

Routes of introduction and spread *Zeugodacus cucurbitae* (Diptera: Tephritidae) in Africa

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Abstract:

The possible worldwide colonization routes of the melon fly, *Zeugodacus cucurbitae* (Diptera: Tephritidae), are mainly inferred from sparse historical records. Here we evaluate possible colonization scenarios of *Z. cucurbitae* in Africa through the Bayesian approach implemented by DIYABC. Populations of *Z. cucurbitae* were sampled from 17 localities in East, West and Central Africa and genotyped at 19 microsatellite loci and 3 mitochondrial gene fragments (COI, COII, ND6). AMOVA suggests the occurrence of four main population groups colonizing Congo, West Africa, Sudan and East Africa. The Bayesian assignment of STRUCTURE shows further genetic structuring in East Africa, with populations from Uganda diverging from those of Tanzania and populations from Burundi and Kenya sharing admixture proportions with West African samples. The analysis of mitochondrial haplotypes suggests that the initial colonization and subsequent demographic expansion of *Z. cucurbitae* in Africa originated from a limited number of introduction events. The most plausible scenario resulting from Bayesian simulations further corroborates the Asian origin of African *Z. cucurbitae*. Invasions originated from a single or from a limited number of introductions (possibly in Tanzania) and resulted in range expansion from East to West Africa. Furthermore simulations suggest a relatively recent origin of *Z. cucurbitae* in Africa (1889-1992) roughly corresponding to the first historical records (1936 for East Africa, 1999 for West Africa).