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APPARENT LOW GENE FLOW OF Aedes Aegypti IN AN URBAN SETTING BASED ON USING NEW MICROSATELLITE MARKERS

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Introduction: *Aedes aegypti* is vector of dengue and others arboviruses including yellow fever. Microsatellite markers would be promising molecular tool for the study of genetic variability of mosquito populations. We investigated genetic variation by studying microsatellite polymorphisms in mosquitoes at 3 sites of Salvador/Bahia/ Brazil. **Objectives:** Find new microsatellites markers for *Ae. Aegypti* and determine if there genetic structure in the populations between different locations in Salvador. **Methods:** *Ae. Aegypti* were obtained from ovitraps and from container-breeding sites in 38 locations distributed in All Saints Bay side from Salvador. All mosquitos were identified as *Ae. Aegypti* by microscopic examination for subsequent DNA analysis. The microsatellite repeat sequences were searched for within available data banks and primer pairs designed. For analysis on the ABI 3100, one primer in the PCR reaction was end-labeled with one fluorescent phosphoramidite dyes (FAM, TED or HEX). To 2.5 µl of each sample 0.5 µl of internal size standard GS-500LIZ and deionized formamide were added for a final volume of 10 µl. Sequencing was processed in the ABI Prism® 3100. BioEdit program (Hall 1999) was used for sequence analysis. Allele frequencies, comparison with Hardy-Weinberg proportions and marker linkage disequilibrium were calculated for each marker and population using the program Genepop (Raymond and Rousset, 1995) and GDA (Lewis 2001). **Results:** Four microsatellite loci were polymorphic, behave as single copy loci and produce interpretable patterns. Homozygotes alleles when sequenced showed deletions in the downstream region. No significant deviations from Hardy-Weinberg equilibrium were found. Deficit of heterozygosity were showed at least one marker for each population studied. **Conclusions:** Based on our results observing that between points in Salvador separated for 25 km and 8 km the *F_{st}* was 0.28 and 0.40 showing a important genetic structure between this populations, through the results not agree with the distance between the populations. The other hand this results show potentially the capacity of our markers for differentiation distinct populations of *Ae. Aegypti* mosquitoes and need enlarge the number of samples for enlarge the power of the our results. This kind of study is important in order to measure the real impact of control programs on mosquito populations and to give significant support for public health efforts principally in Brazil.