

4th World Conference on

SYNTHETIC BIOLOGY AND GENETIC ENGINEERING

November 09-10, 2017 Singapore

Assessment of seed dispersal through metagenomic analysis of the DNA-barcoded fruit-bat species' diet in the tropical lowland forest of Palanan, Isabela**Jessica D Rey¹, Ian Kendrick C Fontanilla¹, Sandra L Yap³, Mariano Roy M Duya¹, Kris A Ortizo¹, Karen Mae R Lego¹, Adrian U Luczon¹, John Gregor P Rono¹, Christopher John A Pueblo¹, Edwino S Fernando^{1,2} and Perry S Ong¹**¹University of the Philippines Diliman, Philippines²University of the Philippines Los Banos, Philippines³Far Eastern University, Philippines

Bats are important parts of the ecosystem. Some serve as predators of insects, while others serve as seed dispersers. In this study, we explore chiropteran diversity and the role of bats in seed dispersal. The dispersal of seeds is oftentimes crucial for survival as it allows the seed to escape from conspecific competition near the mother tree. Fruit bat diversity plays a major role in seed dispersal since different species have distinct diets. Molecular approach to the diet analysis of bats is expected to contribute to the limited number of known food sources of bats in the tropical forest. The main objectives of this study are to determine fruit bat diversity through DNA barcoding and to identify which plant species depend on bats for seed dispersal through diet analysis using the NGS platform. In the Palanan Forest Dynamics Plot, Isabela, Philippines, a total of 32 individuals from eight-species of fruit bats was barcoded. Assessment of variation in bat-dispersed plant species was done across seasons and years in the forest between February 2016 and March 2018. Out of the eight-species captured, only in three species (*Ptenochirus jadori*, *Cynopterus brachyotis* and *Desmalopex leucopterus*) were there enough seeds for DNA extraction. DNA from the pooled samples was extracted and the trnH-psbA intergenic spacer region was amplified with 300 bp long primers with attached adapter sequence. The NGS-generated sequences were cross-referenced to the available database of trnH-psbA sequences of the trees in the plot. Using BLASTn, three tree genera were identified to be the most observed sequences. The tree species were also confirmed by voucher samples in the UP IB Herbarium collection. With this knowledge on the species with which bats consume as food, the next step will be to confirm whether the seeds still germinate after passing through the guts.

Biography

Jessica D Rey is Assistant Professor in University of Philippines, Philippines.

jayrey77@gmail.com

Notes: