NEW APPROACHES IN P. VIVAX MALARIA VACCINE DISCOVERY AND RESEARCH

Sócrates Herrera, Augusto Valderrama-Aguirre, David L Narum, Elizabeth Ampudia, Luz Á. Moreno, Liliana Soto, Omaira Vera, Myriam Arévalo-Herrera

Malaria Vaccine and Drug Development Center (MVDC), Cali, Colombia
Immunology Institute, Universidad del Valle, Cali, Colombia
Primate Center Foundation (FUCEP), Cali, Colombia
Malaria Vaccine Development Branch (MVDB), NIAID/NIH, Rockville, MD

Plasmodium vivax is responsible for more than 50% of malaria cases outside of Africa. It is the most widespread malarial species and negatively impacts infected individuals in terms of both morbidity and socio-economical development. Vaccine discovery and development for P. vivax has been held back to such an extent that only two antigens are in clinical trial evaluations (Pvs25 and PvCS). However the experience, which has been obtained during the past 25 years through the development of the PvCS vaccine candidate and the establishment of a TMRC in Colombia, has enabled us to establish an infrastructure that is capable of overcoming some of the past technical barriers in order to further future development more rapidly.

Based on sequence homology studies with P. falciparum, we identified and are in pre-clinical development with a Pv200L recombinant protein vaccine, which is comprised of an amino-terminal fragment of PvMSP-1. Early efforts showed that Pv200L was antigenic, immunogenic, and induced a protective immune response against a P. vivax blood stage challenge in the Aotus primate model. This vaccine candidate has now been produced at bench-scale as a highly purified, well characterized recombinant protein (EcPv200L) and is currently under pre-clinical evaluation in the Aotus monkey model, formulated in Montanide ISA-720 and ISA-51.

Following a similar homology search with Pf using the unfinished P. vivax genome, we identified Pvs48/45. The orthologous protein in Pf is a transmission blocking vaccine antigen. We are interested to evaluate the vaccine potential of Pvs48.45. Currently, semi-immune individuals are being screened for Pvs48/45 specific antibodies using an eukaryotic expression system. Furthermore the immunogenicity of a Pvs48/45 DNA vaccine is being studied in BALB/c mice.

More recently, a bioinformatics-based approach allowed us to screen the P. vivax genome for conserved non-previously reported genes which might be of importance as vaccine targets across all lifecycle stages. A group of 15 genes is currently being evaluated for their antigenicity using a high-throughput platform based on the previously mentioned eukaryotic expression system.

The new vaccine targets identified by bioinformatics approach plus the platform for rapid screening will allow us to move quicker from P. vivax vaccine antigen discovery to vaccine development.