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INTRODUCTION

In the last 50 years, barn owl populations have suffered a large decline throughout Europe, especially in the Iberian Peninsula. This decline could be due to the intensification and industrialization of agriculture, as well as increased urbanization. These alterations in the barn owl's habitat could be leading to a decrease in the diversity of bird species in their habitat. This may cause generalist parasites to limit host range and increase infections in owl populations, resulting in a higher prevalence and a more vulnerable population. In this context, malaria parasite infection could pose a major threat to barn owl populations in Europe. In order to better understand the conservation status of the species populations, a characterization of the avian malaria parasite community in barn owls has been carried out, as well as a quantification of the presence of parasites in populations in the center of the Iberian Peninsula

MATERIALS AND METHODS

SAMPLE COLLECTION: PROYECTO ALBA (BRINZAL)

- 9 nest boxes (Fig. 1)
 - Location: Community of Madrid and Castilla y León
- Two samples per individual from the jugular vein for smear and molecular analysis

MICROSCOPY

- 51 blood smears reviewed at 1000x (Fig. 2)
- Presence/absence of parasites was observed

MOLECULAR ANALYSIS

- 1st PCR (Ciloglu et al. 2019)
 - 2nd PCR (Hellgren et al. 2004)
 - Sequencing
- The sequences obtained were edited with BioEdit, parasite lineages were identified using local BLAST alignment algorithms in sequence repositories in the MalAvi database (Bensch et al., 2009)



Fig 1. Barn owl nestling found in one of the nest boxes of the present study

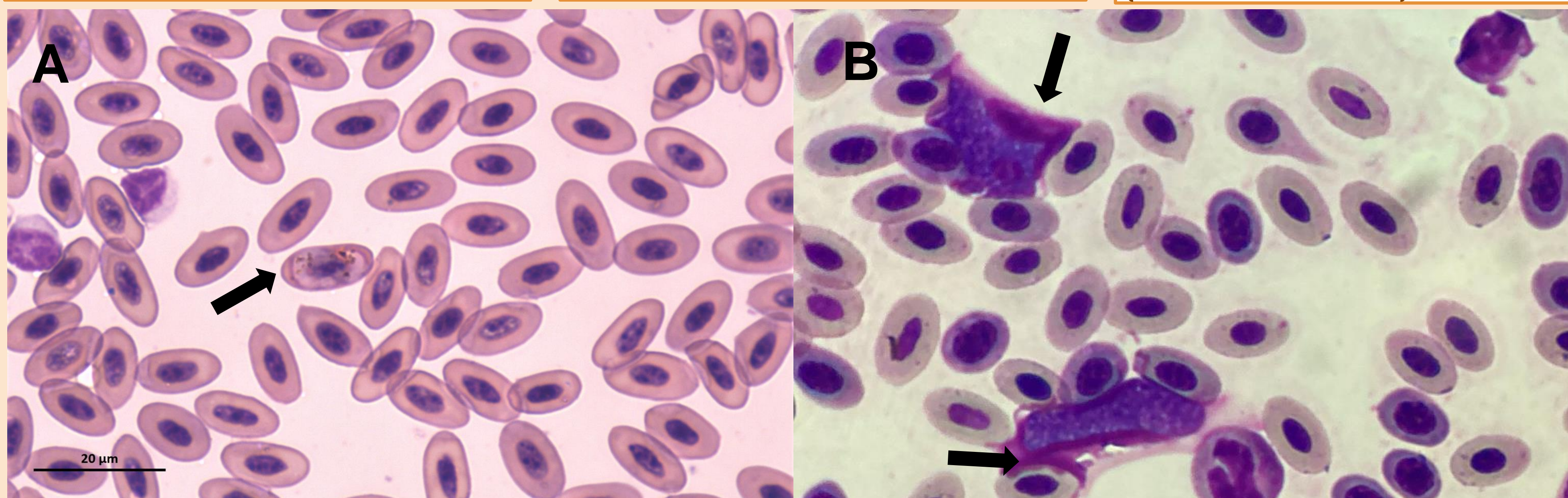


Fig 2. Images at 1000x magnification of blood smears from barn owl specimens observed in the present study, in which avian malaria parasites (arrow) of the genera *Haemoproteus* (A) and *Leucocytozoon* (B) are visible

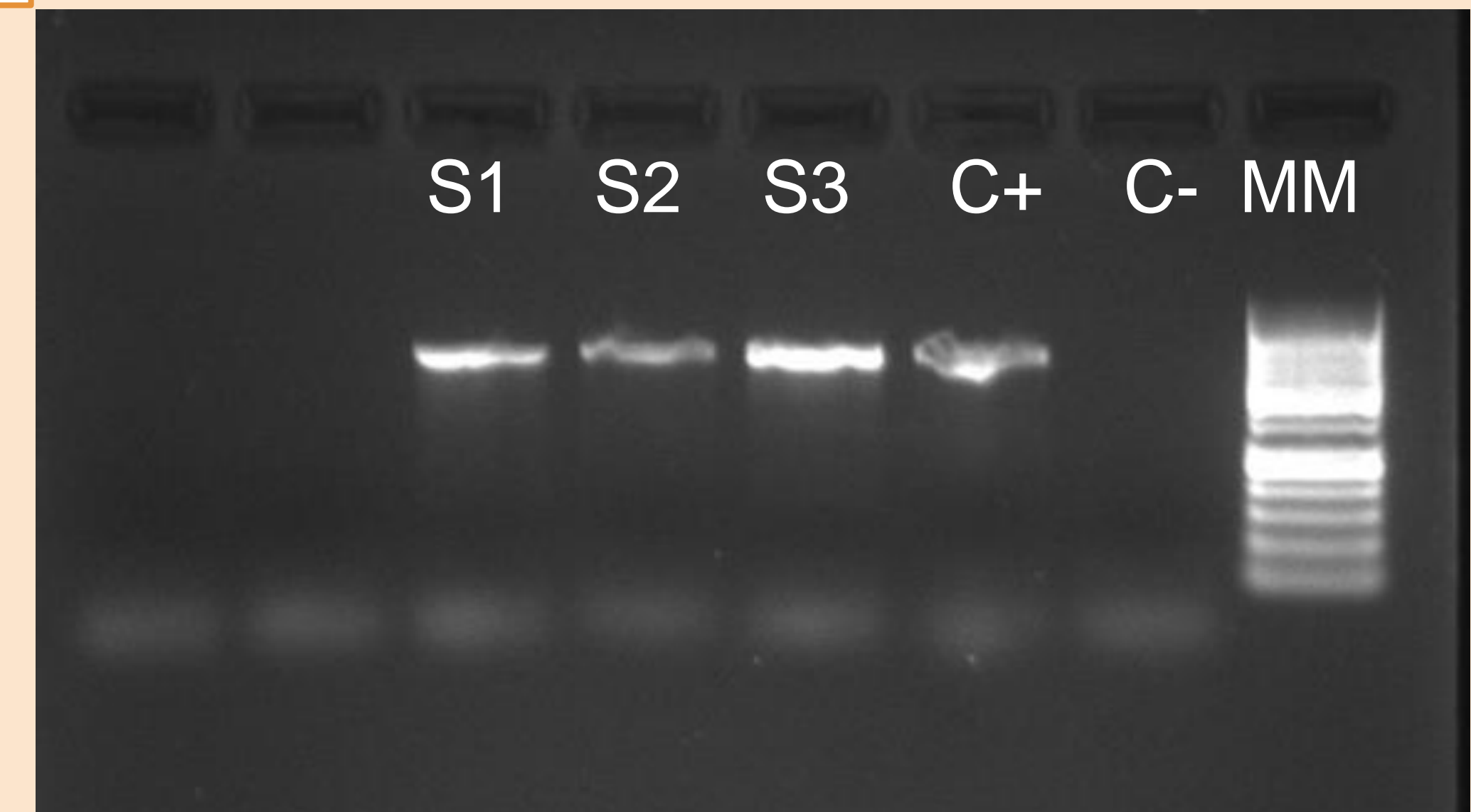


Fig 3. 2% agarose gel showing the result of a PCR (Hellgren et al. 2004). It shows three positive samples (S1, S2, S3), a positive control (C+), a negative control (C-) and a molecular marker

RESULTS

HIGH POPULATION PREVALENCE: 55%

LINEAGE	GENUS	PREVALENCE IN ADULTS (n=7)	PREVALENCE IN NESTLINGS (n=48)	SPECIES IN WHICH IT HAS BEEN DETECTED	FAMILIES IN WHICH IT HAS BEEN DETECTED
L-CIAE02	<i>Leucocytozoon</i>	14%	44%	33	14
L-AEM002	<i>Leucocytozoon</i>	0%	4%	5	3
L-ATN01	<i>Leucocytozoon</i>	28%	0%	2	2
H-TYATL8	<i>Haemoproteus</i>	14%	0%	NEW LINEAGE	
H-TYATL9	<i>Haemoproteus</i>	14%	0%	NEW LINEAGE	

Table 1. Prevalence in adults and nestlings of the parasite lineages identified in the study, and known host taxonomic range of the parasites according to the MalAvi database

GENERALIST:

L-CIAE02
I-AEM002

SPECIALIST:

L-ATN01
H-TYATL8
H-TYATL9

DISCUSSION AND CONCLUSION

- A community of parasites has been observed in which we found both specialist and generalist parasites. The lineage with the highest prevalence in the population is CIAE02, a generalist parasite that has shown a much higher prevalence in nestlings than in adults (Table 1)
- It should be noted that adults spend more time than juveniles in the nest, where the latter become infected, so their exposure to the most prevalent parasite in this system is evident, however prevalences are higher in chicks for the CIAE02 lineage, so apparently parasites that affect nestlings in nests have problems persisting with equal prevalence in the adult population
- The fact that most of the parasites detected in this study were generalists may have great conservation implications, taking into account the results obtained for the prevalence of parasites in nestlings

REFERENCES

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