

**Population structure of a global agricultural invasive pest, *Bactrocera dorsalis* (Diptera: Tephritidae)**

ABSTRACT

*Bactrocera dorsalis*, the Oriental fruit fly, is one of the world's most destructive agricultural insect pests and a major impediment to international fresh commodity trade. The genetic structuring of the species across its entire geographic range has never been undertaken, because under a former taxonomy *B. dorsalis* was divided into four distinct taxonomic entities, each with their own, largely non-overlapping, distributions. Based on the extensive sampling of six a priori groups from 63 locations, genetic and geometric morphometric datasets were generated to detect macrogeographic population structure, and to determine prior and current invasion pathways of this species. Weak population structure and high genetic diversity were detected among Asian populations. Invasive populations in Africa and Hawaii are inferred to be the result of separate, single invasions from South Asia, while South Asia is also the likely source of other Asian populations. The current northward invasion of *B. dorsalis* into Central China is the result of multiple, repeated dispersal events, most likely related to fruit trade. Results are discussed in the context of global quarantine, trade, and management of this pest. The recent expansion of the fly into temperate China, with very few associated genetic changes, clearly demonstrates the threat posed by this pest to ecologically similar areas in Europe and North America.

**Keyword:** *Bactrocera dorsalis*; Geometric morphometrics; Microsatellites; Mitochondrial genes; Population structure