

Molecular systematics and geographical distribution of the *Drosophila longicornis* species complex (Diptera: Drosophilidae)

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Abstract

Here we examine the phylogenetic relationships of eleven species previously hypothesized to be members of the *Drosophila longicornis* complex (*repleta* group, *mulleri* subgroup) using combined analyses of four mitochondrial genes. This complex, as currently redefined, is composed of the *longicornis* cluster (*D. longicornis*, *D. pachuca*, *D. propachuca*, and *D. mainlandi*), the *ritae* cluster (*D. desertorum*, *D. mathisi*, and *D. ritae*), and several miscellaneous species (*D. hamatofila*, *D. hexastigma*, *D. spenceri*, and an undescribed species “from Sonora”). A maximum likelihood inference also includes the *huckinsi* cluster (*D. huckinsi* and *D. huichole*) as the most distant members in the *longicornis* complex, a condition not recovered using maximum parsimony. We were unable to diagnose species in the triad of sibling species *D. longicornis*, *D. pachuca*, and *D. propachuca* using rapidly evolving mitochondrial DNA data, and we discuss possible species concept conflict for this triad. Comprehensive distribution information for these species, gathered over the past 60 years, is synthesized and displayed in range maps. Available information about the ecology and host plants of each species is also included.

Key words: *Drosophila longicornis* complex; molecular systematics; species concept conflict; host cactus

Introduction

The *Drosophila repleta* species group is composed of the *fasciola*, *hydei*, *mercatorum*,