

The prevalence and molecular characterisation of blood parasites infecting the vulnerable Tamarugo Conebill (*Conirostrum tamarugense*) and other birds in the Pampa del Tamarugal, Chile

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Resumen

Blood parasites exert significant selective pressure, which can alter population dynamics, and the introduction of new parasite lineages in a region could lead to the extinction of endemic avian species that have not coevolved with them. The avifauna of the Pampa del Tamarugal in the desert of Atacama, Chile, is highly depauperate, with two species accounting for the greatest numbers: the widespread Rufous-collared Sparrow (*Zonotrichia capensis*) and the endemic Tamarugo Conebill (*Conirostrum tamarugense*). We used molecular and microscopic methods to estimate the prevalence of haemoparasites in birds inhabiting the Pampa del Tamarugal. The molecular screening of the samples from the most common species indicated that the Tamarugo Conebill was only infected by parasites of the genus *Leucocytozoon* (prevalence 3.5%) and the Rufous-collared Sparrow was uninfected. Only two other bird species (of a total of seven) were infected, the House Sparrow (*Passer domesticus*), by *Plasmodium relictum* (prevalence 30%), and the Eared Dove (*Zenaida auriculata*), by *Haemoproteus multipigmentatus* (prevalence 100%). The occurrence of House Sparrows infected with the *Plasmodium* haplotype GRW4 (involved in Hawaiian bird extinctions) may entail the risk of potential host-switching, something particularly relevant for the conservation of the endemic and vulnerable Tamarugo Conebill.

Palabras clave

Palabras clave de autor: [avian malaria](#); [haplotype GRW4](#); [host-switching](#); [House Sparrow](#); [Plasmodium](#); [Leucocytozoon](#)

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