SUMMARY

Molecular characterization of Theileria equi and Babesia caballi genotypes and "like" variants circulating in central Italy

Aims:

1. Define in the study areas the distribution of parasitic variants on biomolecular bases, both in equidae and in vectors.
2. Investigate the biological and taxonomic relationships of T. equi and B. caballi and their variants.
3. Provide useful guidance for the correct interpretation of the results of the different diagnostic tests (ELISA, IFI, PCR).

Methods:

1. Selection of samples based on serological (ELISA) and biomolecular results (PCR Real Time for V4 18S gene and Endpoint for EMA 1).
2. Sequencing and analyzing data.
3. Statistical analysis to correlate the presence of symptomatology, serological result and positivity to PCR for EMA1 with the sequenced genotype.

Results:

Confirmed earlier studies dividing V4 sequences into three groups (A, B and C) for T. equi and three for B. caballi (A, B1 and B2) while confirming the presence of 4 groups for EMA (A, B , C and D).
The groups seem to be associated with the presence or absence of symptoms and the positivity or not to PCR for Ema-1 for T. equi, in particular Group A seems to give rise to symptomatic and positive infections in PCR EMA 1 whereas Group B no . The sampling number for B. caballi did not allow statistical inference.

Discussions and Conclusions:

From this study it has emerged that pyroplasms infection can also start with mild or absent symptoms and therefore must always be taken into account by the veterinarian when compatible symptoms are manifested.
Serologic tests are no longer enough to guarantee the negativity of a subject but a biomolecular test is needed.
The sensitivity of the serological and molecular methods must always be verified.

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