
Genetic reconstruction of *Aedes albopictus* invasion history in Europe

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Abstract

The Asian tiger mosquito, *Aedes albopictus*, is currently the most invasive mosquito in the world. Native to South-eastern Asia, it has rapidly spread across all continents over the past 30 years. In Europe, the first record of *Ae. albopictus* is dated in 1979 in Albania, with a second introduction in Italy in 1990. Although an increasing number of studies revealed the possible sources of the recent invasion in Europe, they were based on a small number of populations. In this study, we sampled a broader range of invasive mosquito populations, representative of the current species range in Europe. We used genome-wide single nucleotide polymorphism (ddRADseq SNPs) to explore patterns of genetic variation and infer the most likely colonization scenario. We found evidence for different and independent introduction events in Albania and Italy. China emerges as the most probable source of populations in Albania, and United States, from an ancestral Japanese source, is the most probable source of populations in Italy. The spatial genetic structure suggests dispersal from established populations in Albania to neighbor countries but most of populations in Western Europe are genetically similar to those in Italy, supporting that Italian populations have played a major role in the rapid demographic expansion of populations throughout Europe. The high levels of genetic diversity observed in most recently invaded populations support that they result from genetic admixture from multiple sources of introduction, which probably accelerated the rapid range expansion of *Ae. albopictus* in Europe.

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