

***Babesia* development within mammalian and tick vectors**

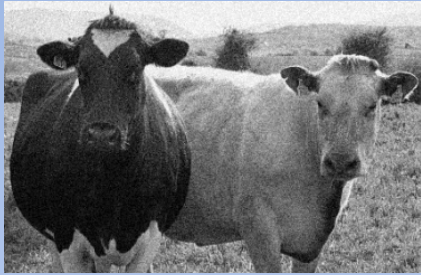
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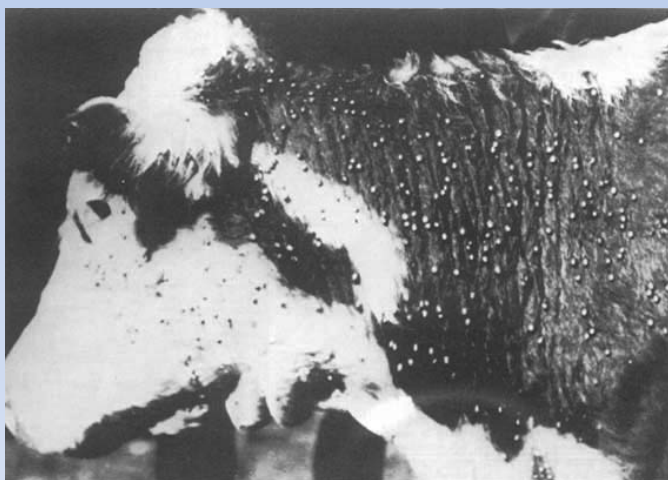


**USDA-SAGARPA Cattle Fever Tick Summit
November 2016**

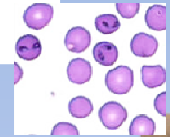


- Solve basic and applied problems concerning persistent infectious diseases of domestic animals
- Tick-borne pathogens of livestock
 - ❖ Strategies to control tick-borne pathogens of cattle and horses

Pathogens transmitted by tick vectors remain the major concern and challenge to improve animal health.



Bovine babesiosis



- Most prevalent tick-borne disease of livestock

- Tropical and subtropical distribution
 - ❖ *Babesia bovis* and *B. bigemina*
 - Asia, Africa, Central and South America, Europe, and Australia

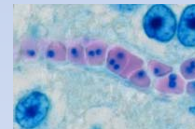
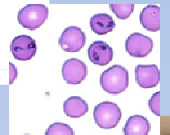
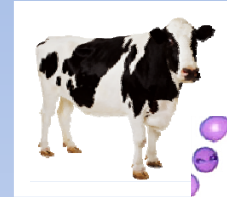
 - ❖ *Babesia divergens*
 - Europe

Tick-borne diseases of livestock

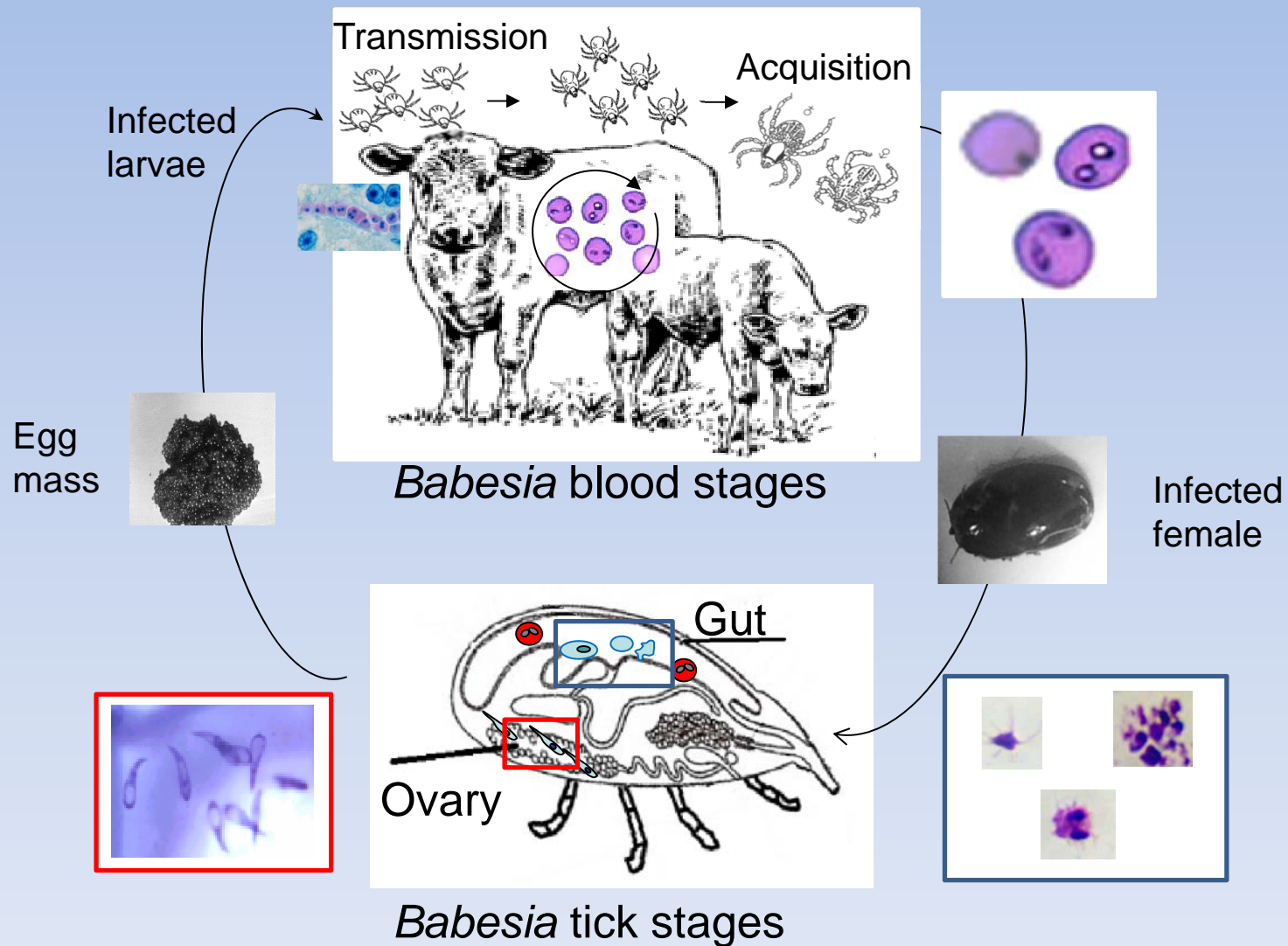
➤ Bovine babesiosis

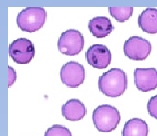
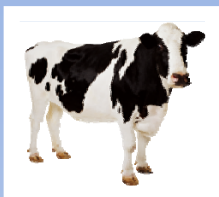
❖ Significant losses

- > \$800 million per year in Latin America
 - High morbidity
 - High mortality (cerebral babesiosis)
 - Abortion
 - Reduction in milk and meat production



Babesia development within vertebrate and invertebrate hosts





Genomic sequence of *B. bovis*



| Features | Species | | |
|--|----------------------|-----------------|-----------------|
| | <i>P. falciparum</i> | <i>T. parva</i> | <i>B. bovis</i> |
| Size (Mbp) | 22.8 | 8.3 | 8.2 |
| Number of chromosomes | 14 | 4 | 4 |
| Total G+C composition (%) | 19.4 | 34.1 | 41.8 |
| Size of apicoplast genome (kbp) | 35 | 39.5 | 33 |
| Size of mitochondrial genome (kbp) | ~6 linear | ~6 linear | ~6 linear |
| Number of nuclear protein coding genes | 5,268 | 4,035 | 3,671 |
| Average protein coding gene length (bp) ^a | 2,283 | 1,407 | 1,514 |
| Percent genes with introns | 53.9 | 73.6 | 61.5 |
| Mean length of intergenic region (bp) | 1,694 | 405 | 589 |
| G+C composition of intergenic region | 13.8 | 26.2 | 37 |
| G+C composition of exons (%) | 23.7 | 37.6 | 44 |
| G+C composition of introns (%) | 13.6 | 25.4 | 35.9 |
| Percent coding | 52.6 | 68.4 | 70.2 |
| Gene density ^b | 4,338 | 2,057 | 2,228 |

^aNot including introns.

^bGenome size/number of protein coding genes.

Brayton K.A., et al. PLoS Pathog. 2007

Proteins expressed by *Babesia* blood stages

➤ RAP-1

- Goff, WL et al. Infect. Immun. 1988; Suarez, CE, et al. Int. J. Parasitol. 2004

➤ BboRhop68

- Baravalle, ME, et al. Parasitol. Int. 2010

➤ Smorf

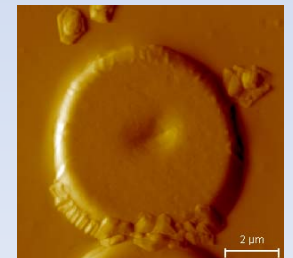
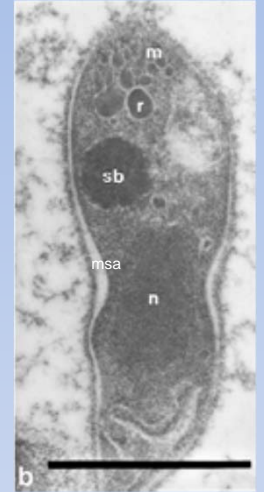
- Ferreri, LM et al. Int. J. Parasitol. 2011

➤ MSA-1 and MSA-2

- Goff, WL et al. Infect. Immun. 1988; Hines, SA, et al. Mol. Biochem. Parasitol. 1989; Jasmer, DP, et al, Mol. Biochem. Parasitol. 1992

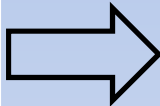
➤ VESA

- Allred, DR, Microbes Infect. 2001; Allred, DR, Vet. Parasitol. 2006; Brayton, KA, et al. PLoS Pathog. 2007

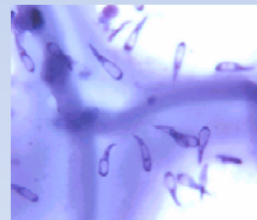
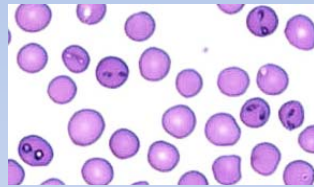


Transcription regulation during *B. bovis* development within vertebrate and invertebrate hosts

Animal infected with
B. bovis stabilate



B. bovis
blood stage



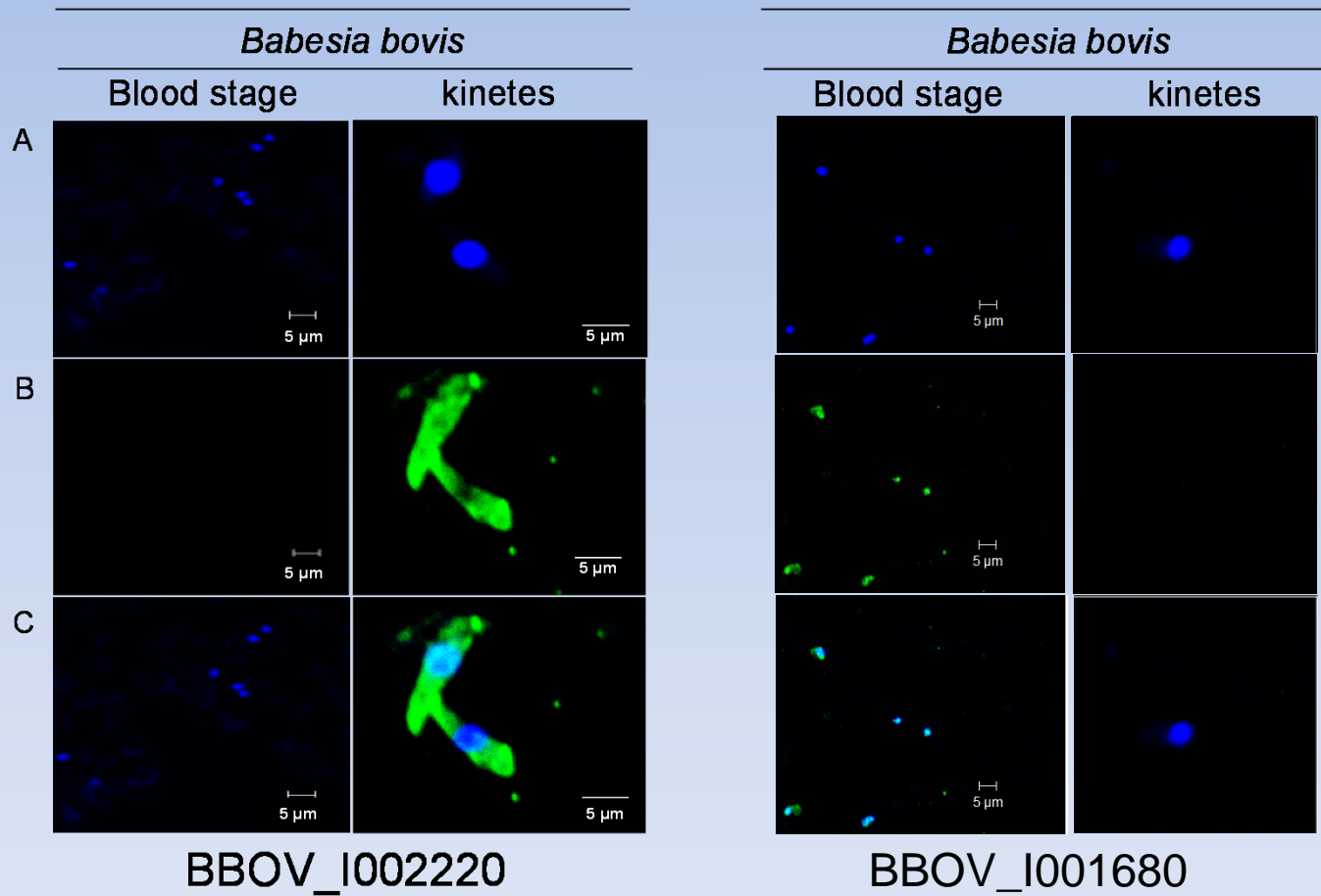
Engorged infected
R. microplus

B. bovis
tick stage

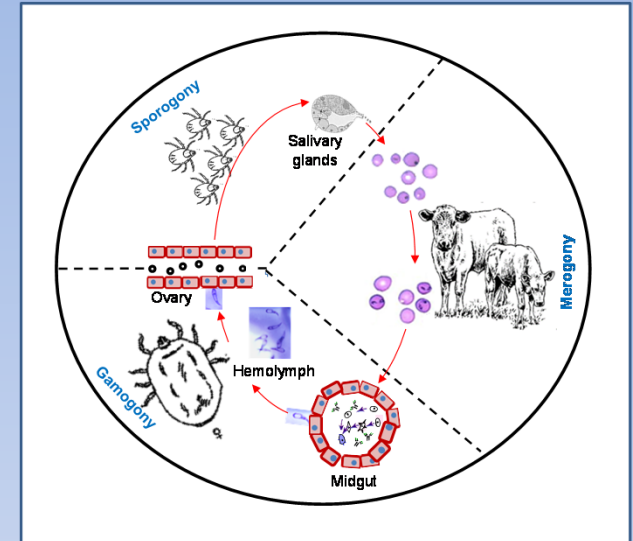
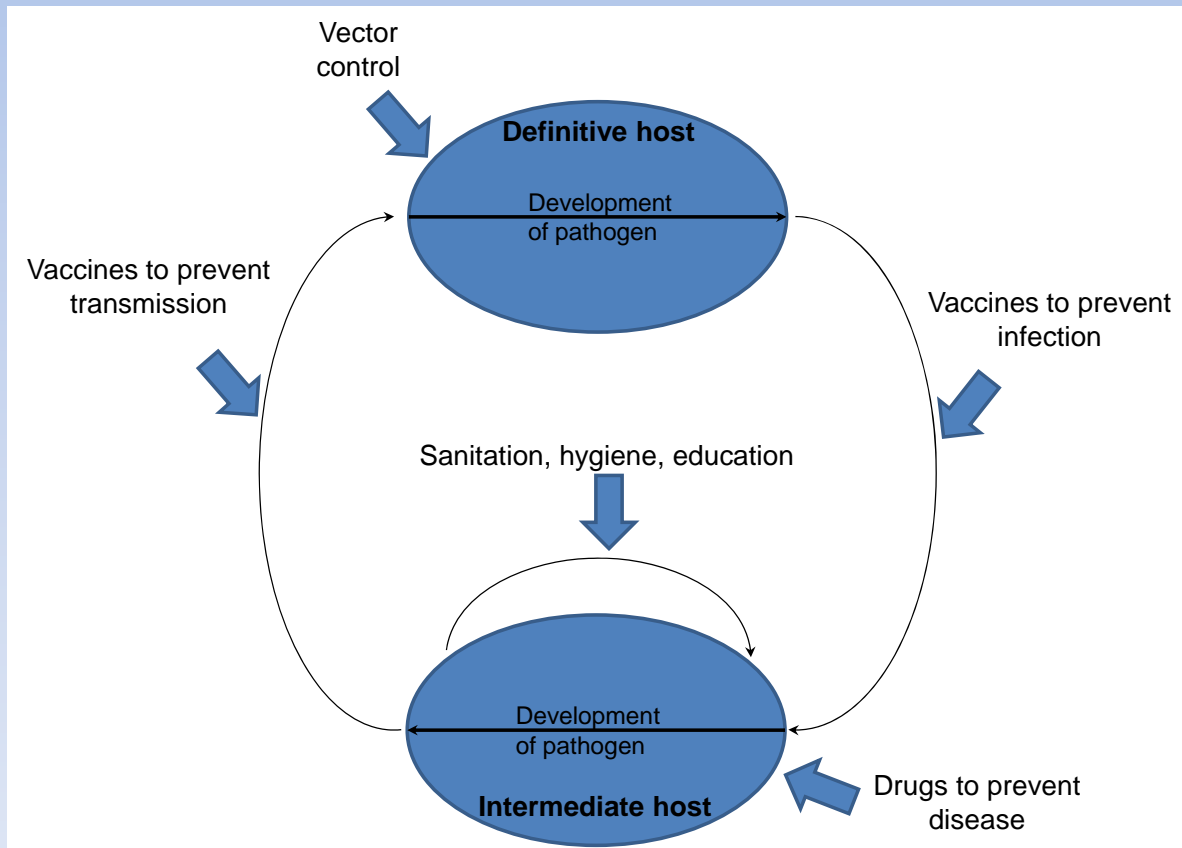
| <i>B. bovis</i> gene name | <i>B. bovis</i> | |
|------------------------------|-----------------|-----------|
| | Blood stages | Kinetes |
| BBOV_IV010280 | 4,240 | 3 |
| BBOV_IV009870 | 4,141 | 2 |
| BBOV_IV009860 | 2,068 | 1 |
| BBOV_IV011230 | 26,438 | 74 |
| BBOV_I003060 | 271,778 | 251 |
| BBOV_I003010 | 23,228 | 14 |
| BBOV_I003020 | 9,038 | 7 |
| BBOV_I002990 | 11,229 | 6 |
| BBOV_I003000 | 8,050 | 1 |
| BBOV_I002220 | 265 | 1,188,531 |
| BBOV_IV000290 | 1,159 | 1,096,089 |
| BBOV_II006620 | 153 | 752,203 |
| BBOV_II006100 | 97 | 176,535 |
| BBOV_II006600 | 29 | 83,939 |

RNA seq data

B. bovis proteins



Control strategies for bovine babesiosis



- Understanding the life cycle will allow us to develop efficient strategies to prevent infection/disease in the mammalian host and/or block parasite transmission via tick vectors.
- These proteins are postulated to be critical for the *Babesia* parasite to complete its life cycle within mammalian and tick hosts.

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Questions

