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Malaria control strategies based on genetic manipulation of vectors will require extensive knowledge of vector population genetics. Critical information includes: patterns of gene flow/dispersal, population size and the breeding structure of populations. The ultimate success of a malaria control program for Africa will require that this be implemented over the entire area affected. It is important to have study sites throughout sub-Saharan Africa that are examined in a coherent and uniform way. Our research project, with Guimogo Dolo, William Black, myself and headed by Gregory Lanzaro is aimed at describing the genetic structure of *An. gambiae* populations within ecologically diverse and geographically disjunct study sites in Mali and Cameroon. This survey is still under way, but significant parts have been accomplished. I will describe our progress and describe our database, which we believe could be useful for the entire *Anopheles* community.

Briefly, our goal is to define the distribution of genetic populations at several hierarchical levels, including within ecological zones in each country, between ecological zones (both within and between countries) and over the entire study area. In addition, temporal variation will be studied at select sites by re-sampling over time. Genetic diversity will be analyzed using four distinct types of markers: chromosome inversions, mitochondrial DNA, microsatellites and single copy nuclear genes. All analyses will be conducted on the same set of samples and will include 100 genomes per site, for a total of 10,000 genomes for the entire study. Genetic methods will be supplemented by an ecological approach (mark-release-recapture) to estimate population parameters. A critical component is mapping variation and correlating genetic information with ecological parameters, employing information from remote sensing, ground measurements and using GIS. Associations between genetic and environmental variables will be established by correlating linear combinations of these variables. These will then be correlated with principal components, canonical correlations, and spatial autocorrelation methods. Associations between gene flow and environmental variables will be established by calculating N_{em} between each pair of locations and forming a matrix of such values. This matrix will then be compared to a matrix of geographical distance values and compared with a Mantel test. We will also perform such tests with matrices where distances are weighted by mean, maximum and minimum NDVI values along straight lines connecting locations. The final product of this effort will be a series of maps defining boundaries of genetically distinct population groups, the identification of ecological/geographic barriers and corridors to gene flow and the identification of association between *An. gambiae* genotypes and specific environmental parameters. Such information should be critical to vector control efforts that require an understanding of dispersal and gene flow (genetic control, insecticide resistance management).