* strain 1P (MTCC 8707) a novel bacterial antagonist from the North Western Indian Himalayas. *World Journal of Microbiology and Biotechnology* 25: 131–137.
- Shi, W., Norton, J.M., Miller, B.E. and Pace, M.G. 1999. Effects of aeration and moisture during windrow composting on the nitrogen fertilizer values of dairy waste composts. *Applied Soil Ecology* 11: 17–28.
- Shin, H.S. and Jeong, Y.K. 2010. The Degradation of Cellulosic Fraction in Composting of Source Separated Food Waste and Paper Mixture with Change of C / N Ratio. *Environmental Technology* 37–41.
- Shuit, S.H., Tan, K.T., and Kamaruddin, A.H. 2009. Oil palm biomass as a sustainable energy source: A Malaysian case study. *Energy*. 34(9):1225-1235.
- Singh R.P., Ibrahim M.H., Esa N. and Iliyana M.S. 2010. Composting of waste from palm oil mill: a sustainable waste management practice. *Review Environmental Science and Biotechnology* 9: 331-344
- Singh, R.P., Embrandirra, A., Ibrahim, M.H. and Esa, N. 2011. Management of biomass residues generated from palm oil mill: Vermicomposting a sustainable option. *Resources conservation and recycling* 55: 423-434

- Singleton, D.R., Furlong, M.A. and Rathbun, S.L. 2001. Quantitative comparisons of 16s rRNA gene sequence libraries from environmental samples. *Applied Environmental Microbiology* 67:4347-4376
- Smårs, S., 2002. Improvement of the composting time for household waste during an initial low pH phase by mesophilic temperature control. *Bioresource Technology* 84: 237–241.
- Sonoki, T., Furukawa, T., Jindo, K., Suto, K., Aoyama, M. and Sánchez-Monedero, M.Á. 2013. Influence of biochar addition on methane metabolism during thermophilic phase of composting. *Journal of Basic Microbiology* 53: 617–621.
- Steger, K., Jarvis, A., Vasara, T., Romantschuk, M. and Sundh, I. 2007. Effects of differing temperature management on development of Actinobacteria populations during composting. *Research in Microbiology* 158: 617–624.
- Stevenson, B.S., Eichorst, S.A., Wertz, J.T., Schmidt, T.M., Breznak, J.A., 2004. New strategies for cultivation and detection of previously uncultured microbes. *Applied and Environmental Microbiology* 70: 4748–4755.
- Stewart, E.J., 2012. Growing unculturable bacteria. *Journal of Bacteriology* 194: 4151–4160.
- Straatsma, G., Samson, R.A., Olijnsma, T.W., Op Den Camp, H.J.M., Gerrits, J.P.G. and Van Griensven, L.J.L.D. 1994. Ecology of Thermophilic Fungi in Mushroom Compost, with Emphasis on *Scytalidium thermophilum* and Growth Stimulation of *Agaricus bisporus* Mycelium. *Applied and Environmental Microbiology* 60: 454–458.
- Strom, P.F., 1985. Identification of thermophilic bacteria in solid-waste composting. *Applied and Environmental Microbiology* 50: 906–913.
- Su, C., Lei, L., Duan, Y., Zhang, K.Q. and Yang, J. 2012. Culture-independent methods for studying environmental microorganisms: methods, application, and perspective. *Applied Microbiology and Biotechnology* 93: 993–1003.
- Suárez-Estrella, F., Vargas-García, M.C., López, M.J., Capel, C. and Moreno, J. 2007. Antagonistic activity of bacteria and fungi from horticultural compost against *Fusarium oxysporum* f.sp. melonis. *Crop Protection* 26: 46–53.
- Sudirman, L.I., Sutrisna, A., Listiyowati, S.R.I., Fadli, L. and Tarigan, B. 2011. The potency of oil palm plantation waste for mushroom production pp. 378–384.
- Suhaimi, M., Ong, H.K., 2001. Composting empty fruit bunches of oil palm. *Extension Bulletin- Food Fertilizer Technology Center* p. 1–8.

- Sulaiman, F., Abdullah, N., Gerhauser, H. and Shariff, A. 2011. An outlook for Malaysian energy, oil palm industry and its utilization of wastes as useful resources. *Biomass Bioenergy* 35:3775-3786
- Sulaiman, A., Busu, Z., Tabatabaei, M., Yacob, S., Abd-Aziz, S., Hassan, M.A. and Shirai, Y. 2009. The effect of higher sludge recycling rate on anaerobic treatment of palm oil mill effluent in a semi-commercial closed digester for renewable energy. *American Journal of Biochemistry and Biotechnology* 5:1-6.
- Sumathi, S., Chai, S. P. and Mohamed, A. R. 2007. Utilization of oil palm as a source renewable energy in Malaysia. *Renewable Sustainable Energy Review* 12: 2404-2421.
- Sundberg, C. and Jönsson, H. 2008. Higher pH and faster decomposition in biowaste composting by increased aeration. *Waste Management* 28: 518–26.
- Sunitha, S. and Varghese, P.T. 1999. Composting of oil palm wastes for efficient recycling of nutrients in palm plantations. *Planter* 75: 677–681.
- Sundquist, A., Ronaghi, M., Tang, H., Pevzner, P., Batzoglou, S., 2007. Whole-genome sequencing and assembly with high-throughput, short-read technologies. *PLoS One* 2: 484.
- Szanto, G.L., Hamelers, H.V.M., Rulkens, W.H. and Veeken, A.H.M. 2007. NH₃, N₂O and CH₄ emissions during passively aerated composting of straw-rich pig manure. *Bioresource Technology* 98: 2659–70.
- Székely, A.J., Sipos, R., Berta, B., Vajna, B., Hajdú, C. and Márialigeti, K. 2009. DGGE and T-RFLP analysis of bacterial succession during mushroom compost production and sequence-aided T-RFLP profile of mature compost. *Microbiology Ecology* 57: 522–533.
- Takaku, H., Kodaira, S., Kimoto, A., Nashimoto, M. and Takagi, M. 2006. Microbial communities in the garbage composting with rice hull as an amendment revealed by culture-dependent and -independent approaches. *Journal of Bioscience and Bioengineering* 101: 42–50.
- Tamaki, H., Sekiguchi, Y., Hanada, S., Nakamura, K., Nomura, N., Matsumura, M., Kamagata, Y., 2005. Comparative analysis of bacterial diversity in freshwater sediment of a shallow eutrophic lake by molecular and improved cultivation-based techniques. *Applied and Environmental Microbiology* 71: 2162–2169.
- Tamaki, H., Wright, C.L., Li, X., Lin, Q., Hwang, C., Wang, S., Thimmapuram, J., Kamagata, Y. and Liu, W. 2011. Analysis of 16S rRNA Amplicon Sequencing Options on the Roche / 454 Next-Generation Titanium Sequencing Platform. *PLoS One* 6: 6–8.

- Tamura, K., Dudley, J., Nei, M. and Kumar, S. 2007. Molecular evolutionary genetic analysis (MEGA4) Software Version 4.0. *Molecular Biology and Evolution* 24: 1596-1599.
- Tang, J.-C., Kanamori, T., Inoue, Y., Yasuta, T., Yoshida, S. and Katayama, A. 2004. Changes in the microbial community structure during thermophilic composting of manure as detected by the quinone profile method. *Process Biochemistry* 39: 1999–2006.
- Tang, J.-C., Maie, N., Tada, Y. and Katayama, A. 2006. Characterization of the maturing process of cattle manure compost. *Process Biochemistry* 41: 380–389.
- Tang, J.-C., Shibata, A., Zhou, Q. and Katayama, A. 2007. Effect of temperature on reaction rate and microbial community in composting of cattle manure with rice straw. *Journal of Bioscience and Bioengineering* 104: 321–328.
- Thambirajah, J.J. and Kuthubutheen, A.J. 1989. Composting of palm press fibre. *Biological Wastes* 27: 257–269.
- Thambirajah, J.J., Zulkali, M.D. and Hashim, M.A. 1995. Microbiological and biochemical changes during the composting of oil palm empty-fruit-bunches. Effect of nitrogen supplementation on the substrate. *Bioresource Technology* 52: 133–144.
- Tian, W., Sun, Q., Xu, D., Zhang, Z., Chen, D., Li, C., Shen, Q. and Shen, B. 2013. Succession of bacterial communities during composting process as detected by 16S rRNA clone libraries analysis. *International Biodeterioration & Biodegradation* 78: 58–66.
- Ting, A.S.Y., Hermanto, A., Peh, K.L., 2014. Indigenous actinomycetes from empty fruit bunch compost of oil palm: Evaluation on enzymatic and antagonistic properties. *Biocatalysis and Agricultural Biotechnology* 3: 310-315
- Ting, A.S.Y., Tay, H., Peh, K.L., Tan, W.S., Tee, C.S., 2013. Novel isolation of thermophilic *Ureibacillus terrenus* from compost of empty fruit bunches (EFB) of oil palm and its enzymatic activities. *Biocatalysis and Agricultural Biotechnology* 2: 162–164.
- Tiquia, S.M., 2005. Microbial community dynamics in manure composts based on 16S and 18S rDNA T-RFLP profiles. *Environmental Technology* 26: 1101–1113.
- Tiquia, S.M., Ichida, J.M., Keener, H.M., Elwell, D.L., Burt, E.H. and Michel, F.C. 2005. Bacterial community profiles on feathers during composting as determined by terminal restriction fragment length polymorphism analysis of 16S rDNA genes. *Applied Microbiology and Biotechnology* 67: 412–419.

- Tiquia, S.M., Tam, N.F.Y. and Hodgkiss, I.J. 1996a. Effects of composting on phytotoxicity of spent pig-manure sawdust litter. *Environmental Pollution* 93: 249–256.
- Tiquia, S.M., Tam, N.F.Y. and Hodgkiss, I.J. 1996b. Microbial activities during composting of spent pig-manure sawdust litter at different moisture contents. *Bioresource Technology* 55: 201–206.
- Tiquia, S.M., Tam, N.F.Y. and Hodgkiss, I.J. 1997. Effects of turning frequency on composting of spent pig-manure sawdust litter. *Bioresource Technology* 62: 37–42.
- Tkachuk, V.L., Krause, D.O., Knox, N.C., Hamm, A.C., Zvomuya, F., Ominski, K.H. and McAllister, T.A. 2014. Targeted 16S rRNA high-throughput sequencing to characterize microbial communities during composting of livestock mortalities. *Journal of Applied Microbiology* 115: 1181–1194
- Touzel, J. P., O'Donohue, M., Debeire, P., Samain, E. and Breton, C. 2000. "Thermobacillus xylanilyticus gen. nov., sp. nov., a new aerobic thermophilic xylan degrading bacterium isolated from farm soil," *International Journal of Systematic Evolutionary Microbiology* 50: 315–320.
- Tuomela, M., Vikman, M., Hatakka, A. and Itävaara, M. 2000. Biodegradation of lignin in a compost environment: A review. *Bioresource Technology* 72: 169–183.
- Umikalsom, M.S., Arif, A.B., Zulkifli, H.S., Tong, C.C., Hassan, M.A and Karim, M.I.A. 1998. The pretreatment of oil palm empty fruit bunch fibre for subsequent use as substrate for cellulase production by *Chaetomium globosum* kunze. *Bioresource Technology* 62: 1–9.
- Valles, S.M., Oi, D.H., Yu, F., Tan, X.-X., Buss, E.A., 2012. Metatranscriptomics and Pyrosequencing Facilitate Discovery of Potential Viral Natural Enemies of the Invasive Caribbean Crazy Ant, *Nylanderia pubens*. *PLoS One* 7: 31828.
- Vargas-García, M.C., Suárez-Estrella, F., López, M.J. and Moreno, J. 2007. In vitro Studies on lignocellulose degradation by microbial strains isolated from composting processes. *International Biodeterioration and Biodegradation* 59: 322–328.
- Vaz-Moreira, I., Silva, M.E., Manaia, C.M. and Nunes, O.C. 2008. Diversity of bacterial isolates from commercial and homemade composts. *Microbiology Ecology* 55: 714–722.
- Viau, E. and Peccia, J. 2009. Evaluation of the enterococci indicator in biosolids using culture-based and quantitative PCR assays. *Water Research* 43: 4878–4887.

- Vishnivetskaya, T. A., Lucas, S., Copeland, A., Lapidus, A., Glavina del Rio, T., Dalin, E., Tice, H., Bruce, D. C., Goodwin, L. A., Pitluck, S., Saunders, E., Brettin, T., Detter, C., Han, C., Larimer, F., Land, M. L., Hauser, L. J., Kyrpides, N. C., Ovchinnikova, G., Kathariou, S., Ramaley, R. F., Rodrigues, D. F., Hendrix, C., Richardson, P. and Tiedje, J. M. 2011. Complete genome sequence of the thermophilic bacterium *Exiguobacterium* sp. AT1b. *Journal Bacteriology* 193: 2880-2881.
- Vuorinen, A.H. and Saharinen, M.H. 1999. Cattle and Pig Manure and Peat Cocomposting in a Drum Composting System: Microbiological and Chemical Parameters. *Compost Science & Utilization* 7: 54-65.
- Wakase, S., Sasaki, H., Itoh, K., Otawa, K., Kitazume, O., Nonaka, J., Satoh, M., Sasaki, T. and Nakai, Y. 2008. Investigation of the microbial community in a microbiological additive used in a manure composting process. *Bioresource Technology* 99: 2687-2693.
- Wang, C.M., Shyu, C.L., Ho, S.P. and Chiou, S.H. 2007. Species diversity and substrate utilization patterns of thermophilic bacterial communities in hot aerobic poultry and cattle manure composts. *Microbiology Ecology* 54: 1-9.
- Wang, C.M., Shyu, C.L., Ho, S.P. and Chiou, S.H. 2008. Characterization of a novel thermophilic, cellulose-degrading bacterium *Paenibacillus* sp. strain B39. *Letters in Applied Microbiology* 47: 46-53.
- Wang, Y. and Qian, P.Y. 2009. Conservative fragments in bacterial 16S rRNA genes and primer design for 16S ribosomal DNA amplicons in metagenomic studies. *PLoS One* 4: 7401.
- Watts, J.E.M., Fagervold, S.K., May, H.D. and Sowers, K.R. 2005. A PCR-based specific assay reveals a population of bacteria within the Chloroflexi associated with the reductive dehalogenation of polychlorinated biphenyls. *Microbiology* 151: 2039-2046.
- Wei, H., Tucker, M.P., Baker, J.O., Harris, M., Luo, Y., Xu, Q., Himmel, M.E., Ding, S.-Y., 2012. Tracking dynamics of plant biomass composting by changes in substrate structure, microbial community, and enzyme activity. *Biotechnology for Biofuels* 5: 20.
- Weisburg, W.G., Barns, S.M., Pelletier, D.A. and Lane, D.J. 1991. 16S ribosomal DNA amplification for phylogenetic study. *Journal of Bacteriology* 173: 697-703.
- Wéry, N., Lhoutellier, C., Ducray, F., Delgenès, J.P. and Godon, J.J. 2008. Behaviour of pathogenic and indicator bacteria during urban wastewater treatment and sludge composting, as revealed by quantitative PCR. *Water Research* 42: 53-62.

- Wilson, D.B. 2004. Studies of *Thermobifida fusca* plant cell wall degrading enzymes, chemical record , New York, 4, pp. 72–82.
- Wong, Y.S., Teng, T.T., Ong, S.-A., Norhashimah, M., Rafatullah, M. and Leong, J.Y. 2014. Methane gas production from palm oil wastewater—An anaerobic methanogenic degradation process in continuous stirrer suspended closed anaerobic reactor. *Journal of The Taiwan Institute Chemical Engineers* 45: 896–900.
- Wu, T.Y., Mohammad, A.W., Jahim, J.M. and Anuar, N. 2010. Pollution control technologies for the treatment of palm oil mill effluent (POME) through end-of-pipe processes *Journal of Environmental Management* 91:1467–1490.
- Xiao, Y., Zeng, G. M., Yang, Z. H., Ma, Y. H., Huang, C., Shi, W. J., Xu, Z. Y., Huang, J. and Fan, C. Z. 2011a. Effect of continuous thermophilic composting (CTC) on bacterial community in the active composting process,” *Microbiology Ecology* 62: 599-608.
- Xiao, Y., Zeng, G.M., Yang, Z.H., Ma, Y.H., Huang, C., Xu, Z.Y., Huang, J. and Fan, C.Z. 2011b. Changes in the actinomycetal communities during continuous thermophilic composting as revealed by denaturing gradient gel electrophoresis and quantitative PCR. *Bioresource Technology* 102: 1383–1388.
- Yacob, S., Hassan, M.A., Shirai, Y., Wakisaka, M. and Subash, S. 2005. Baseline study of methane emission from open digesting tanks of palm oil mill effluent treatment. *Chemosphere* 59: 1575–1581.
- Yacob, S., Shirai, Y., Hassan, M.A., Wakisaka, M. and Subash, S. 2006. Start-up operation of semi-commercial closed anaerobic digester for palm oil mill effluent treatment. *Process Biochemistry* 41: 962–964.
- Yahya, A., Sye, C. P., Ishola, T. A. and Suryanto, H. 2010. Effect of adding palm oil mill decanter cake slurry with regular turning operation on the composting process and quality of compost from oil palm empty fruit bunches. *Bioresource Technology* 101: 8736-8741.
- Yamada, T., Miyauchi, K., Ueda, H., Ueda, Y., Sugawara, H., Nakai, Y. and Endo, G. 2007. Composting cattle dung wastes by using a hyperthermophilic pre-treatment process: characterization by physicochemical and molecular biological analysis. *Journal of Bioscience and Bioengineering* 104, 408–415.
- Yamada, T., Suzuki, A., Ueda, H., Ueda, Y., Miyauchi, K. and Endo, G. 2008. Successions of bacterial community in composting cow dung wastes with or without hyperthermophilic pre-treatment. *Applied Microbiol and Biotechnology* 81: 771–781.

- Yamada, Y. and Kawase, Y. 2006. Aerobic composting of waste activated sludge: kinetic analysis for microbiological reaction and oxygen consumption. *Waste Management* 26: 49–61.
- Yamamoto, N., Asano, R., Yoshii, H., Otawa, K. and Nakai, Y. 2011. Archeal community dynamics and detection of ammonia oxidizing archaea during composting of cattle manure using culture-independent DNA analysis. *Applied Microbiology and Biotechnology* 90: 1501-1510.
- Yasin, N.H.M., Rahman, N.A., Ismail, F., Mohd Yusoff, M.Z. and Hassan, M.A. 2009. Effect of Different Temperature, Initial pH and Substrate Composition on Biohydrogen Production from Food Waste in Batch Fermentation. *Asian Journal of Biotechnology* 1: 42-50.
- Ye, L. and Zhang, T. 2011. Pathogenic bacteria in sewage treatment plants as revealed by 454 pyrosequencing. *Environmental Science and Technology* 45: 7173–7179.
- Yeoh, C.Y., Chin, N.L., Tan, C.S. and Ooi, H.S. 2011. Acceleration effects of microbial inoculum on palm oil mill organic waste composting. *Compost Science & Utilization* 19: 135-142
- Yin, L.-J., Huang, P.-S., Lin, H.-H., 2010. Isolation of Cellulase-Producing Bacteria and Characterization of the Cellulase from the Isolated Bacterium *Cellulomonas* Sp. YJ5. *Journal of Agricultural and Food Chemistry* 58: 9833–9837.
- Yoshizaki, T., Shirai, Y., Hassan, M.A., Baharuddin, A.S., Raja Abdullah, N.M., Sulaiman, A. and Busu, Z. 2013. Improved economic viability of integrated biogas energy and compost production for sustainable palm oil mill management. *Journal of Cleaner Production* 44: 1–7.
- Yu, H., Zeng, G., Huang, H., Xi, X., Wang, R., Huang, D., Huang, G. and Li, J. 2007. Microbial community succession and lignocellulose degradation during agricultural waste composting. *Biodegradation* 18: 793–802.
- Zahran, H.H., 1999. Rhizobium -Legume Symbiosis and Nitrogen Fixation under Severe Conditions and in an Arid Climate. *Microbiology and Molecular Biology Reviews* 63: 968–989.
- Zainudin, M.H.M., Abd-Aziz, S., Abdul Rahman, N.A., Funaoka, M., Shinano, T., Shirai, Y., Wakisaka, M. and Hassan, M.A. 2012. Utilization of Glucose recovered from Oil Palm Empty Fruit Bunch through Phase Separation System for Bioethanol production. *Pertanika Journal of Tropical Agricultural Science* 35: 117-126

- Zeng, G., Zhang, J., Chen, Y., Yu, Z., Yu, M., Li, H., Liu, Z., Chen, M., Lu, L. and Hu, C. 2011. Relative contributions of archaea and bacteria to microbial ammonia oxidation differ under different conditions during agricultural waste composting. *Bioresource Technology* 102: 9026–9032.
- Zhang, J., Yan, L., Chi, L., Long, X., Mei, Z. and Zhang, Z. 2008. Start-up and operation of anaerobic EGSB reactor treating palm oil mill effluent. *Journal of Environmental Science* 20: 658-663.
- Zhang, J., Zeng, G., Chen, Y., Yu, M., Yu, Z. and Li, H. 2011. Effects of physico-chemical parameters on the bacterial and fungal communities during agricultural waste composting. *Bioresource Technology* 102: 2950–2956.
- Zhao, H., Li, J., Liu, J., Lü, Y., Wang, X. and Cui, Z. 2013. Microbial Community Dynamics During Biogas Slurry and Cow Manure Compost. *Journal of Integrative Agriculture* 12: 1087–1097.
- Zheng, H. and Wu, H. 2010. Gene-centric association analysis for the correlation between the guanine-cytosine content levels and temperature range conditions of prokaryotic species. *BMC Bioinformatics* 11: S7.
- Zhu, N., 2007. Effect of low initial C/N ratio on aerobic composting of swine manure with rice straw. *Bioresource Technology* 98: 9–13.

BIODATA OF STUDENT

Mohd Huzairi b. Mohd Zainudin was born on 26th October 1983 in Kuala Kangsar, Perak. He received his primary education at Sekolah Kebangsaan Pasukan Polis Hutan, Ulu Kinta, Perak from 1990 to 1995. He continued his secondary education at Sekolah Izzuddin Shah, from 1996 until 2000 and continuing his study under matriculation program at Chermat College, Negeri Sembilan in 2001. A year later, he had been offered to continue his study in Bachelor degree of Biotechnology at Universiti Putra Malaysia (UPM) and graduated in Julai 2005. He was admitted to join a Master Degree in Environmental Biotechnology at UPM under the supervision of Prof. Dr. Mohd Ali Hassan and graduated in 2009 with one manuscript. In December 2009, he continued his PhD project in the same field of Master's study at UPM. He has been given the opportunity to carry out collaborative research as his PhD work with AJINOMOTO Co. Inc., the prominent food and chemical company in Japan. During his doctorate study, he guided undergraduate on the final year project, assisted in handling the laboratory class and paper publishing. Throughout his study, he has also been given the opportunity to carry out his research in Kyushu University under the joined research work. He has published several manuscripts and also participated in the Workshops on the Molecular Typing of Microorganism by Pulse Field Gel Electrophoresis (PFGE) in July 2010.

LIST OF PUBLICATIONS

- Zainudin, M.H.M., Hassan, M.A., Tokura, M. and Shirai, Y. 2013. Indigenous Cellulolytic and Hemicellulolytic Bacteria Enhanced Rapid Co-Composting of Oil Palm Empty Fruit Bunch with Palm Oil Mill Effluent Anaerobic Sludge. *Bioresource Technology* 147:632-635. doi:1016/j.bior- tech.2013.08.061
- Zainudin, M.H.M., Hassan, M.A., Abdullah, N., Md Shah, U.K., Tokura, M., Yasueda, H., Sakai, K. and Shirai, Y. 2014. Bacterial Community and Biochemical Changes During Composting of Lignocellulose Oil Palm Empty Fruit Bunch. *BioResources* 9:316-335. ISSN: 1930-2126
- Harun, N.A.F., Baharuddin, A. S., Zainudin, M.H.M., Bahrin, E.K., Naim, M.N. and Zakaria, R. 2013. Cellulase Production from Treated Oil Palm Empty Fruit Bunch Degradation By Locally Isolated *Thermobifida fusca*. *BioResources* 8:676- 687. ISSN: 1930-2126

Proceeding of conferences

- Zainudin, M.H.M., Yusoff, M.Z.M., Nordin, N., Hassan, M.A., Md Shah, U.K., Abdullah, N. and Shirai, Y. (2014) Characterization of thermophilic cellulolytic bacterium *Thermobifida fusca* strain EBT20D-1 producing thermostable endoglucanase. AFOB Regional Symposium 2014 (ARS2014), Kuala Lumpur, Malaysia. (Poster Presentation)
- Mohd Huzairi Mohd Zainudin, Mohd Ali Hassan and Yoshihito Shirai (2014) Pyrosequencing-based analysis of bacterial community during enhanced rapid co-composting of oil palm empty fruitbunch with palm oil mill effluent anaerobic sludge. Symposium of Applied Engineering and Science (SAES). 20-21th December 2014, Kyushu Institute of Technology, Japan. (Oral Presentation)