

Thesis Title                    Some Biological Aspects of the  
   *Anopheles dirus* Complex.  
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#### ABSTRACT

In the present study, three different biological aspects, i.e. polytene chromosome relationships, hybridization and morphology of 5 members of the *Anopheles dirus* complex, species A, B, C, D and F, were studied.

Photomaps and rearrangements of each salivary gland polytene chromosome arm of species A, B, C, D and F of the *An. dirus* complex from natural populations in Thailand were presented. Structural conformation of heterokaryotypes and comparison of chromosome banding sequences revealed 10 paracentric inversions.

Reciprocal cross-mating between species F and species A, B, C and D were performed by induced copulation. The number of eggs per female, the hatchability, the viability and the fertility of the F<sub>1</sub> hybrids were investigated. Sterile F<sub>1</sub> hybrid males, as determined from backcrossing and selfcrossing, were observed

in all combination crosses accompanied by various degrees of abnormality in reproductive systems of the hybrid males. Completely asynaptic salivary gland polytene chromosomes were observed among the F<sub>1</sub> hybrids. These results suggest there existed reproductive isolation between species F and the other species. The relationships between species F and species A, B, C and D were discussed.

Morphology of eggs of species F was studied. Twelve characteristics of the eggs were observed. Some of the data were compared to previously studied parameters of species A, B, C and D. Eggs of species F were larger in size than the other species and also had the greatest entire egg length, float length, and number of ridges on floats. Number of teeth per maxilla and length of maxillary tooth row of females of the 5 members of the *An. dirus* complex were studied. Species rank based on both characteristics, from the largest to the smallest, were the same: F - C - A - D - B. Differences among species were discussed and found to be statistically significant ( $P \leq 0.05$ ).

Based on the present data, a phylogenetic relationship can be constructed. Species D seems to be the common ancestor from which the hypothetical species originated. Species A, B and F derived from this hypothetical ancestor with their specific genetic differentiation. Species C derived from species A by ecological adaptation.