



Finding Vaccine Candidates for Malaria

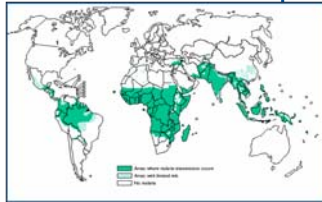
A Bioinformatics Approach



Background

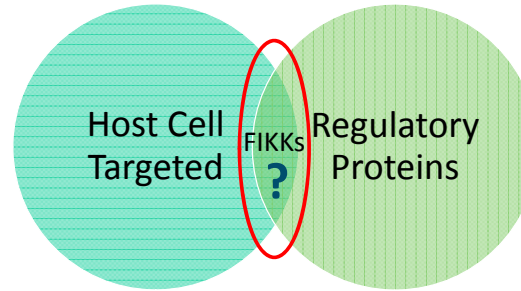
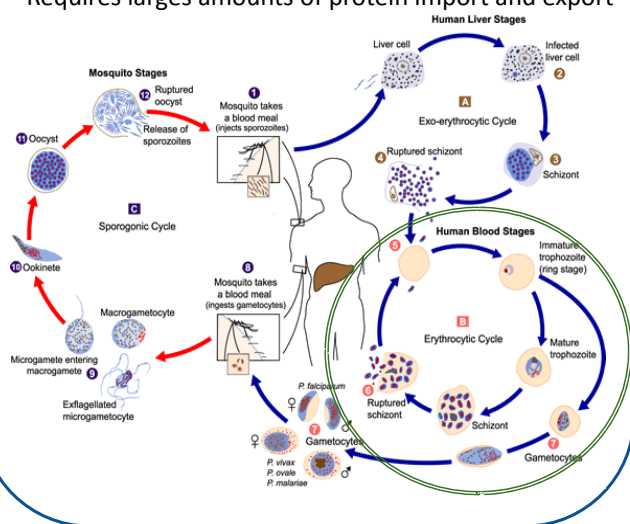
A disease of the underprivileged

- 2.5 billion largely impoverished people are at risk for malaria
- More than 1 million people die of malaria a year
- 1 in every 5 child deaths in Africa is due to malaria
- Malaria is both worsened by and contributes to the poverty level of the communities it infects



Parasitic Lifecycle

- Complex and multi-stage
- Requires large amounts of protein import and export



Objective

- Find good vaccine candidates among malaria proteins

Assumptions

- The parasite is affecting the host cell through direct regulatory processes
- Most regulatory domains are intracellular
- To affect the human proteins, the parasitic proteins need to be exported or presented on the membrane surface

Rationale

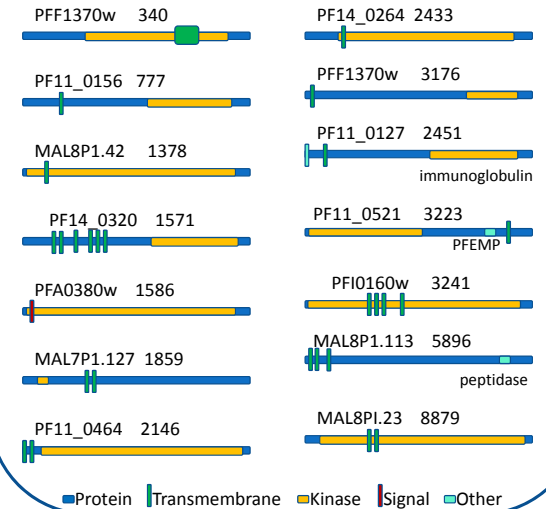
- Regulatory proteins contain highly conserved genes that could be consistently recognized by the body's immune system

Our Methods

1. Find malarial proteins containing regulatory domains
2. Investigate the other domains identified for these proteins
3. Check for predicted transmembrane regions
4. Check for annotated signal peptide

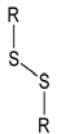
Current Results

- 13 transmembrane, non-FIKK proteins
- 1 signal peptide, non-FIKK protein



Continuing Work

- Expression data
Is the protozoa expressing this protein while in the human red blood cell?
- Discover more signaling motifs
- Predict disulfide bridges
Indicates extracellular location
- Assess the rate of regulatory and transmembrane proteins in non-parasitic eukaryotes
- Assess accuracy of annotations and predictions for malaria



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