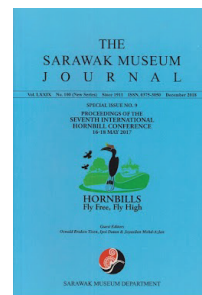




The Sarawak Museum Journal

Vol. LXXIX No. 100

December 2018



ISSN: 0375-3050

Citation: *Sarawak Museum Journal*, LXXIX (100) (2018): 109-116**CAVITY MANAGEMENT ENHANCED THE ALLELIC DISTRIBUTION OF GREAT HORN BILLS IN EASTERN KHAO YAI NATIONAL PARK**Nareerat Viseshakul¹, Pipat Jirapiti¹, Kanchid Srinapawan² and Pilai Poonswad³¹Department of Pathology, Faculty of Veterinary Science, Chulalongkorn University, 39 Henri Dunant Road, Pathumwan, Bangkok 10330²National Park Office, Department of National Parks, Wildlife and Plant Conservation, Paholayothin Rd., Chatujak, Bangkok 10900³Thailand Hornbill Project, Department of Microbiology, Faculty of Science, Mahidol University, Rama 6 Rd, Ratchthevee, Bangkok 10400

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ABSTRACT

Khao Yai National Park, covering an area of 2,168 km², is very rich in wildlife. The park includes mainly monsoon evergreen forests inhabited by four species of hornbills, namely *Anthracoceros albirostris*, *Buceros bicornis*, *Ptilolaemus austeni* and *Rhyticeros undulatus*. Among these species, Great Hornbills, *B. bicornis*, are the largest birds and require the most in terms of quantity and quality of natural resources. They require very large cavity which is in short supply in the wild. The western part of the park supports a high population of Great Hornbills while in the eastern part has low density. From 2009, the study has been expanded to cover the eastern part. Following seven consecutive years (2009–2015) of nest management, we studied the uses of nests with 4 microsatellites DNA markers specific for each allele of Great Hornbills. This study is to examine non-invasively the 49 DNA samples from mainly tailed feathers. We collected DNA from the shed feathers at or near the nests from Eastern and Western Khao Yai. The population structure analysis revealed by microsatellites markers, showed the inbreeding coefficient (*F_{is}*) of the local hornbills of Western Khao Yai improved from 0.45 in 2009 to -0.028 in 2015 with great genetic diversity. In 2014, these hornbills introduced 6 of 9 alleles into the Eastern Khao Yai (locus Bbi 3). Data showed the population connectivity between the two subpopulations. The gene flows potentially increase between the west and the east. Nonetheless, heterozygosity of Great Hornbills in the Eastern Khao Yai significantly improved from *H_{Obs}* = 0.615 to 0.750. Results also showed the availability of suitable nest cavities attracted hornbills from the western to eastern Khao Yai. This molecular approach indicates that the nest cavity management is one of the important strategies to secure the longterm survival of hornbills.

Keywords: DNA microsatellites, genetic diversity, population connectivity

CAVITY MANAGEMENT ENHANCED THE ALLELIC DISTRIBUTION OF GREAT HORNBILLS IN EASTERN KHAO YAI NATIONAL PARK

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