ABSTRACT

Mosquitoes, the main vectors of multiple parasites and viruses, are one of the most dangerous animals on the planet, causing over a million deaths annually. The large number of deaths attributed to them makes the need to control insect vectors imperative. The most common and effective way of limiting mosquitoes is the use of insect repellents.

Odorant binding proteins (OBPs) participate in the initial step of the olfactory transduction pathway making them ideal targets for the discovery and design of new insect repellent chemical compounds and mixtures.

The determination of the tertiary structure of OBPs as well as their complexes with ligands provides detailed information both on the overall structure and on the individual protein-protein and protein-ligand interactions, evidence that may lead to finding more effective, safer, and friendly to the environment chemical mosquito control agents.

In the context of this thesis, the proteins of the mosquito Anopheles gambie AgamOBP1, AgamOBP4 and AgamOBP5, as well as the AealOBP1 protein of the mosquito Aedes albopictus were studied. Regarding the proteins AgamOBP1, AgamOBP4, a total of 6 new ligands were found with the RCE (Reverse Chemical Ecology) method. The crystal (tertiary?) structures of AgamOBP5 and AealOBP1 were also determined. Two binding sites in AgamOBP5 that bind monoterpenes (carvacrol, thymol) were identified, identifying it as the first molecular target among monoterpene specific OBPs. At the same time, the determination of the three-dimensional structure of AealOBP1 makes it possible to highlight a molecular target in a mosquito species, widespread and responsible for spreading various diseases.

The research results of this thesis contribute to the expansion of the available molecular targets and by extension the number of repellent compounds discovered, paving the way for the discovery of new ones, thus strengthening the chemical arsenal for the control of mosquito-borne diseases.