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Detoxification enzymes associated with insecticide resistance and exposure to entomopathogenic fungi in Anopheles arabiensis

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2014-02-06
http://hdl.handle.net10539/13675

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ABSTRACT

Anopheles arabiensis is one of the major African malaria vectors, and DDT and pyrethroid resistance in this species is widespread. The aim of this study was to investigate, in detail, what detoxification enzymes are associated with insecticide resistance using the *An. gambiae* "detox chip", a small-scale microarray based on genes that are putatively involved in metabolic detoxification of insecticides. The first part of the study focused on two DDT and pyrethroid resistant laboratory strains of *An. arabiensis* – one that originated from Sudan, and a second that originated from South Africa. One P450 was over-transcribed in the Sudanese strain, while 20 genes were over-transcribed in the South African strain. The majority of these were P450s although GSTs and redox genes were also over-transcribed. The use of synergist assays indicated that DDT and permethrin resistance were related to the presence of a *kdr* mutation (determined by PCR), while deltamethrin resistance was based on insecticide metabolism. In order to evaluate the role of enzymatic detoxification in permethrin resistance, a permethrin selected strain was used. No *kdr* mutations were present in this strain. Here, 29 genes were over-transcribed. Most of these were CYP genes (55%), followed by redox genes (21%), and GSTs (14%). A certain degree of overlap in the gene over-transcription was observed between the deltamethrin and permethrin resistant phenotypes. These genes are potentially functional against both pyrethroids, while those that differed were possibly more substrate specific. The final part of the study aimed to assess whether genes that are associated with insecticide resistance are also induced in mosquitoes infected with the entomopathogen, *Beauveria bassiana*. Using microarray data, a subset of important insecticide resistance genes was chosen for analysis following fungal infection. This study was based on the use of qPCR

to detect changes in expression. None of the genes that were investigated were over-transcribed suggesting that virulence factors, such as toxins, produced by *B. bassiana* may not be inhibited by genes that are already over-expressed in insecticide resistant mosquito populations. This is promising for biological control and suggests that the fungi are viable alternatives to insecticides.