

ISME SPONSORED EVENT REPORT

A. Title of Event: Philippine Society for Microbiology, Inc. (PSM) 48th Annual Convention and Scientific Meeting

B. Date and Venue: July 18-19, 2019 at Clark Marriott Hotel, Pampanga, Philippines

C. Conference theme and goals:

The Philippine Society for Microbiology, Inc. (PSM) is the primary society for microbiologists in the Philippines. It was established in 1971 and since then held annual conventions and scientific meetings. The PSM recognizes the challenge posed by zoonotic diseases, antimicrobial resistance and food safety to the community of microbiologists thus, for this year, the theme of its 48th Annual convention was **“Promoting One Health through Microbiology Education, Research and Practice.”** Since the One Health approach is a collaborative, multisectoral, and trans-disciplinary approach — working at the local, regional, national, and global levels, the PSM invited experts from the World Health Organization, UN Food and Agriculture Organization, National Training Center for Biosafety and Biosecurity, the US and Japan to discuss how optimal health outcomes can be achieved through recognizing the interconnection between people, animals, plants, and their shared environment. The importance and role of the One Health approach in food safety, control of different zoonoses and in addressing the current war on antibiotic resistance were also discussed. The two-day scientific meeting and convention showcased a multi-disciplinary sharing of breakthroughs, collaborative research and innovations directing to the One Health approach through plenary lectures, quick talk format on vaccines, parallel technical sessions of submitted papers, and poster presentations. The convention was able to inform the Philippine microbiology community of the latest scientific information and results that have been worked on by a pool of experts to monitor and control public health threats and to learn about how diseases spread among people, animals, and the environment. PSM hoped that through this event, Philippine microbiologists were able to recognize their role in One Health’s goal.

The convention was attended by members of related professional organizations, leaders in the industry, science teachers, microbiologists, professors and scientists and the enthusiasts in the field, as well as graduate and undergraduate students from different universities in the Philippines (Table 1).

Table 1. Number of conference participants

	TOTAL
Total Number of Participants	393
Number of participants by institutional affiliation	
a. Academe	193
b. Government	31
c. Industry	35
d. Students	34
Number of plenary speakers/resource persons/presentors	
Local	98
Foreign	2

D. Highlights of the event supported by ISME

The PSM website carried the ISME logo prior to the convention and to date (Annex 1).

The ISME funding supported in part the accommodations of our invited Plenary Speakers who came from abroad or from the Philippines, as well. They are:

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| a. Dr. Bernadette L. Ramirez
(Keynote Speaker)
World Health Organization,
Geneva, Switzerland | b. Dr. Mary Joy N. Gordoncillo
Food and Agriculture
Organization of the United
Nations Regional Office for
Asia and the Pacific | c. Dr. Raul V. Destura
National Training Center for
Biosafety and Biosecurity
(Philippines) |
|--|---|--|

- | | | |
|---------------------------------------|---|---|
| d. Dr. Isagani Padolina
ADP Pharma | e. Dr. Kozo Watanabe
Ehime University, Japan | f. Dr. Matthew Bramble
National Children's Hospital,
Washington DC, USA |
|---------------------------------------|---|---|

The cover of the printed conference souvenir program also carried the ISME logo (p. 3).

The PSM gives free conference registration fee/travel award to young researchers (graduate students) through the Young Researcher's Grant (YRG). For the 48th annual convention, we have provided an **ISME Young Researcher's Grant** (pp. 4-5) to two MS students, who were chosen by a technical panel based on the merit of their graduate research. They gave oral presentations of their paper in parallel technical sessions of the conference. The recipients of the ISME YRG are:

a. **Joseph Martin Q. Paet**

Title of paper: Characterization of Rice Blast Fungus [*Magnaporthe oryzae* (Cavara) B. Couch]- Induced Hypersensitive Response- Related Programmed Cell Death in Lesion Mimic Mutant Rice (*Oryza sativa* L.)

b. **Michael P. Gatpatan**

Title of paper: Metagenomic Analysis of Bacterial Communities Associated with Ants (Hymenoptera: Formicidae) from Canopy and Understory of Selected Trees at Mt. Makiling Forest Reserve

We have also given an **ISME Best Poster Award** to **Sofia B. Ibañez** (p. 6) for her poster, "Molecular Identification of *Leptospira* spp. in Bats Found in Davao City". The ISME best poster award will include the student's membership fee to ISME.

Submitted by:

Leslie Michelle M. Dalmacio, PhD, DPAM
PSM 48 President

PHILIPPINE SOCIETY FOR MICROBIOLOGY, INC.

48TH

ANNUAL CONVENTION
AND SCIENTIFIC MEETING

PROMOTING **ONE HEALTH** THROUGH
MICROBIOLOGY EDUCATION, RESEARCH
AND PRACTICE

CLARK MARRIOTT HOTEL
CLARK FREEPORT ZONE
MABALACAT, PAMPANGA,
PHILIPPINES

JULY 18-19, 2019



In Partnership with:

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Characterization of Rice Blast Fungus [*Magnaporthe oryzae* (Cavara) B. Couch]-Induced Hypersensitive Response-Related Programmed Cell Death in Lesion Mimic Mutant Rice (*Oryza sativa* L.)

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Hypersensitive response (HR) is a key feature of plant immunity that sacrifices through programmed cell death (PCD) the already infected cells and thereby restricts the growth and further invasion of pathogens. Rice (*Oryza sativa*) **lesion mimic mutants** (LMM) manifest disease phenotype in the absence of pathogen and are monocots' model organisms in unraveling the molecular mechanism of HR-induced PCD. The aim of the current basic research was to characterize phenotypically and genotypically a rice LMM from an EMS-generated mutant accession obtained from the International Rice and Research Institute, Philippines. LMM 6321-2, used in this study, is an initiator type of LMM that showed significantly reduced agronomic yield potential as a penalty for dysregulated PCD. However, it exhibited increased or partial resistance against virulent rice blast fungus, *Magnaporthe oryzae* (PO6-6 and CA89 isolates) and induced HR-mediated PCD after incompatible isolate inoculation (V86010, CA41 and M101-1-2-9-1) using rice blast nursery spray and punch inoculation assays. The recessive mutation was successfully identified using bulk segregation analysis to be a nonsynonymous mutation in a highly conserved amino acid residue of the sixth transmembrane domain of a cyclic nucleotide-gated ion channel (CNGC). *OscNGC13* mutation was validated by sequencing and localized by quaternary protein model prediction in an important Ca²⁺ conducting pore of the channel. This brought about significant changes in its expression profile in *M. oryzae* post-inoculated experiment where genes related to Ca²⁺ conduction and sensing, NADPH oxidases, ROS scavengers, LMM-, phytohormone-, and pathogenesis-related genes were found to be significantly expressed with a different timing of expression than its IR64 parent. In brief, the mutant showed delayed expression of PCD-related genes peaking 48 hpi compared to IR64, which heightened 24 hpi. Taken together, it was proposed that LMM 6321-2 have a Ca²⁺-dependent ROS-mediated PCD where mutated *OscNGC13* plays a key role in the lesion mimicking phenotype.

Diversity of Bacteria in Ants (Hymenoptera: Formicidae) from Canopy and Understory of Selected Trees at Mt. Makiling Forest Reserve

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The Mt. Makiling Forest Reserve (MFR) is a biodiversity hotspot that is listed as one of the 170 conservation priority areas established by the Philippine government. Its flora and fauna diversity has been reported but knowledge gap has been identified as regard to the **bacterial communities** associated with the flora and fauna. This study focused on ants (Hymenoptera:Formicidae), which are dominant in forest canopy and play essential role in the ecosystem functionality. NGS-based metagenomic sequencing were employed to investigate the bacterial communities associated with five arboreal ants species collected from MFR. Ants were identified as *Dolichoderus thoracicus*, *Myrmecaria sp.*, *Colobopsis leonardi*, *Polyrhachis mindanaoensis*, and *Polyrhachis semiinermis*. The 16S rDNA metagenomic sequencing using V3-V4 region showed that Proteobacteria, Spirochaetes, Firmicutes, Bacteroides, and Actinobacteria were the most abundant phyla. Individual analysis of bacterial genera associated with the five species showed that unclassified members of Rhizobiaceae, Orbaceae and Burkholderiaceae were dominant in *D. thoracicus*. Unclassified members of Rhizobiaceae, Spirochaetaceae, and Ruminococcaceae were dominant in *Myrmecaria sp.* On the otherhand, *Candidatus Blochmannia* and *Wolbachia* were abundant in *Camponoti* ants *C. leonardi*, *P. mindanaensis*, and *P.semiinermis*. Comparative analysis of bacteria associated with arboreal ant species using Bray-Curtis distance and UPGMA cluster analyses showed that the microbiomes of the *Camponoti* group clustered together, while *D. thoracicus* and *Myrmecaria sp.* exhibited unique bacterial profiles. Predictive gene profile analysis showed that the most functional categories were those associated with metabolism and biosynthesis of amino acids, pathways for metabolism of nucleotide, amino sugars, nitrogen, and utilization of different carbon sources.

Non-Professional Category

α -amylase- Conjugated Biogenic Silver Nanoparticles as Innovative Strategy against Biofilm-forming Multi-drug Resistant Bacteria

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The evolution of multi-drug resistance in pathogenic bacteria instigates the decline in effectiveness of antibiotics and antimicrobial agents. Nanoparticle-enzymes conjugates (bioconjugates) is a recent interest in countering biofilm related infections due to its stability and targeted delivery. In this study, silver nanoparticles (AgNPs) were

synthesized using cell-free supernatants of alkaliphilic bacteria isolated from a hyperalkaline spring in Zambales, Philippines. The biosynthesized AgNPs exhibited an absorbance peak at 400-470nm corresponding to the surface plasmon resonance of AgNPs. Scanning electron microscopy (SEM) coupled with energy dispersive X-ray (EDX) spectroscopy showed stable irregular and spherical particles with high elemental silver composition. Fourier-transform infrared (FTIR) spectroscopy revealed functional groups in the supernatant involved in the reduction of Ag⁺ to AgNP. These biosynthesized AgNPs were then conjugated with α -amylase extracted from *Bacillus subtilis*. The modification in α -amylase protein structure was exhibited by a concentration-dependent increase in its absorbance intensity at around 280nm and increase in fluorescence quenching as revealed by UV-vis analysis and Stern–Volmer relation, respectively. FTIR spectroscopy revealed slight characteristic peak shifts upon interaction of AgNP with α -amylase. The biosynthesized AgNP and bioconjugates showed significant inhibition of biofilm formation and dispersion of pre-formed biofilms of multi-drug resistant strains of *Klebsiella pneumoniae* and methicillin-resistant *Staphylococcus aureus* (MRSA) in a dose-dependent manner as determined by microtiter plate assay. *K. pneumoniae* and MRSA were found to be susceptible in concentration-dependent manner to both AgNP and bioconjugate as established by Kirby-Bauer assessment. Notably, the bioconjugates exhibited higher efficiency than AgNPs alone when used against the biofilm-forming strains. This study demonstrates that biosynthesized AgNPs from alkaliphilic bacteria can be conjugated with α -amylase with promising biomedical applications.

Molecular Identification of *Leptospira* spp. in Bats Found in Davao City

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Leptospirosis is a zoonotic disease with worldwide prevalence. It is caused by pathogenic species of *Leptospira* with established reservoir hosts such as domestic and wild animals. Bats are considered potential vectors of *Leptospira*

pathogens as reported in other countries. However, association between *Leptospira* and bats in the Philippines remains to be elucidated. This study aimed to profile bat species and examine the occurrence of leptospires in bats found in Malagos, Davao City. Blood, urine and/or kidney samples were obtained from the 50 trapped bats. Whole blood and the urine and/or kidney samples were cultured in modified Korthof's medium with 5-fluorouracil for isolation of *Leptospira*. DNA were also extracted from the kidney samples and subjected to *flagellin B* polymerase chain reaction (*flaB* PCR) to determine if the bats carried pathogenic leptospires. DNA samples that turned out *flaB* PCR-positive were further subjected to sequencing using the same target gene. No leptospires were isolated from the kidney or body fluids of the bats. However, 1 out of 50 individuals was found to be positive in *flaB* PCR, suggesting that it harbored pathogenic *Leptospira*. The *flaB* PCR-positive bat belongs to the colonial species *Rousettus amplexicaudatus*. Result of the *flaB* gene sequence analysis showed close similarity of the sample with *Leptospira borgpetersenii* serovar Hardjobovis with a 93.82% identity. Phylogenetic analysis also showed that the DNA sequence was closely related to *Leptospira borgpetersenii* serovars Hardjobovi Javanica, Dehong, and Balcanica. It also revealed that the sample was more closely related to species and serovars found in reservoir or maintenance hosts such as rats and goats than those seen in incidental hosts such as humans. This suggests that bats may be important hosts to the transmission cycle of *Leptospira* to other animals. Animals and humans that coexist and live in close proximity to bats may be at risks of acquiring the infection. The large distribution of bats, their colonial nature, and their ability to fly and cover large areas makes them potential vectors in spreading leptospires. This study serves as the first evidence of *Leptospira-bat* association in Mindanao.