

Abstract of thesis entitled

**GENETIC VARIATION IN *EUPLOEA*  
(LEPIDOPTERA: NYMPHALIDAE) POPULATIONS  
IN SOUTH CHINA**

submitted by  
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The ecology of winter aggregation of *Euploea core anymone* and *E. midamus midamus* in South China were investigated.

272 *E. core* individuals from nine populations and 226 *E. midamus* individuals from eight populations were captured from Hong Kong, Hainan and Guangdong for three consecutive seasons from November 2007 to January 2009. No *E. core* samples were captured from Guangdong in the wet season and no *E. midamus* were sampled from Hainan in either season or from Guangdong in the dry season.

Mating status of 187 *E. core* and 171 *E. midamus* females was examined by bursa copulatrix dissection. Both studied species in Hong Kong breed in the wet season as supported by a significantly greater proportion of mated females with fresh spermatophores while overwintering populations are reproductively dormant. No sound generalisation for the region could be given due to insufficient sample size from some populations. However, 42.9% and 31.3% of freshly-mated females were sampled from Deep Water Bay during the middle

of aggregation period suggested possible mating within aggregation site, but further investigation on the population origin would be needed to deduce if inter-population breeding occurred. Multiple mating was found to be common in both studied species, with a maximum of seven and six spermatophores in *E. core* and *E. midamus* respectively.

The population genetic structures of both species were studied by inter-simple sequence repeats (ISSR) with six loci. Consistent results were generated using POPGENE and AFLP-SURV. Low genetic diversity was found in both *E. core* (8.56-14.02%) and *E. midamus* (9.57-15.09%). Large and significant overall genetic differentiation was found in both species (*E. core*:  $G_{ST} = 0.2617$ ,  $F_{ST} = 0.2342$ ; *E. midamus*:  $G_{ST} = 0.3811$ ,  $F_{ST} = 0.3686$ ). A reduction in spatial genetic divergence between populations of Hong Kong and Hainan from wet to dry season in 2008, together with a slight rise in  $N_m$  value, revealed possible movement of individuals by migration between two populations. Seasonal differentiation between residential, breeding and aggregating, reproductively dormant populations from Hong Kong was greater than that from Hainan, indicating that the change in population genetic composition in Hainan was less significant. Shek Pik (Hong Kong) had the most diverse *E. core* and the least diverse *E. midamus* populations among all overwintering populations, which could be originated from a different area. UPGMA dendrograms and nMDS three-dimensional plots showed a possibly local residential *E. core* population from Shangchuan Dao (Guangdong), and a *E. midamus* population from a pre-wintering site at Fan Lau were the most distinct from the others.

Supported by results from this study and observation records, winter migration of both studied species between Hong Kong and Hainan was possible. Two hypothesized migration routes are suggested, of which migrating along coastal areas from Hong Kong to islands in Guangdong, then to Hainan seems more probable than direct flight across the South China Sea. Potential threats and conservation implication of this study are discussed. Finally, studies by microsatellites and stable isotopes are recommended for future research to confirm the danaine migration route in the region.