

*Theretra alecto* (Linnaeus, 1758)

# Historical biogeography of the hawkmoth genus *Theretra* Hübner, 1819 (Sphingidae) based on mitochondrial genes



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## Introduction

The family Sphingidae includes more than 1600 species. With more than 70 already described species, *Theretra* Hübner, 1819 is among the three most diverse genera in the subfamily Macroglossinae. It occurs throughout the Old World, from Africa across Asia and Australia up to New Caledonia and Melanesia. Many studies were published about different groups of insects with the Old World distribution (Kodandaramaiah & Wahlberg 2007; Müller et al. 2010, etc.). From these studies, we can deduce some general colonisation trends for each group of animals with the origin in South Asia. The main aim of the study was to find the centre of radiation and to reconstruct the dispersal routes of these hawkmoths.

## Results and discussion

Our results revealed that the dispersion of the hawkmoths in this region followed similar colonization patterns of other groups of animals and also the monophyly of the genus *Theretra*. The origin of the genus and center of radiation were most probably in South Asia (SA). From there hawkmoths firstly colonized Middle Asia (MA) and the Far East (FE). Before 10 Ma Indonesia (IN) was colonized and the mass diversification started. Soon hawkmoths reached the borders of Papua New Guinea and Australia (AU). Oceania and Polynesia (OP) where colonized multiple times through South Asia, Indonesia and Australia. Before 6 Ma Africa (AF) was colonized for the first time and then re-colonized by the dispersal across the ocean 4 Ma later. According our analysis species with a good ability of dispersal appeared multiple times in the evolution of the genus *Theretra*.

## Material and methods

In our study, we used 89 sequences of mitochondrial COI gene from 59 species and 10 subspecies (Fig. 2). Alignment was done in Bioedit v. 7.2.5. For phylogenetic analyses we performed Maximum Likelihood (10 million generations, sampling 1000 generation). The dating analyses were run in BEAST 1.8.0, we used two calibration points based on results of the study by Kawahara & Barber (2015). We computed the ancestral distribution in the R package BioGeoBEARS, which implements the DEC model similar to Lagrange C++. We allowed the founder-event speciation parameter  $j$  to be estimated in NS1- $j$  and TS1- $j$  to evaluate the importance of long-distance dispersal across islands (Fig. 1).

Fig. 2. The map of sampled areas in Old World .

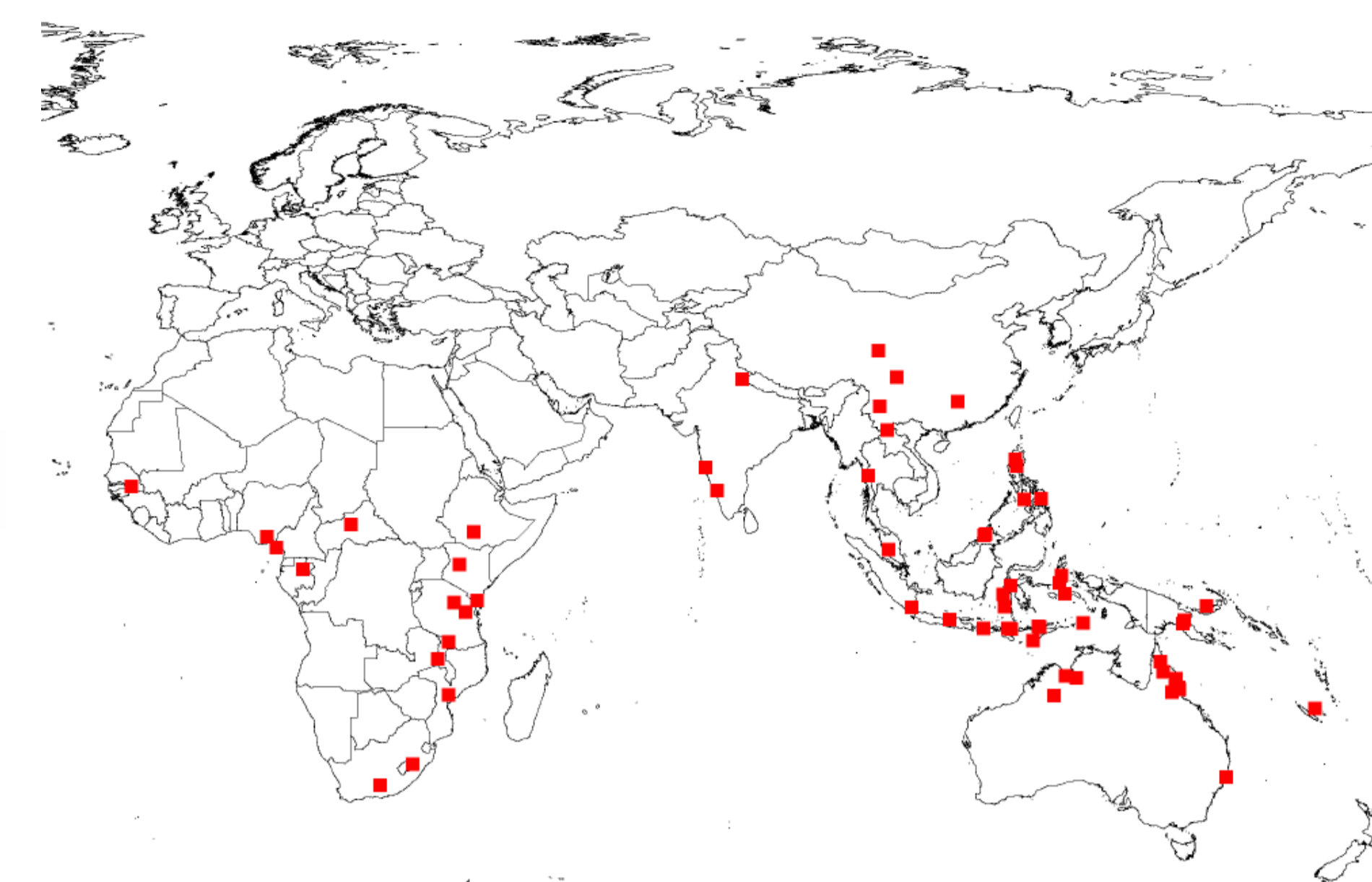


Fig. 1. The calibrated phylogenetic tree estimated by Beast 1.8.0 with the ancestral distribution points analysed in the R package BioGeoBEARS.

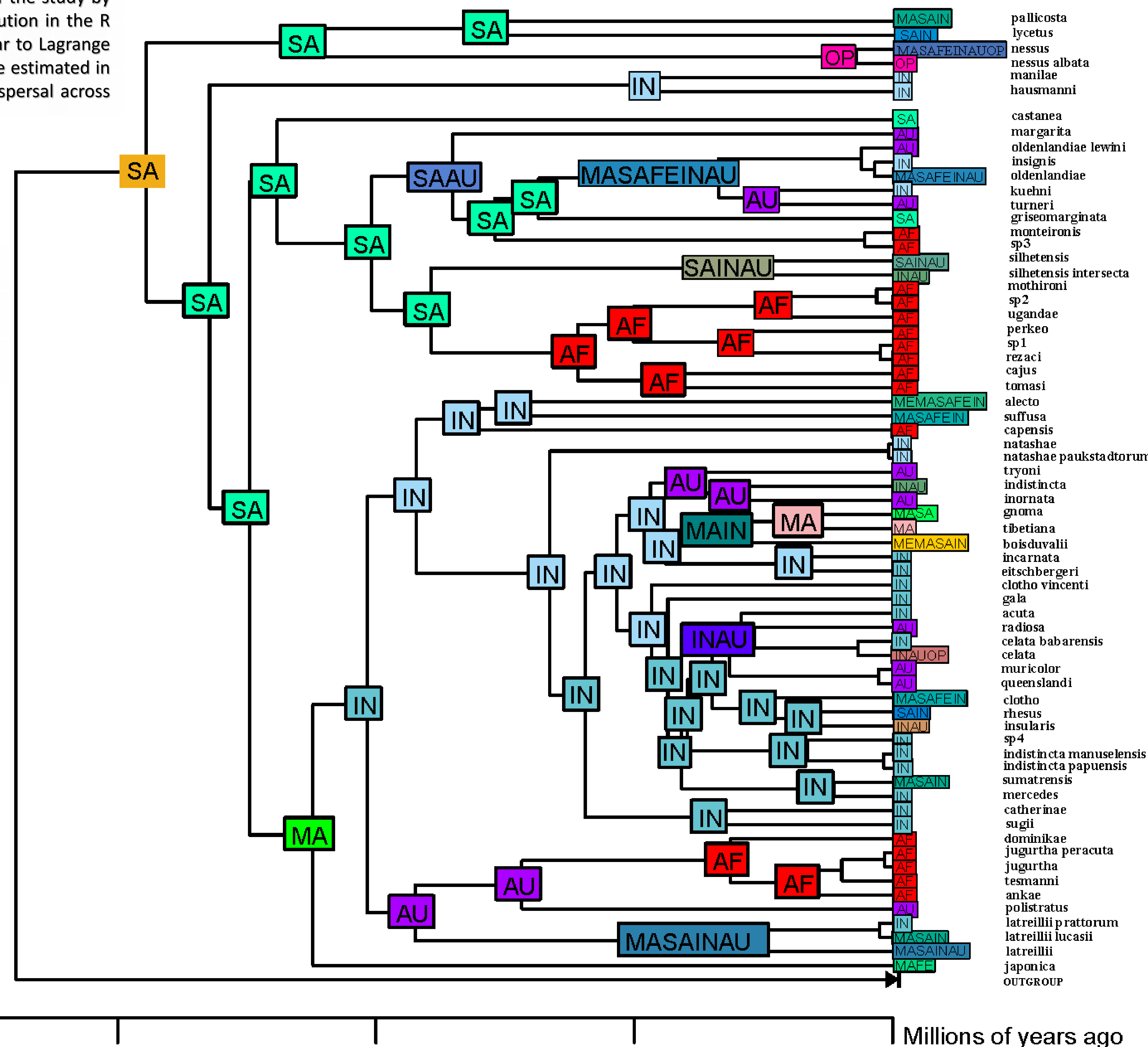
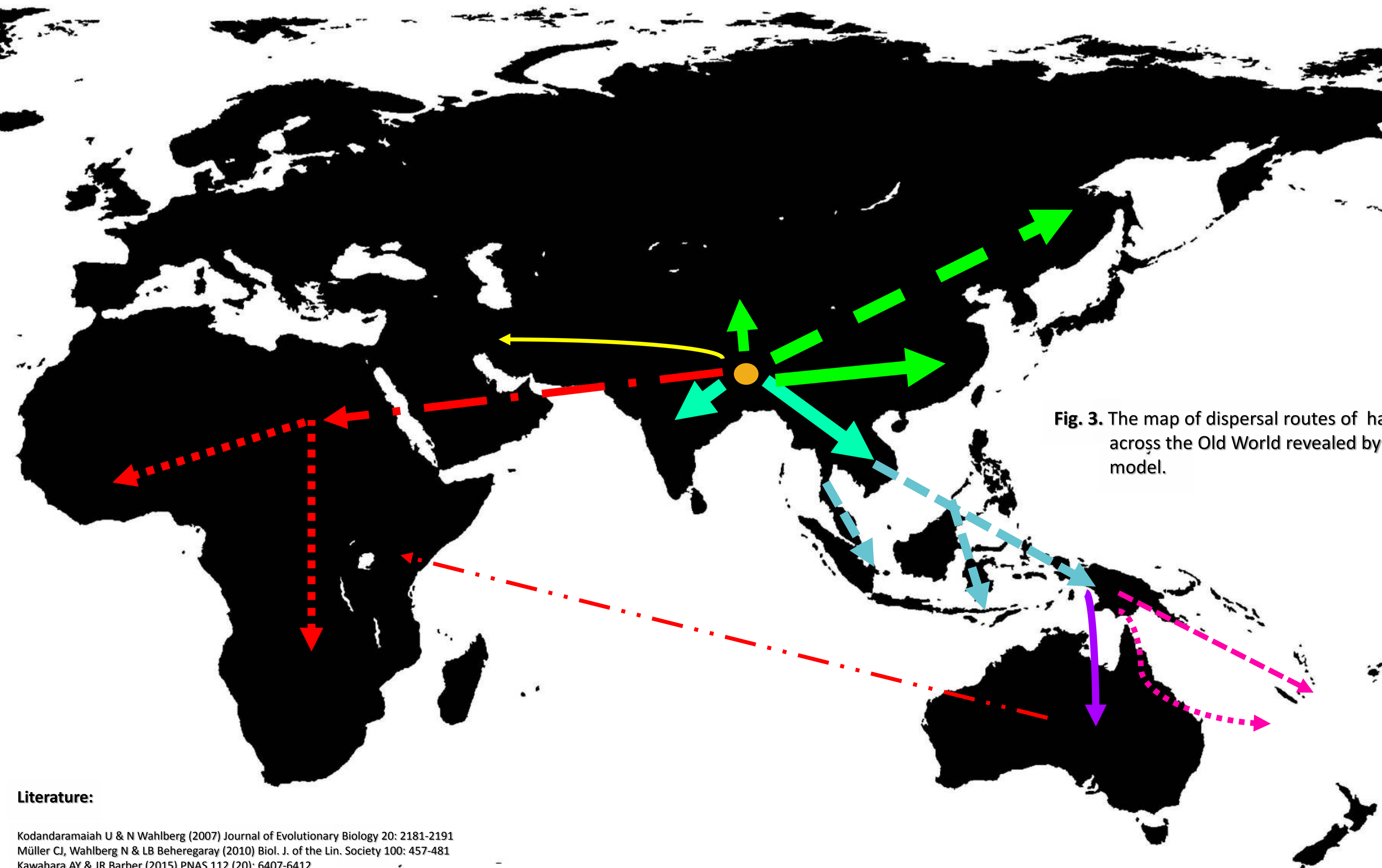


Fig. 3. The map of dispersal routes of hawkmoths across the Old World revealed by BioGeoBEAR model.



Literature:

Kodandaramaiah U & N Wahlberg (2007) Journal of Evolutionary Biology 20: 2181-2191  
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Kawahara AY & JR Barber (2015) PNAS 112 (20): 6407-6412