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CAVITY MANAGEMENT ENHANCED THE ALLELIC DISTRIBUTION OF GREAT HORNBILLS IN EASTERN KHAO YAI NATIONAL PARK**Nareerat Viseshakul^{1*}, Pipat Jirapiti¹, Kanchid Srinapawan² and Pilai Poonswad³**

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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 (Fis) 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 HObs = 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

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JABATAN MUSEUM SARAWAK

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Abstract

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INTRODUCTION

Khao Yai National Park, a world heritage park of Thailand, is a lush monsoon evergreen forest covering a large habitat of wildlife, 2,168 square kilometres. This park provides an excellent resource of food and nest trees for four species of large and small hornbills namely, *Anthracoceros albirostris*, *Buceros bicornis*, *Ptilolaemus austeni* and *Rhyticeros undulatus* (Poonswad 1995). Among these species, Great Hornbills (Gh), *B. bicornis*, is the largest bird and require the most in terms of quantity and quality of natural resources. They are frugivorous feeding on fruits from big trees and nest in a hole cavity of reasonable size at a height of 15–25 metres. The habitat of the Great Hornbill therefore tends to be more critically depleted than the other three species.

The western part of the park (KYW) situated around the park head quarter receives regular patrolling by wildlife rangers. Subsequently, the western part of the park is more tightly populated with hornbills than the eastern area. In 2009–2015, the Hornbill Research Foundation initiated the programme of cavity management of all species of hornbills including the Great Hornbills. The project was extended to include the eastern part of the park (KYE) restoring the abandoned nest cavities into more usable ones. It is hoped that the Great Hornbills will return to the repaired hole cavities in the next breeding season. We also expect that birds from the western area will migrate in the new repaired nest cavities around the eastern part of the park. This will reduce the competition over the nests in the west and move to the lower populated area of the east.

Our research is to determine the situation of nest cavity management of which is not only successful for the newer nest usage but also for their gene flow between the western part back to the east. We used four microsatellites markers to track bird genetic material collected from shed feathers during the breeding season. The Bbi3, is the most useful loci marker showing the allelic distribution of birds from the west gradually establishing a new and small population of the east.

MATERIAL AND METHOD

Sixty feather samples were collected from both KYW and KYE around and at the nest of 49 Great Hornbill cavities. Total DNA from each separate sample was extracted using Neucleospin extraction kit. The following micro-