



Species delimitation in the *Drosophila aldrichi* subcluster (Diptera: Drosophilidae) using DNA sequences

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Abstract

DNA sequence data has been successfully used to verify current species-level taxonomic hypotheses based on morphology and other characters. Setting species boundaries in the *Drosophila repleta* group has been challenging because this group contains several cryptic taxa and morphologically polymorphic populations. Mitochondrial (*cox1* and *nad2*) and nuclear (*sina* and *Marf*) genes were employed to assess species limits for two traditionally recognized, closely related, and taxonomically problematical species, *D. aldrichi* and *D. wheeleri*. Both tree-based and character-based methods were used to show that *D. wheeleri* is indeed a distinct species; however, our data shows that *D. aldrichi* is a paraphyletic assemblage of two lineages as previously suggested based on patterns of reproductive isolation. One lineage is sister to *D. wheeleri* and includes populations originating from southern and western Mexico (western-*aldrichi*). The second, basal group also contains flies from southern Mexico, along with populations from the northern and eastern regions within the species boundaries traditionally described as *D. aldrichi* (eastern-*aldrichi*). The populations of *D. aldrichi* that were introduced into Australia were found to be included in the eastern-*aldrichi* group. Our results, particularly those based on the rapidly evolving mtDNA sequences, confirm the presence of at least two cryptic species previously referred as “*D. aldrichi*”.

Key words: *Drosophila repleta* group, cactophilic *Drosophila*, cryptic species, molecular phylogenetics

Introduction

Many species in the *Drosophila repleta* species group are not readily identifiable using external morphological characters. As a result, male genitalia, reproductive isolation, and polytene chromosome inversions have been used to determine species limits and to discover cryptic species. However, this approach is unwieldy and in some instances species resolution is still problematical. This is the case for *D. aldrichi* Patterson & Crow and *D. wheeleri* Patterson & Alexander. These species are homosequential for polytene chromosome banding (Wasserman 1954), and there are no obvious morphological differences in male genitalia suggesting that their status as valid species is questionable (Vilela 1983). Nevertheless, patterns of reproductive isolation, often in the form of F₁ male sterility, have been indicative of multiple species as seen in reciprocal crosses between *D. aldrichi* and *D. wheeleri* (Patterson & Alexander 1952). Furthermore, Wasserman (1992) suggested that *D. aldrichi* likely consists of a number of cryptic species based on incompatible crosses among several different populations. Krebs and Barker (1994) also proposed that an introduced population of *D. aldrichi* in Australia and a population of *D. aldrichi* from northwestern Mexico were different species based on observed hybrid sterility.