

As climate and other environmental factors associated with latitude may affect the abundance of ectoparasite vectors (Linardi and Krasnov 2013), we examined the effects of study area and season on pathogen prevalence. We also explored the effect of host-related factors such as sex and age. We analysed differences in prevalence with generalized linear models (GLM), specifying binomial errors and logit link. When model fit was not possible due to very little variability in the response or redundancies/missing levels in predictors, we used standard contingency table analysis for binomial data. We also analysed differences in ectoparasite intensity using Poisson errors and log link. If needed, models were adjusted for overdispersion by setting the scale parameter as the deviance divided by its degrees of freedom. We assessed the percentage of deviance explained by the models. We compared alternative models containing different combinations of predictors (Burnham and Anderson, 2002) using the Akaike Information Criterion (AIC). We considered competing models those with $\Delta AIC \leq 2.0$. PCR fragments were sequenced and manually assembled. All sequences obtained were compared to those of the GenBank database and aligned using the CLUSTALW algorithm (Geneious®). Phylogenetic trees were constructed based on maximum-likelihood analysis and the Tamura-Nei model with RaXML software version 1.5 (Stamatakis et al., 2008). The data set was resampled 1000 times to generate bootstrap values. The best model of evolution was selected by the program jModelTest2 (version 2.1.6) (Darriba et al., 2012), under the Akaike Information Criterion (AIC) (Posada and Buckley, 2004). Genetic p-distances among the hemoplasmas were calculated with MEGA 7.0 (Tamura et al., 2007) using 616bp of the 18S ribosomal RNA gene.