

## Patterns of Genetic Variation Between the Checkered Skippers *Pyrgus communis* and *Pyrgus albescens* (Lepidoptera: HesperIIDae)

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**ABSTRACT** We examined patterns of genetic variation between the transcontinental species *Pyrgus communis* (Grote) and *Pyrgus albescens* Plötz (HesperIIDae) to examine whether patterns of molecular variation are congruent with the taxonomy. Sequence data from mitochondrial DNA and nuclear DNA failed to distinguish the two taxa. Although substantial genetic variation is explained by the two nominal taxa, more variation is explained by geography. Specifically, our molecular data indicate that the Transverse Ranges of southern California and the Sierra Nevada are important features affecting patterns of genetic variation. The possibility of recent divergence and secondary contact is discussed. Although *P. communis* and *P. albescens* do not adhere to a phylogenetic species concept, diagnostic morphological and distributional differences exist between the two entities that merit consideration regarding their taxonomic status.

**KEY WORDS** genitalia, introgression, phylogeography, sibling species, Sierra Nevada

The taxonomic status of the checkered skippers *Pyrgus communis* (Grote) and *P. albescens* Plötz has been debated for a century. The designated status of *P. albescens* has ranged from a distinct species to a mere geographical form of *P. communis* (for a detailed history, see Burns 2000). The two entities can be diagnosed by the morphology of the valves (or claspers) of the male genitalia. The valves of *P. communis* are higher from dorsal to ventral margin in lateral view, more massive, and marked by a prominent posterior process that curves anterodorsad and typically ends in a pair of prongs, whereas the valves of *P. albescens*, in lateral view, are relatively low throughout (Fig. 1a) (Burns 2000: figs. 9–12, 19–20, and 23–375). Intermediate valval shapes have been reported in regions of contact between the two entities (Powell 1958, Tilden 1965, Austin 1986), but those reports were refuted by Burns (2000). Based on wing length, *P. communis* averages slightly larger than *P. albescens* [analysis of data reported in Burns (2000):  $t = 8.01$ ,  $df = 115$ ,  $P < 0.001$ ].

*P. communis* ranges into southern Canada (southeastern British Columbia, southern Manitoba, Saskatchewan

and Alberta, and southernmost Ontario), through most of the continental United States, and south to southern Mexico; *P. albescens* ranges across the southern United States to southern Mexico (Fig. 1b) (Layberry et al. 1998: 45; Burns 2000: figs. 21–22). Although *P. communis* and *P. albescens* are broadly sympatric in the American Southwest and montane Mexico, they narrowly replace each other elsewhere (Burns 2000: figs. 21–22).

We examine genetic variation between these two species as an initial assessment of geographic and taxonomic structure, focusing particularly on Californian portions of its range. The high endemism of other taxa in this region, coupled with the fact that the Sierra Nevada and the Transverse Ranges have been shown to be important barriers for gene flow in other systems, make this region especially interesting (Calsbeek et al. 2003, Swenson and Howard 2005, Chatzimanolis and Caterino 2007). In California, *P. albescens* occurs in the southern Coast Ranges, southern San Joaquin Valley, southern Sierra Nevada, and in the Transverse Ranges and points south and east, including desert areas, whereas *P. communis*, despite limited overlap locally, occurs primarily to the north (Fig. 1b) (Burns 2000: fig. 21). The mountains of this region have been shown to be congruent with genetic discontinuities of other butterfly species complexes (Forister et al. 2004, Nice et al. 2005, Oliver and Shapiro 2007). We examine patterns of genetic variation to assess congruence with species-level taxonomy based on morphology and geographic distribution, and to examine the effect of geography and topography on genetic variation.

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