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Mapping Landscape Friction to Locate Isolated Tsetse Populations that are Candidates for Elimination

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Abstract

Tsetse flies are the cyclical vectors of deadly human and animal trypanosomes in sub-Saharan Africa. Tsetse control is a key component for the integrated management of both plagues, but local eradication successes have been limited to less than 2% of the infested area. This is attributed to either resurgence of residual populations that were omitted from the eradication campaign or reinvasion from neighboring infested areas. Here we focused on *Glossina palpalis gambiensis*, a riverine tsetse species representing the main vector of trypanosomoses in West Africa. We mapped landscape resistance to tsetse genetic flow, hereafter referred to as friction, to identify natural barriers that isolate tsetse populations. For this purpose, we fitted a statistical model of the genetic distance between 37 tsetse populations sampled in the region, using a set of remotely sensed environmental data as predictors. The least-cost

path between these populations was then estimated using the predicted friction map. The method enabled us to avoid the subjectivity inherent in the expert-based weighting of environmental parameters. Finally, we identified potentially isolated clusters of *G. p. gambiensis* habitat based on a species distribution model and ranked them according to their predicted genetic distance to the main tsetse population. The methodology presented here will inform the choice on the most appropriate intervention strategies to be implemented against tsetse flies in different parts of Africa. It can also be used to control other pests and to support conservation of endangered species.

The full paper was published in: *PNAS*: 112 (47) 14575-14580 (2015).

Symbiotic Bacteria Enable Olive Fly Larvae to Overcome Host Defenses

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Abstract

Ripe fruit offer readily available nutrients for many animals, including fruit fly larvae (Diptera: Tephritidae) and their associated rot-inducing bacteria. Yet, during most of their ontogeny, fruit remain chemically defended and effectively suppress herbivores and pathogens by high levels of secondary metabolites. Olive flies (*Bactrocera oleae*) are uniquely able to develop in unripe olives. Unlike other frugivorous tephritids, the larvae maintain bacteria confined within their midgut caeca. We examined the interaction between larvae, their associated bacteria, and fruit chemical defence, hypothesizing that bacterial contribution to larval development is contingent on the phenology of fruit defensive chemistry. We demonstrate that larvae require their natural complement of bacteria (*Candidatus Erwinia dacicola*: Enterobacteriaceae) in order to develop in unripe olives. Conversely, when feeding on ripe fruit, larval development proceeds independently of these bacteria. Our experiments suggest that bacteria counteract the inhibitory effect of oleuropein—the principal phenolic glycoside in unripe olives. In light of these results, we suggest that the unique symbiosis in olive flies, compared with other frugivorous tephritids, is understood by considering the relationship between the fly, bacteria and fruit chemistry. When applied in an evolutionary context, this approach may also point out the forces which shaped symbioses across the Tephritidae.