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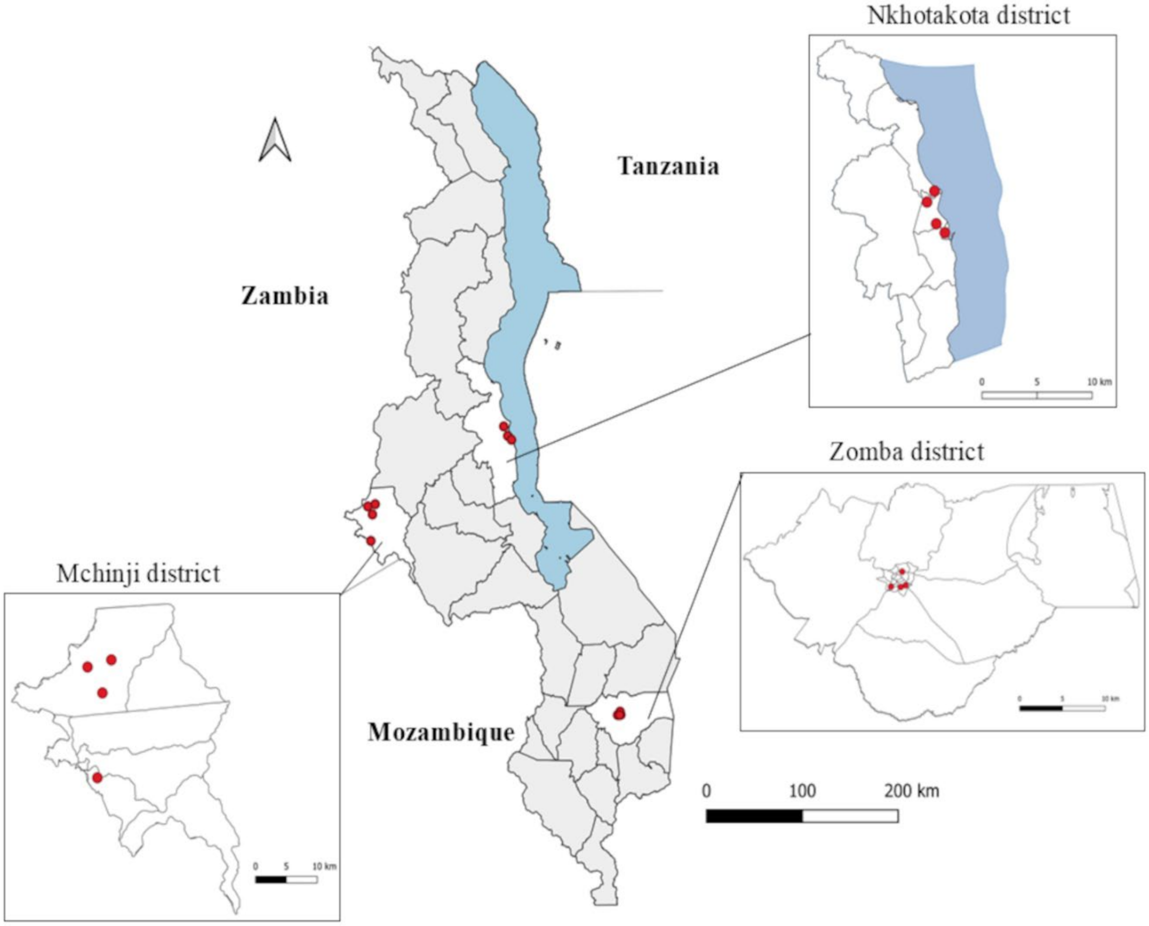
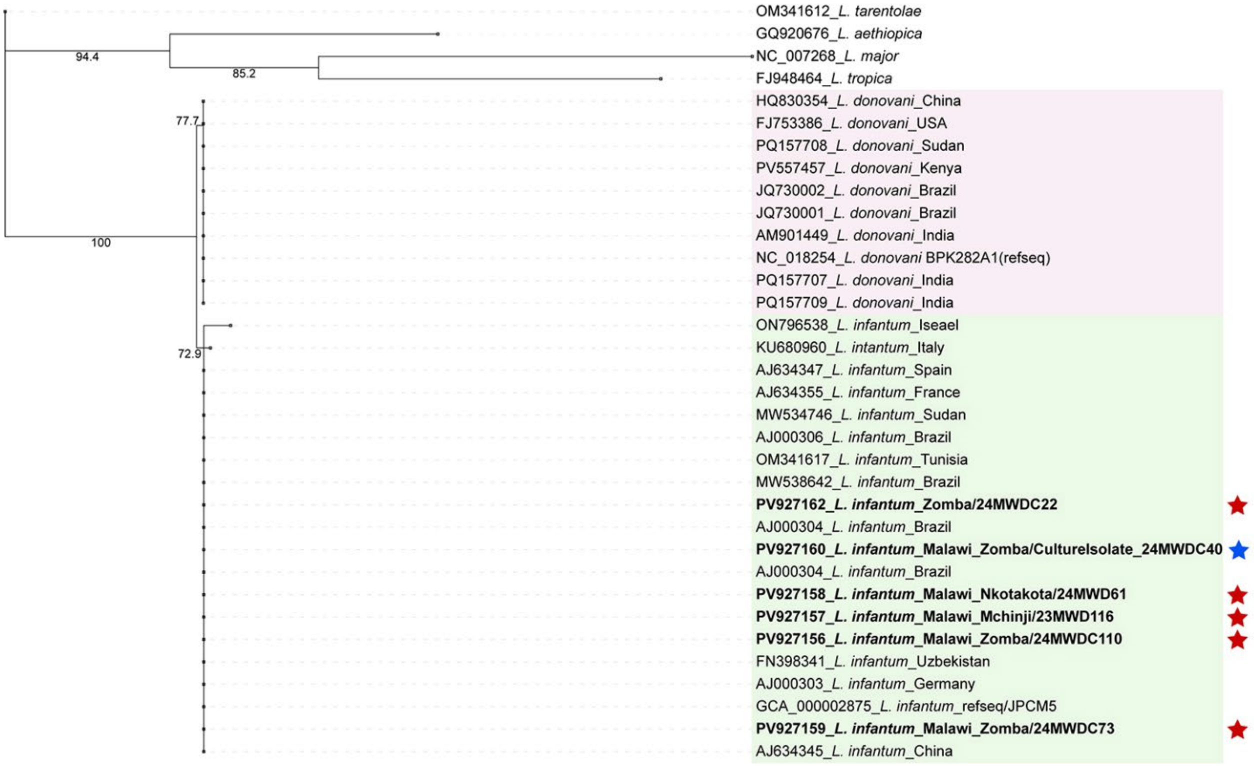
Presence or Emergence of Canine Leishmaniasis, Malawi

Appendix 1



Appendix 1 Figure 1. Map of Malawi showing sampling sites. The map was generated using QGIS software (version 3.40.1).



Appendix 1 Figure 2. Maximum likelihood phylogenetic tree showing the relationship between entire ITS sequences (ITS1, 5.8S, ITS2) of the study (bold) and selected *L. infantum* sequences obtained from NCBI GenBank. Red stars: sequences obtained from blood samples. Blue star: sequence obtained from an in vitro cultured isolate from Zomba dog 24MWD_C040. Sequences were aligned using MAFFT with L-INS-i method. After manual trimming, a maximum likelihood tree was conducted using IQ-TREE 3 using TPM2u+F+I, which was selected by ModelFinder Plus. All bootstrap values greater than 75% from 1000 replications are shown on the branch nodes. *Leishmania tarentolae* (OM341612) was used as the outgroup.