Title: In *Silico* Study of the Complex Mechanisms of Anopheles gambiae Insecticide Resistance

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Abstract: Insecticide resistance is an inherited characteristic involving changes in one or more insect gene. Insecticide resistance is a major public health problem which hinders the control of malaria. Since early 1950s the sensitivity of the malaria vectors to insecticides has been on the decline. Newer insecticides were discovered in an effort to tackle this problem, but these insecticides are either expensive or have undesirable side effects.

The socioeconomic impact is beyond measure and the negative effect is enormous. Since the influence is particularly prominent in the African continent, there is a huge and urgent need to discover and validate mechanisms which *A. gambiae* deploys to resist these existing insecticides to enable the introduction of new insecticidal compounds and improvement / development of additional control strategies.

Analyzing the metabolic or target site changes in mosquitoes computationally may yield insight to important mechanisms of insecticide resistance. Thus, In this work, we used data obtained with the application of microarray technology to produce gene expression data for various mosquito under many conditions at the genome level. A desirable advancement is the need to extract from this gene expression data, information that will be useful towards giving answers to the questions targeted at the design of the microarray experiment.

Analysis of gene expression data of Mosquitoes (*Anopheles gambiae)* when induced with two chemical insecticide (such as DDT and Permethrin) has shown that the *A. gambiae* resistance mechanisms is eluci-date-able at both the genomics and on a proteomic level. Biochemical research has elucidated an increasingly complete image of the metabolic architecture of organisms that included that of mosquito. In this work, we used the biochemical network of *A. gambiae* to deduce its resistance mechanism(s) using expression data obtained when *A. gambiae* is sprayed with chemical insecticide. We do this by mapping these gene expression data onto the enzymatic reaction nodes of the metabolic net-work. A consecutive ones clustering method is used to derived important clusters (pathways) of genes that represents crucial changes in the metabolic regulation and stress response of the mosquito. Further, a feature extraction method is applied to study these clusters. Based on previous findings, it is expected that these clusters will give us important insight into the mechanisms that *A. gambiae* deplores for resisting these insecticides.