

## Population genetics of mosquitoes vectors from Recife, Brazil

Constância F. J. Ayres Dept. de Entomologia, Centro de Pesquisa Aggeu Magalhães/FIOCRUZ. [tans@cpqam.fiocruz.br](mailto:tans@cpqam.fiocruz.br)

Recife is the capital of the state of Pernambuco, North-eastern Brazil. Filariasis and The Dengue virus are endemic in this city, with high incidences of both diseases. My group works on population genetics of the mosquitoes vectors *Aedes aegypti*, *Ae. albopictus* and *Culex quinquefasciatus*, trying to develop better strategies for vector control and we have found some interesting results. Some of them are described below.

### ***Aedes aegypti* and *Ae. albopictus*:**

A twelve-month survey of seasonal variation in allele frequencies in *Ae. aegypti* and *Ae. albopictus* populations was undertaken to determine possible changes in the genetic structure and their relationship with environmental conditions. Patterns of genetic diversity were examined by using Random Amplified Polymorphic DNA and haplotypes of a mtDNA gene (cytochrome oxidase c subunit II). Samples of the two species were collected from December 2003 to November 2004 in two areas of Recife. Evidence of significant genetic differentiation was detected throughout the year for both species, without the loss of genetic diversity within populations (heterozygosity and polymorphism). Samples of *Ae. albopictus* from sylvan and urban areas showed intensive gene flow ( $N_m = 4.2$  and  $22$ ) during two different moments. The data obtained could be very useful in improving vector control strategies by indicating the best moment to interfere. Besides that, we are using the genetic data analysis to monitor the success of the vector program implemented since 2002. The entomological indexes (number of eggs by ovitraps) were congruent with the genetic data.

### ***Culex quinquefasciatus* receptor:**

The larvicidal activity of the *Bacillus sphaericus* (*Bs*) is due to the interaction of its binary toxin (Bin) with a specific receptor present in the midgut epithelium of Culicidae larvae. We have cloned and sequenced the gene encoding this receptor obtained from *Culex quinquefasciatus* larvae from susceptible and resistant colonies to *Bs*, in order to elucidate the molecular mechanism of resistance. The sequencing of the receptor gene from the susceptible colony revealed a 1925 pb sequence composed of 5' and 3' untranslated regions, coding sequence and introns. The corresponding sequence from the resistant colony showed a deletion of 19 nucleotides, which generates a change in the reading frame for 28 amino acids and one premature translation stop codon. The presence of this premature stop codon can destabilize the respective mRNA, and prevent its translation, as well as lead to the synthesis of a truncated protein lacking the GPI anchor required for its positioning in the epithelial membrane. In both cases the absence of the receptor in the midgut epithelium could be the reason for the resistance.

### ***Culex quinquefasciatus* x *Wuchereria bancrofti*:**

On May 2003, single course DEC mass treatment was administered to 20.000 individuals from Água Fria, a district of Recife with high filarial prevalence. We have collected adult *C. quinquefasciatus* samples from houses in the area before, during and after treatment, in order to monitor vector infection rate and to detect the decreasing of mf due to the drug administration. Using PCR we observed a reduction in the vector infection rate from 1.29 % (before treatment) to 0.27 % after 10 months of treatment.

### ***Wolbachia* endosymbiont:**

We are also trying to describe the infection by *Wolbachia* in the three species mentioned above. Assays for *Wolbachia* infection were performed by PCR amplification using primers for the *wsp* gene. Different infection rates of *Wolbachia* were observed for *Ae. albopictus* and *C. quinquefasciatus* populations from different areas. *Ae. aegypti* populations were all *Wolbachia* free.