

Transcriptional profile of detoxifying genes in the malaria vector *Anopheles gambiae*. Effect of permethrin exposure, mosquito aging and sugar feeding.

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Abstract

The small-scale microarray '*Anopheles Detox Chip*' containing more than 200 genes putatively involved in insecticide detoxification in the mosquito *Anopheles gambiae* was used to monitor changes in expression of detoxifying genes after females emergence and permethrin exposure. Transcriptional changes were comparatively investigated 2h, 6h and 24h after emergence in sugar-fed females (controls) and sugar-fed females exposed to a sub-lethal dose of permethrin using the *RSP (Reduced Susceptibility to Permethrin)* laboratory strain. Transcription of 14 genes belonging to various enzyme families appear modulated either by sugar feeding or mosquito aging while 12 genes mainly belonging to cytochrome P450s, glutathione S-transferases and peroxidases were significantly related to insecticide exposure. Kinetic analysis reveals that CYP6Z genes react almost immediately (2h) to insecticide exposure while other genes including esterases, superoxide dismutases, peroxidases and glutathione S-transferases show a delayed response (mainly at 24h) to insecticide exposure. This differential response may emphasize the difference between the direct response to the insecticide and the later enzymatic response to partially degraded insecticides metabolites and/or oxidative stress. Verification of microarray data and further investigations of the role of CYP6Z genes in response to permethrin was performed. Effectiveness of microarray technology to study responses to xenobiotics and other specific mosquito metabolic pathways are discussed.

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