

RESISTANCE GENE REPLACEMENT IN THE MOSQUITO *CULEX PIFIENS*

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How adaptation appears and is later refined by natural selection has been the object of intense theoretical work. However the testing of these theories is limited by our ability to estimate the strength of natural selection in nature and to identify precisely its target at the molecular level. For some particular adaptations such as resistance to insecticide, it is now possible to bridge the knowledge from the genes implied in the adaptation to the dynamics observed in natural populations. We will present here how we estimated the selection coefficients acting on different alleles at the same locus using long-term cline series. We specifically analysed the allele replacements observed in the insecticide resistance genes Ester and ace-1 in the mosquito *Culex pipiens* in the Montpellier area, southern France. Several alleles have been identified for both genes and the effect of these genes on the fitness of mosquitoes have been measured in the lab. More recently we managed to measure the fitness coefficients associated with the different alleles in natural populations. At the Ester locus, a first resistance allele appeared early, which was replaced by a second resistance allele providing the same advantage but at a lower cost, itself being replaced by a third resistance allele with both higher advantage and cost. At the ace-1 locus a different path has been followed which implies duplication of the gene. More generally, we will discuss how the systemic understanding of the insecticide resistance, from the molecular mechanisms at the gene level to precise estimates of the strength of selection obtained from field data, help to understand more fully the process of adaptation.