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Co-circulation of *Chlamydia psittaci*, *C. gallinacea*, and *Chlamydiaceae* DNA in Brazilian Wild Birds and Reptiles

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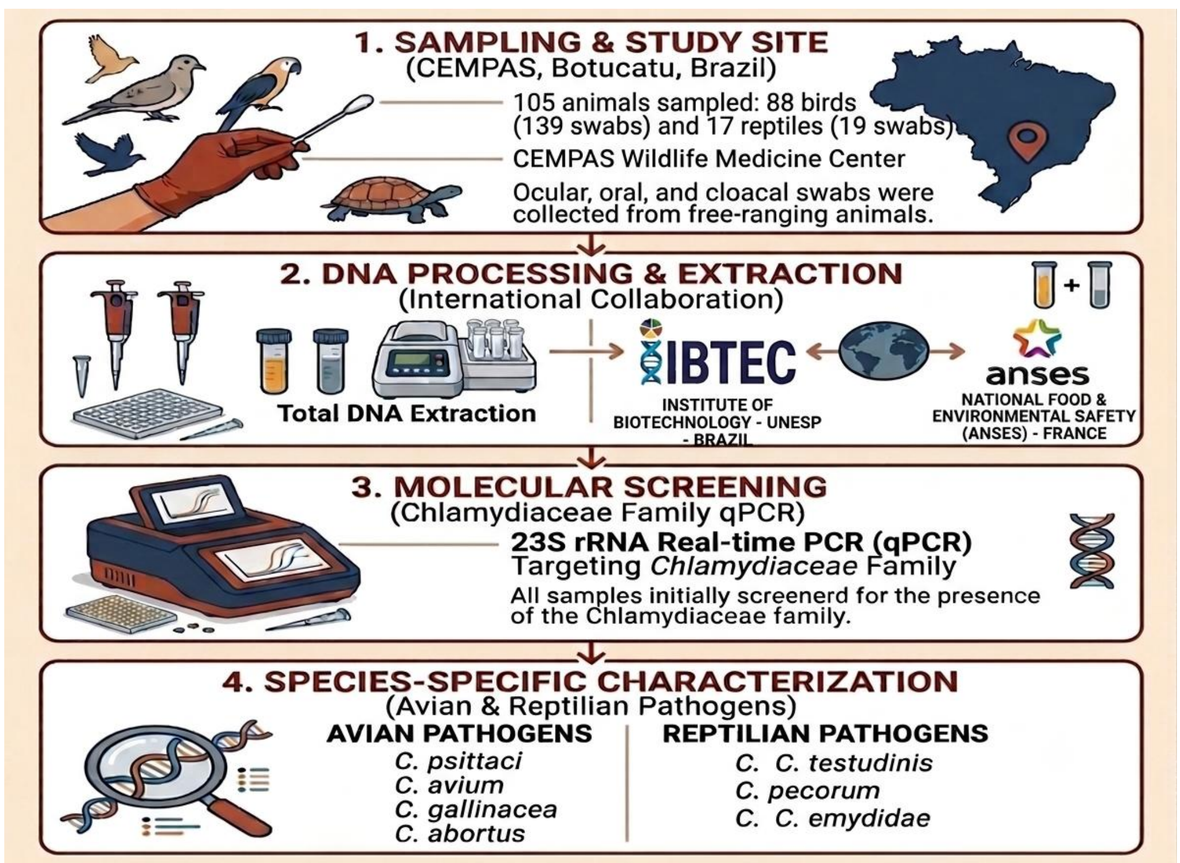
INTRODUCTION & AIM

The *Chlamydiaceae* family comprises versatile obligate intracellular pathogens affecting mammals, birds, and reptiles, leading to systemic, respiratory, and reproductive diseases [1]. Free-ranging wildlife acts as a critical reservoir for these agents, maintaining a complex diversity that includes established zoonotic pathogens like *Chlamydia psittaci (*the cause of avian chlamydiosis and human psittacosis) and emerging species such as *Chlamydia gallinacea [2]*. In Brazil, molecular surveillance has increasingly detected *C. psittaci* in wild and illegally traded birds [3]. Regarding reptiles, global studies report family-level positivity and the alarming circulation of atypical, uncharacterized chlamydial lineages in chelonians and lizards [4,5]. When admitted to rehabilitation centers, these diverse hosts create a high-density human-wildlife interface. Infected animals shed high bacterial loads via feces and secretions that persist in the environment, posing a silent occupational hazard to veterinarians and staff through aerosol inhalation [6]. **Therefore, this study aimed to investigate the prevalence and molecular diversity of chlamydial agents in wild birds and reptiles admitted to a Brazilian rehabilitation center (CEMPAS, Botucatu, Brazil), evaluating potential zoonotic risks under a One Health approach.**

METHOD

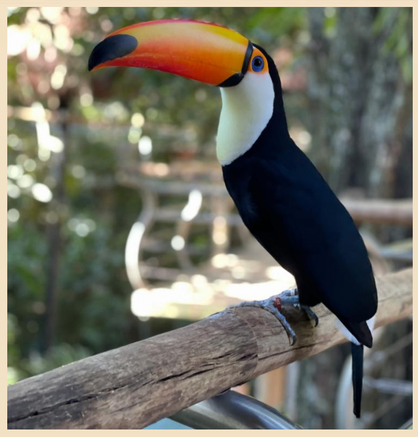


RESULTS & DISCUSSION

A total of 9/105 wild animals tested positive for the *Chlamydiaceae* family, representing an overall prevalence of 8.5%. When analyzed by group, reptiles (*Chelonoidis* spp.) showed a remarkably high positivity rate of 35.3% (6/17), exceeding the global estimate of 23.5%, while birds presented 3.4% (3/88), falling below the South American avian average of 16.5% [5]. Among these, specific qPCR identified *Chlamydia psittaci* in an eared dove (*Zenaida auriculata*), matching Brazilian data that points to columbids as major urban reservoirs and highlighting an occupational hazard for rescue center staff via aerosol inhalation [3]. Additionally, *Chlamydia gallinacea* was detected in a toco toucan (*Ramphastos toco*), supporting international evidence that this emerging avian pathogen is expanding its host range beyond domestic poultry [2]. In sharp contrast, all 6 positive samples from *Chelonoidis* spp. tested negative for all targeted species. This discrepancy strongly suggests low DNA load, primer incompatibility, or the circulation of novel, host-specific *Chlamydiaceae* clades that standard species-specific assays fail to detect [4,5], reinforcing the urgent need for genetic sequencing to map South American wildlife chlamydial diversity.

35.3%
REPTILE PREVALENCE
Exceeding the 23.5% global estimate

Chelonoidis spp. high positivity rate suggests potential novel, host-specific chlamydial lineages



Ramphastos toco positive for ***C. gallinacea***, demonstrating expanding wild avian host range

3.4%
AVIAN PREVALENCE
Below the 16.5% South American average.

Zenaida auriculata sample positive for ***C. psittaci***, a well-documented urban **zoonotic reservoir**

**Image credits: Unsplash / Wikimedia Commons*

CONCLUSION

The identification of *C. psittaci* and *C. gallinacea* in wild birds, alongside a high prevalence of uncharacterized *Chlamydiaceae* in *Chelonoidis* spp., underscores significant zoonotic risks and hidden microbial diversity at the urban-wildlife interface. These findings highlight the urgent need for strict biosafety protocols, consistent use of PPE by veterinarians and staff, and advanced genetic sequencing to mitigate potential spillover events and protect public health under a One Health perspective.

REFERENCES

[1] Borel N & Sachse K. *Zoonoses*, 2023. **[2]** Zhang F, et al. *Emerg Microbes Infect*, 2021. **[3]** Braz MS, et al. *Braz J Microbiol*, 2022. **[4]** Mitura A, et al. *BMC Vet Res*, 2017. **[5]** Inchuai R, et al. *Vet Res*, 2021. **[6]** Beeckman DS & Vanrompay DC. *Vet Comp Oncol*, 2009.

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