

Incidences of hemoparasitic...
Koonyosyning et al.

Editor's comments"

Please pay careful attention to the comments by Reviewers 1 and 2 and edit your manuscript accordingly. In addition, some comments from the editor:

- Abstract
 - o lines 46-48: "exhibited homology with other isolates obtained from different countries in ranges between xx-yy%...". Break this sentence in two and reword this segment of the sentence as follows: "exhibited considerable sequence similarity to homologous sequences from isolates obtained from other countries. Sequence similarity ranged between xx-yy% , etc, etc, for genex, geney and genez, respectively."
- Intro
 - o Ln65-66: "extremely prevalent worldwide via their" -> "extremely prevalent throughout their"
- Materials and Methods
 - o Ln94: that were located -> that are located
 - o Ln125: Geomic -> Genomic
 - o Ln139-149: methods need to be explained more clearly. If I understand correctly, microscopy was first used to ascertain presence of pathogens and determine genus. Was PCR conducted only on the samples that were positive by microscopy or in all samples? Were all samples analyzed with all primers (all Babesia and Theileria and Anaplasma primers)? If yes, pls say so. If not, what determined which primers to use in which samples? Carefully explain the decision process.
 - o Ln 142: what do you mean by "B bovis and N bigemina were detected among B bovis rap-1.. etc"? The sentence as is does not make sense.
 - o Line 150:"the primer specific gene sequences listed" -> "the gene-specific primers for which the sequence is listed"
 - o Ln159-183: there should be no space between digits and "°C".
- "DNA sequencing and phylogenetic tree analysis"
 - o Lines 186-187: is the number of samples listed the number collected "from each province or was that the total number of samples for each species? If the latter (I believe that is the case), delete "collected from each province" from the sentence.
 - o Describe the data used for phylogenetic reconstruction: nucleotide or aa sequences?
 - o the method used for phylogenetic tree reconstruction (eg, Neighbor Joining, Maximum likelihood, Bayesian), model of evolution (eg, Jukes-Cantor, Nei-Gojobori, etc) and any other parameters selected.
- Results
 - o Ln 256: genetic homology -> sequence similarity
 - o Ln257: Columbia -> Colombia
- Discussion

- Ln269: explain the sentence "Babesia spp. and Theileria spp were screened." D=For example, do you mean "All samples were first screened for the presence of Babesia or Theileria species using 18S primers."
- Ln269: "the specific genus" -> "the species"
- Figures
 - Figures and their respective legends should tell the whole story. Accordingly, several figure legends need a lot more information:
 - Fig 3: Figure legend needs more detail. Which marker was used for each species?
 - Fig 5-7: add information to figure legend regarding the length of the alignment, whether it is composed of nucleotide or amino acid sequences, the phylogenetic method used, the model of evolution used, any other parameters, what the numbers on the nodes represent and how they were obtained, how many replicates, etc.