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BIOGEOGRAPHY OF FRUIT BATS IN SOUTHEAST ASIA¹

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ABSTRACT

A study on the biogeography and diversity of fruit bats (Megachiroptera) was carried out in 32 selected areas in Southeast Asia from April 1994 to May 1997. There are a number of factors that are associated with the patterns of distribution, species diversity and abundance of fruit bat species. These factors include ecological and geographical barriers and possible past Pleistocene or vicariant events. The distribution of fruit bats in SE Asia is consistent with Huxley's Line and Pleistocene land-bridge theory. Fourteen species of the known 21 megachiropterans were mist-netted in Borneo, Peninsular Malaysia and Thailand. Apparently, the species diversity and composition of the fruit bat community was related to the available ecological habitats and structural diversity of the habitat. Higher species diversity was observed in the primary forest (closed habitat), probably due to high structural diversity of the forest. In the secondary habitat (open area) species diversity was lower and dominated by few species. *C. brachyotis* was dominant, widespread, occupying all habitats sampled, and outnumbered all other species mist-netted; and it occurred in high abundance in open habitat but was lowest in the closed habitat. MacroGLOSSINAE were always associated with flowering *Musa* species found in the ecotones between primary forest and open habitats. *D. spandiceus* and *E. major* were relatively rare species that occurred in restricted habitats with low abundance and probable have specialised life requirements and niches. Contrary to Payne et al. (1985), there was no recent observation of *C. sphinx* in Borneo during this study.

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* This is the first part, out of three major studies on the biogeography and evolution of fruit bats in Malaysia.

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INTRODUCTION

The patterns of geographical distribution of fauna and flora in their present habitats generally reflect the historical biogeography of the area (Whitmore, 1981; Morley and Flenley, 1987). Historical biogeography and tectonic models have been used to understand distribution patterns and to explain the geographic changes of animals in an area (Hall and Holloway, 1998). Evidence from all fields of biogeography is therefore necessary to test these models and identify the origin of the present biogeographic patterns (Hall and Holloway, 1998).

Biogeography is a science that attempts to document and understand the spatial patterns of biodiversity of fauna in an area (Brown and Lomolino, 1998). This involves study about both the past and the present in order to understand the patterns of differences in diversity. The diversity of an area can be measured by species richness or the number of species in a sample from a local or geographic area (Brown and Lomolino, 1998). The type of diversity is conveniently divided into three categories (Ricklefs and Schluter, 1993; Brown and Lomolino, 1998). Alpha diversity refers to the species richness of a local community, i.e. the number of species recorded within a standardised area or some naturally delineated habitat patch. Beta diversity refers to the overall change or turnover in species composition between two distinct habitats. Gamma diversity refers to the total species richness of a large area, which reflect, the influence of both alpha and beta diversity.

The patterns of alpha diversity in a geographic area can be found by ecological surveys, as long as the taxonomy is well known. Changes in species composition and richness can be observed by conducting field surveys of selected geographical areas and habitats.

Changes in the species composition reflect certain interactions within the community (Ricklefs and Schluter, 1993). The observed patterns of diversity in the fruit bat community would be useful knowledge in our understanding about the factors that might influence or control the divergence in a species in terms of genetics and morphology.

During a long expedition into the forest of the Far East, Alfred Russel Wallace collected a large number of specimens and a vast amount of information on the distribution of fauna (Wallace, 1860, 1896). He observed that there were prominent differences in the patterns of distribution of insects, birds and mammals between Borneo and Sulawesi (Wallace, 1860). Based on that information, he described a boundary between the Asian and Australasian fauna, later to be called Wallace's Line. This line is one of the best examples of its kind and it became the first area where the importance of biogeography and evolution was recognised. Wallace's Line runs from between the Philippines and Moluccas in the north, bends southwest between Borneo and Sulawesi and then south between the islands of Bali and Lombok (Fig. 1) (Mayr, 1944; Smith, 1980). Wallace's line has been recognized by many investigators and has initiated much interest in the study of biogeography in Southeast Asia (SE Asia). In 1868, Huxley extended the idea by modifying Wallace's Line to run between Palawan and the rest of the Philippines Archipelago and south of the Taiwan islands (Fig. 1) (Mayr, 1944; Corbet and Hill, 1992). Authors in biogeography have accepted Huxley's Line to represent the major regional biogeographic division. Lydekker's Line was proposed in 1896, drawn between New Guinea and the Moluccas to mark the eastern limit of distribution of the Oriental species (Mayr, 1944; Corbet and Hill, 1992). In 1904, Webers's Line was drawn east of Wallace's Line to separate a group of islands with the most Oriental faunal species from those with the Australian animals. Weber's Line can be considered as a halfway line between those of Wallace and Lydekker (Mayr, 1944). These lines drawn by previous researchers were based on limited knowledge of the distribution and numbers of animals in the area, and were subjected to refinement as more information became available.