COMPUTATIONAL IDENTIFICATION OF PROTEIN KINASES (KINOME) IN *AEDES AEGYPTI* GENOME.

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Mosquitoes are the vectors of the most prevalent human diseases since ancient times; including malaria, filariasis, yellow fever and dengue. However methods to block disease transmission by such vectors are still scarce. Protein kinases (PK) are enzymes able to catalyze protein phosphorylation and are the ultimate effectors of most signaling pathways. Host and vector infection cause changes in their own signaling pathway which once blocked could avoid disease development (Silva-Neto et al, 2002). Mosquito PKs were identified by Hidden-Markov-Model searches using PK domains. Selected sequences were analyzed by similarity comparison programs and manually curated. The conservation of PK domains was also analyzed when applicable. Atypical PKs contain 13 families, but only 7 were identified (A6, ABC1, FAST, HistK, PDHK, PIKK and RIO) totalizing 24 sequences. Typical PKs account for 241 sequences divided in 9 groups (AGC, CAMK, CK1, CMGC, STE, TK, TKL, RGC and Others). A total number of 265 PKs was found, representing 1.2% of 20995 unique sequences in *A. aegypti* gene index (release 4.0). This result is within the 1-2% interval found in other kinome projects. The next steps include differential expression analysis for all PKs during the time course of mosquito infection by malaria parasite and dengue virus. The identification of essential PKs involved in infection process will allow the design of novel strategies to block disease transmission by mosquitoes. Supported by CNPq and CEFET-Química.