



Husbandry guide for the ex-situ recovery of wild born European roller *Coracias garrulus* nestlings.

F. Valera¹, Cortés De Arévalo, M.², Bolonio, L. ³, A. Martínez², F. Castaño-Vázquez⁴, J.Sánchez², J.M. Rodríguez-Linde².

¹ Estación Experimental de Zonas Áridas (EEZA-CSIC). Ctra. de Sacramento s/n. La Cañada de San Urbano. 04120; ² MiniHollywood Oasys, Reserva Zoológica del Desierto de Tabernas. Ctra. Nacional 340-km 464, Tabernas, Almería. 04200; ³ CEBIME. Conservación y estudio de la biodiversidad en medios esteparios (www.CasaCarraca.org). C/ Castrillo de Aza, 5. 7D. Escalera centro. 28031, Spain; ⁴ Universidad Complutense de Madrid (UCM). Departamento de Biodiversidad, Ecología y Evolución. C/ de José Antonio Novais, 12, Moncloa. 28040. Madrid, Spain.

In the current context of global change, habitats are undergoing a rapid transformation, significantly affecting host-parasite relationships. Avian-malaria like parasites constitutes an ideal system to study such consequences due to their high prevalence and well-documented biology. However, research has focused primarily on passerines while other bird taxa, such as steppe birds, are seldom investigated. To fill this gap, it is essential to first characterize the patterns of avian malaria parasitism and subsequently examine how habitat perturbations might influence these interactions. We monitored the malaria-like parasite lineages of the transaharian migrant European roller breeding in a semiarid area in southeastern Spain, which is experiencing substantial habitat alterations due to solar plant expansion. Three species of avian malaria-like parasites have been morphologically described for rollers (*Haemoproteus coraciae*, *Leucocytozoon eurystomi* and *L. bennetti*), but there is only one molecular lineage of *H. coraciae* described. We surveyed during three years adult rollers (N= 140 samples) to identify the linages present, and explore the prevalence and diversity of malaria-like parasites. We found high prevalence of *Haemoproteus* (97.8%) and *Leucocytozoon* (90%) by means of PCR in adults. The screening of smears produced similar results for *Haemoproteus* (98.6%) but not for *Leucocytozoon* (23.7%). We found 9 lineages of *Haemoproteus* (8 not described), and 5 lineages of *Leucocytozoon* (all not described). Coinfections with *Haemoproteus* and *Leucocytozoon* were relatively frequent (88%), while coinfections with different *Haemoproteus* lineages were common (69.11%) and with different *Leucocytozoon* lineages were scarce (7.94%). Our findings revealed a highly efficient transmission network and high parasite diversity in rollers breeding in semi-arid environments, contrasting with prior studies in extreme habitats. Understanding these parasitic relationships before a significant habitat disruption is crucial for assessing the ecological and evolutionary impact of such changes and allowing to identify effects over steppe birds population dynamics and conservation.