Abstract

Malaria is a problem in today's world. It affects millions of people and causes many deaths in the world each year. Today, due to the evolution of drug resistance in parasite and insecticide resistance in mosquito vector, malaria control has been complicated. On the other hand, due to the high price of drugs to treat malaria, Preparation by poor countries it is not possible. Therefore, prepare a safe, effective and cheap vaccine is a priority for global health. Transmission blocking vaccines (TBVs) block the completion of sexual cycle of parasite inside the mosquito or inhibit the transmission of malaria parasite from mosquitoes to humans. Invasion of the sporozoite to salivary glands of Anopheles mosquito is a necessary step to transmission of the parasite to human. In this stage, the interaction between Plasmodium Sporozoite TRAP Protein and the mosquito salivary glands Saglin protein is happened. Down regulation of Saglin expression results in strong inhibition of salivary gland invasion. In this study, at first conserved areas Saglin gene identified and was collected data by using PCR ,TA-Cloning and 3'-RACE. Molecular data analyzed by using different software. Bioinformatics analysis of the molecular data which obtained from experimental studies, indicate that *Saglin* and *SG1B* genes are ortholog in *Anopheles gambiae* and *Anopheles stephensi*. Comparoson of *SG1B* genes *Anopheles stephensi* from different areas and their genetic diversities and the effect of natural selection on *SG1B* gene was performed in this study. Natural selection analysis determined that this gene plays an important role in the life cycle of the Anopheles mosquito. Therefore, introduced *SG1B* gene can be introduced as a new target for designing transmission blocking vaccine.

Key word: Malaria,Vaccine, *Anophele Stephens, Saglin, SG1B,* PCR, TA-Clong

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Molecular identification of *Saglin* and *SG1B* genes of *Anophele Stephensi* (vector of malaria) candidates for design transmission blocking vaccines

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