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Molecular heterogeneity of Rhipicephalus sanguineus sensu lato and screening for

Ehrlichia canis in mainland Portugal

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Abstract

The present study aimed to expand knowledge regarding the molecular characterization of R.

sanguineus s.l. in Portugal and to screen for ticks naturally infected with E. canis. A total of

113 R. sanguineus s.l. were collected questing or attached to domestic and wild animals from

the 18 administrative regions of mainland Portugal. All the ticks were analyzed for the 16S

rRNA and the partial sequences obtained showed high genetic similarities with specimens

belonging to the temperate lineage. These sequences revealed eight haplotypes (H1–H8), with

a genetic distance ranging from 0.3% to 1.4%. A convenience sample representing

approximately 75% of all the R. sanguineus s.l. ticks collected was tested for the presence of

E. canis by qPCR for the dsb gene. No ticks were found to be infected with this pathogen.

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