

An interspecific QTL study of *Drosophila* wing size and shape variation to investigate the genetic basis of morphological differences

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ABSTRACT. The Drosophila wing has been used as a model in studies of morphogenesis and evolution; the use of such models can contribute to our understanding of mechanisms that promote morphological divergence among populations and species. We mapped quantitative trait loci (QTL) affecting wing size and shape traits using highly inbred introgression lines between D. simulans and D. sechellia, two sibling species of the *melanogaster* subgroup. Eighteen QTL peaks that are associated with 12 wing traits were identified, including two principal components. The wings of D. simulans and D. sechellia significantly diverged in size; two of the QTL peaks could account for part of this interspecific divergence. Both of these putative QTLs were mapped at the same cytological regions as other QTLs for intraspecific wing size variation identified in D. melanogaster studies. In these regions, one or more loci could account for intra- and interspecific variation in the size of Drosophila wings. Three other QTL peaks were related to a pattern of interspecific variation in wing size and shape traits that is summarized by one principal component. In addition, we observed that

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female wings are significantly larger and longer than male wings and the second, fourth and fifth longitudinal veins are closer together at the distal wing area. This pattern was summarized by another principal component, for which one QTL was mapped.

Key words: Quantitative variation; QTL mapping; Transgressive segregation; *Drosophila simulans*; *Drosophila sechellia*; *Drosophila melanogaster*

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