

PATHOGEN GENETIC DIVERSITY A CHALLENGE FOR VACCINE DEVELOPMENT: LOOKING FOR THE PATHOGEN'S ACHILLES' HEEL

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Creation of variant forms has serious consequences in diagnostic, treatment strategies and the future vaccine development. Thus, the actual and future roles of the altered or emergent pathogens in the global pandemic of AIDS, Malaria, Flu and Ebola must be monitored in new molecular epidemiological studies. During the last 5 years, we studied the genetic structure of several pathogens such as 1] malaria parasite showing that gene deletion, recombination can occur and lead to false RDT negative and to the creation of new antigens (hybrid parasites); 2] in HIV, our findings indicate a shift in the virus population circulating over time in Mali. Those observations are suggesting that a vaccine development against those pathogens such *Plasmodium falciparum* parasite and HIV will be a challenge. Our approach that is to target pieces of antigens within a genome which must be well conserved across the specie and immunogenic enough in boosting the immune response. Four steps were identified in that approach which are: 1] Genome mining using computational and experimental tools to identify genes that encode proteins with promising vaccine antigens properties, 2] use of the Immunoinformatics tools to map protein sequences for short, linear putative T-cell epitopes CTL/ T helper, 3] then candidates are synthesized as peptides and evaluated for HLA binding and antigenicity (*in vitro* evaluation) and then 4] Prototype epitope-based vaccines are evaluated for immunogenicity in human Host (*in vivo* evaluation). Our laboratory has partnered with the GAIA foundation to test this approach in Mali.