

**Smith, P. T., Kambhampati, S.\* & Armstrong, K. A.:** Phylogenetic relationships and character evolution among selected species of *Bactrocera* (Diptera: Tephritidae) based on multiple mitochondrial genes. *Insect Syst. Evol.* 36: 343-359. Copenhagen, September 2005. ISSN 1399-560X

Several species within the fruit fly genus *Bactrocera* (Diptera: Tephritidae) are serious pests of cultivated fruit. The number of species within the genus and the relationships among them are not well understood. Therefore, we inferred phylogenetic relationships among thirty-nine *Bactrocera* species from 1819 base pairs of portions of the mitochondrial 16S rRNA, 12S rRNA, NADH 1 dehydrogenase, and cytochrome oxidase II + tRNA-Lys + tRNA-Asp genes. Maximum parsimony analysis suggested the following relationships: (1) *Bactrocera* is monophyletic, (2) *B. (Zeugodacus)* is polyphyletic, (3) *B. (Daculus)* is a sister group to *B. (Bactrocera)*, (4) *B. (Bactrocera)* is monophyletic, and (5) the *B. (B.) dorsalis* complex is polyphyletic. Character evolution, biogeography, and male-lure response were evaluated in a phylogenetic context by mapping selected character states onto the parsimony tree. Our mapping analysis suggested that in most cases the morphological characters exhibit a simple evolutionary transition from one character state another. Within the subgenus *B. (Bactrocera)* four distinct clades were identified which correlated with geographic distribution. Male-lure response was identified as being a labile behavior that has been lost on multiple occasions. Cue-lure response was plesiomorphic to methyl-eugenol response and the latter has evolved independently within the *Bactrocera* and *Zeugodacus* groups. The implications of our results toward a coherent, consolidated classification for *Bactrocera* are discussed.

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