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ANCHALEE SAELEE: ELECTROPHORETIC STUDY OF THE *BACTROCERA TAU* COMPLEX (DIPTERA: TEPHRITIDAE) IN CERTAIN POPULATIONS IN THAILAND. THESIS ADVISORS: VISUT BAIMAI, Ph.D., JOHN MILNE, Ph.D., SANGVORN KITTHAWEE, Ph.D., PREECHA PRATHEPHA, Ph.D. 124 P. ISBN 974-663-006-7

The *Bactrocera* (*Zeugodacus*) *tau*-like flies are some of the most important agricultural pests of south-east Asian cucurbit crops and form a complex of species. There has always been taxonomic confusion regarding the separation of species within this species complex. This is because it is difficult to determine if differences between *B. tau* flies are due to genetic variation within species or genetic differentiation between species. Morphological observations coupled with cytological evidence has revealed at least seven genetic species within this taxon, temporarily designated as species A (=*B. tau*), C, D, E, F, G and I. In this thesis electrophoretic evidence is used to verify the existence of these seven genetic species within the *B. tau* complex. Genetic markers for species separation and phylogenetic relationships of these species are also described.

The genetic variability of and differences among 43 collected samples of seven species of the *B. tau* complex were evaluated electrophoretically. Nine enzyme systems, which were composed of twelve loci, were used. Twenty-eight populations of *B. tau* were characterized by low genetic variability as indicated by low values of average heterozygosity ($\overline{H}_o$) and mean genetic distance ($\overline{D}$). No geographical pattern relationships were displayed because the level of genetic differentiation was similar between populations in the same geographical region and between populations originating from different geographical regions. In the same manner, populations from the same host plant species had similar levels of genetic differentiation as those from different host species. Single diagnostic alleles with specific relative mobilities, which can be used as genetic markers for species classification within the *B. tau* complex, were discovered only in species D. Although, no single allele was diagnostic for the other six species, the use of more than two alleles permitted the correct classification of nearly all individuals of even the two most closely related species. A phylogenetic tree was estimated by using a UPGMA clustering of Nei's unbiased genetic distance. The tree indicates that three main lineages exist in the *B. tau* complex. The first group consists of a complex of extremely similar species (*B. tau*, species E, F and G). The second group consists of species C and I and the last group consists of species D.