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Characterizing *Babesia* genes for candidate vaccine peptides

Babesiosis is a tropical cattle disease caused by the parasite *Babesia bovis*. This parasite infects red blood cells in cattle in much the same way as the malaria parasite *Plasmodium falciparum* infects red blood cells in humans. It also shares other characteristics that make babesiosis a good model disease for malaria. Using a phage-display strategy, certain peptides have previously been selected which could serve as components in a vaccine for babesiosis. The main goals of this project are to determine if the selected peptides are "natural" peptides, that is, parts of actual parasite proteins; and to gather available information about the function of those proteins. To accomplish this, we probed a *B. bovis* cDNA library with the coding sequences of selected phage-displayed peptides. The sequenced cDNA clones were used to determine if the phage-displayed peptide sequence matched the open reading frame of the cDNA clones. These cDNA clones were further used to learn about our peptides' function and location in *B. bovis* by comparison of the cDNA sequence to that of homologous proteins and known motifs. So far we have characterized clones from 24 different probes. Out of those clones 10 showed homology to known or hypothetical proteins, and 5 are putative membrane proteins. Membrane-associated proteins and other proteins that are expressed on the outer side of the parasite fit the mold of good vaccine components.

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