



UNITED STATES ANIMAL HEALTH ASSOCIATION

2013 RESOLUTION

117TH ANNUAL MEETING

OCTOBER 17-23, 2013 ~ SAN DIEGO, CA

RESOLUTION NUMBER: 7 and 14 Combined - APPROVED

**SOURCE: COMMITTEE ON PARASITIC DISEASES
COMMITTEE ON INFECTIOUS DISEASES OF HORSES**

**SUBJECT MATTER: EQUINE PIROPLASMOSIS (EP) - GENETIC STRAIN
TYPING OF EP ORGANISMS**

BACKGROUND INFORMATION:

Equine piroplasmosis (EP) is classified as a foreign animal disease. The identification of EP-positive imported equids and the recent large-scale EP incident in a domestic population of horses have increased the need to identify the genotypic strains of organisms in positive EP equids detected in the United States. While natural, endemic transmission of EP is occurring at a very low level in the United States, a small number of EP positive horses continue to be detected. Many of these positive EP horses have direct ties to foreign countries endemic for EP, where the horse was believed to be infected. Currently, however, there is no validated method to determine different strains of each organism (*Theileria equi* and *Babesia caballi*) complicating the epidemiological and trace back investigations.

RESOLUTION:

The United States Animal Health Association urges the United States Department of Agriculture, Animal and Plant Health Inspection Services, Veterinary Services, Agricultural Research Services and the National Veterinary Services Laboratory to research, develop and validate genetic strain typing capabilities for the equine piroplasmosis organisms *Theileria equi* and *Babesia caballi*.

INTERIM RESPONSE:

The U.S. Department of Agriculture, Animal and Plant Health Inspection Service (APHIS), Veterinary Services and the Agricultural Research Services (ARS) recognize the concerns of the U.S. Animal Health Association and appreciate the opportunity to respond. The National Veterinary Services Laboratories and the Animal Disease Research Unit at Pullman, Washington, have begun discussions on a collaboration to address this need. A single isolate (Florida strain) of *T. equi* has been sequenced, and sequencing of the *B. caballi* genome (Puerto Rico strain) is in progress. Comparative



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genomics at the levels of specific genes will be utilized toward identification of potential strain markers. The decreasing cost and efficiency of whole genomic sequencing makes that method a potential avenue toward strain marker identification. APHIS and ARS will continue discussions to consider these and additional laboratory approaches and formulate a long-term work plan to meet the objectives of this resolution.