

Faecal microbiome of wild mammals: a source of pathogenic bacteria and antibacterial resistance

Diana Dias¹, Tânia Caetano¹, Carlos Fonseca^{1,2}, Sónia Mendo¹

¹ Department of Biology & CESAM, Universidade de Aveiro, 3810-193 Aveiro, Portugal
² ForestWISE - Collaborative Laboratory for Integrated Forest & Fire Management, Quinta de Prados, 5001-801 Vila Real, Portugal

BACKGROUND

A high number of human infectious diseases arise from wildlife. Zoonoses are diseases shared between animals (including livestock, wildlife, and pets) and humans. In 2018 about 360 000 zoonoses were reported in European Union by the EFSA and the ECDC. Shiga toxin-producing *Escherichia coli* (STEC) and *Salmonella* spp. Infections were among the most reported causes of these zoonotic diseases.

Since 2014, WHO considers antimicrobial resistance (AMR) an emerging global problem and a threat to public health. However, wild animals are rarely exposed to antibiotics and therefore low levels of AMR are expected.

The purpose of our work is to characterize the AMR in wild mammals while investigating the possibility that they could be reservoirs of pathogenic bacteria.

REFERENCES:

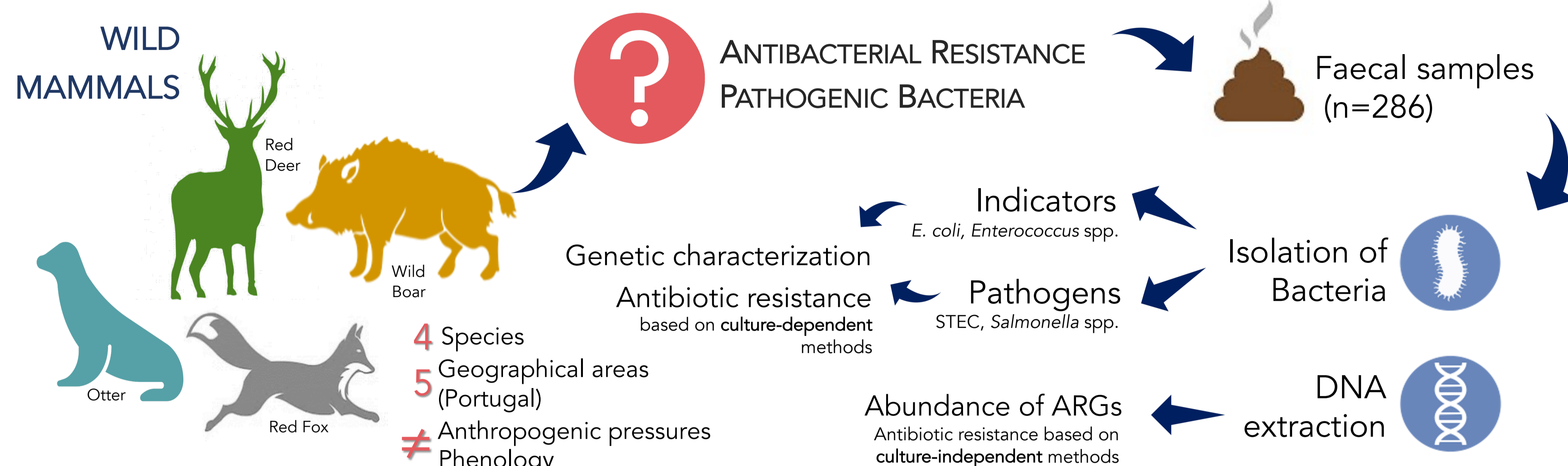
The European Union One Health 2018 Zoonoses Report, 2019. . EFSA J. 17. <https://doi.org/10.2903/j.efsa.2019.5926>

The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2017/2018, 2020. . EFSA J. 18. <https://doi.org/10.2903/j.efsa.2020.6007>

ACKNOWLEDGMENTS

Diana Dias was supported by the Fundação para a Ciência e a Tecnologia (FCT) grant (SFRH/BD/ 118618/2016). Tânia Caetano was funded by national funds (OE), through FCT – Fundação para a Ciência e a Tecnologia, I.P., in the scope of the framework contract foreseen in the numbers 4, 5 and 6 of the article 23, of the Decree-Law 57/2016, of August 29, changed by Law 57/2017, of July (CEECIND/01463/2017). Thanks are due to FCT/MCTES for the financial support to CESAM (UIDP/50017/2020+UIDB/50017/2020), through national funds. We thank Rita T. Torres, Ana Figueiredo and Dário Hipólito from the Wildlife Research Unit (UA), for their contribution to the collection of samples.

OBJECTIVES/METHODS

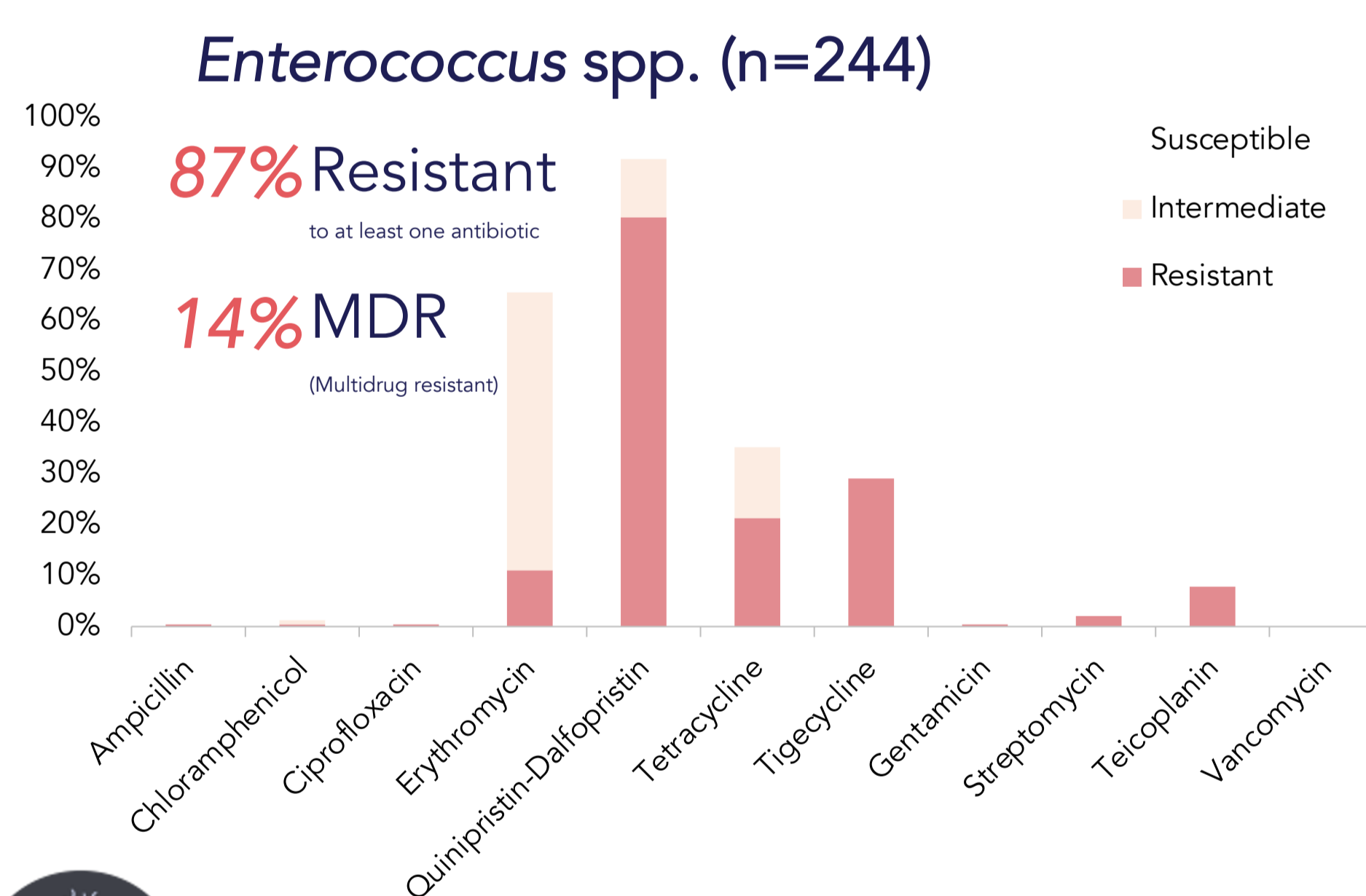
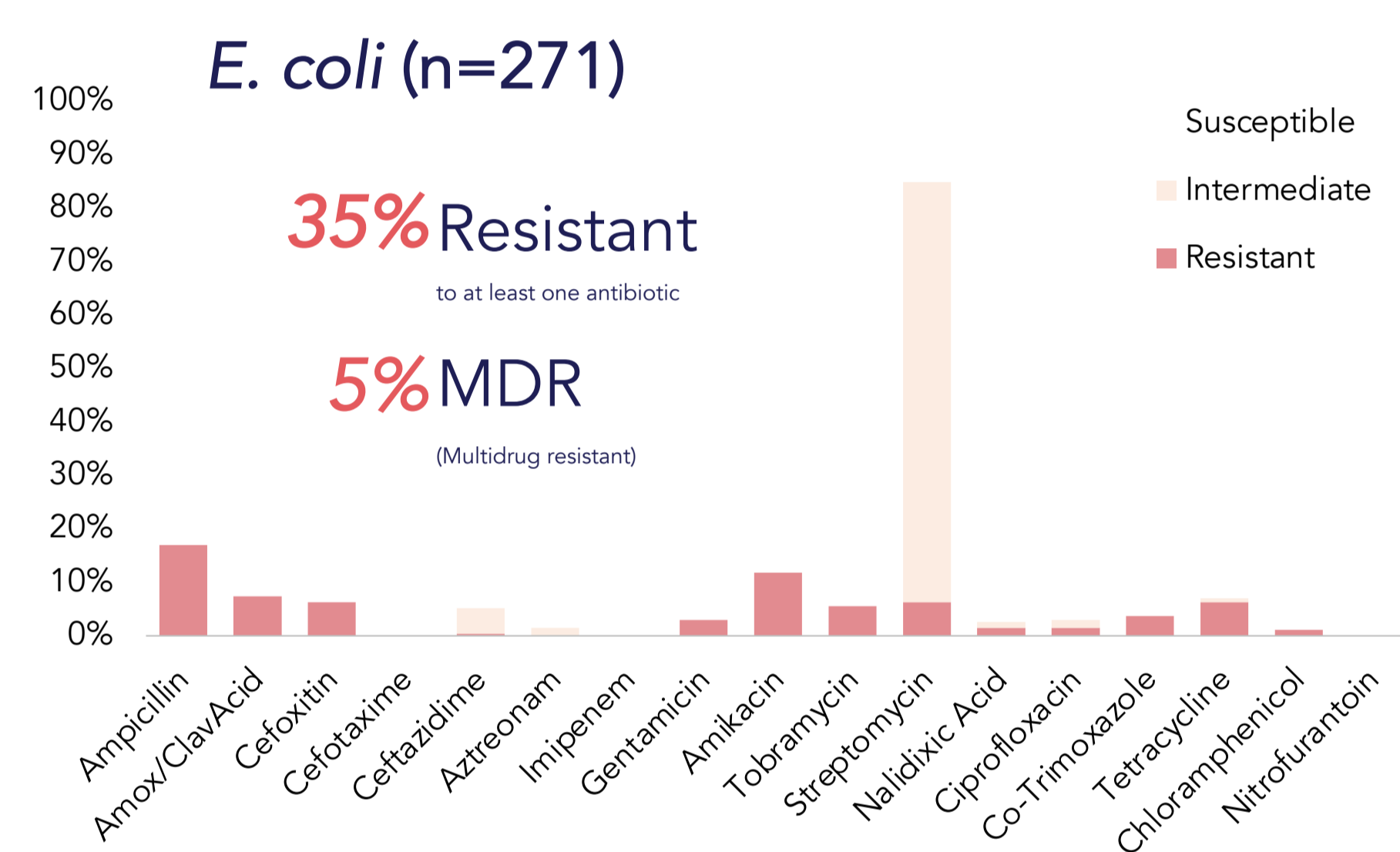


RESULTS AND DISCUSSION

ANTIBACTERIAL RESISTANCE

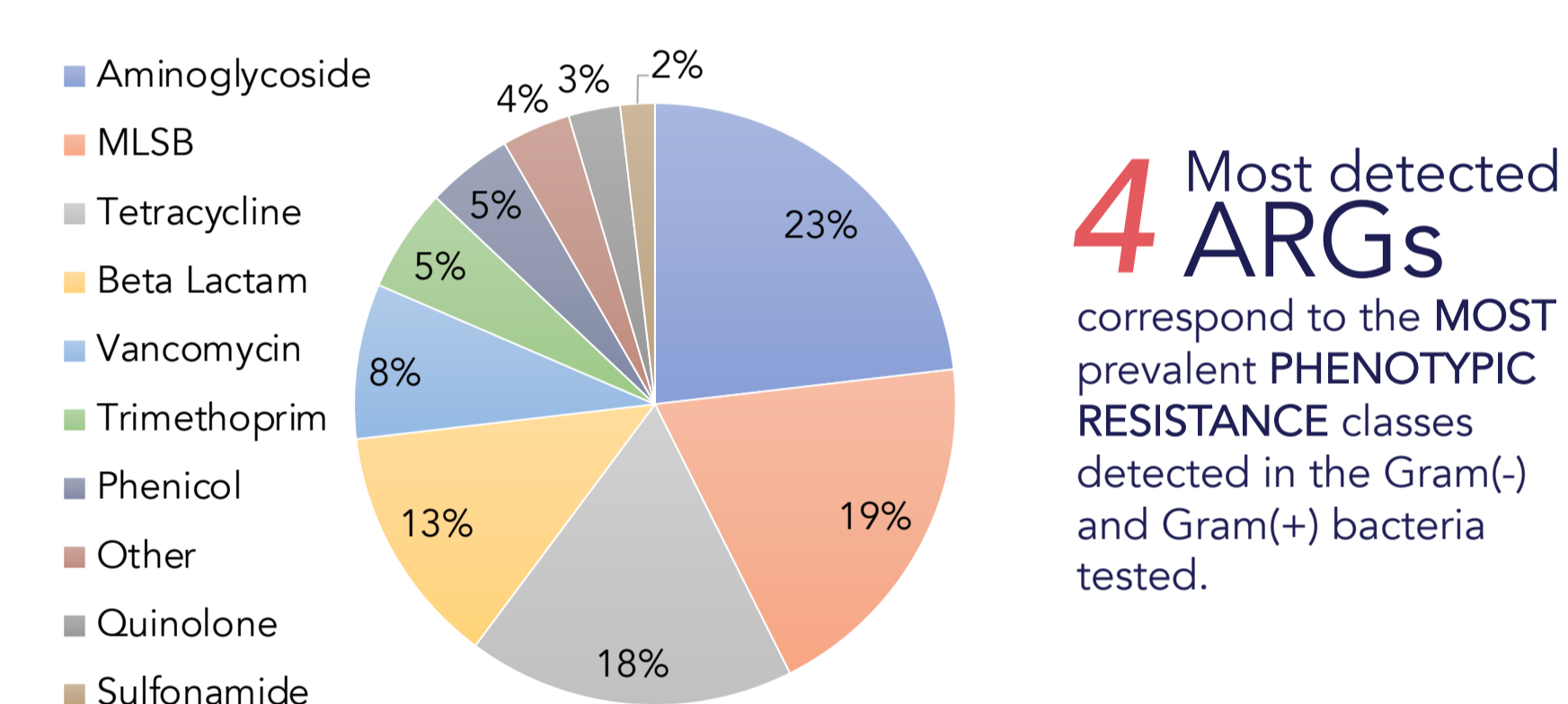


CULTURE-DEPENDENT APPROACH:
Phenotypic resistance of indicators

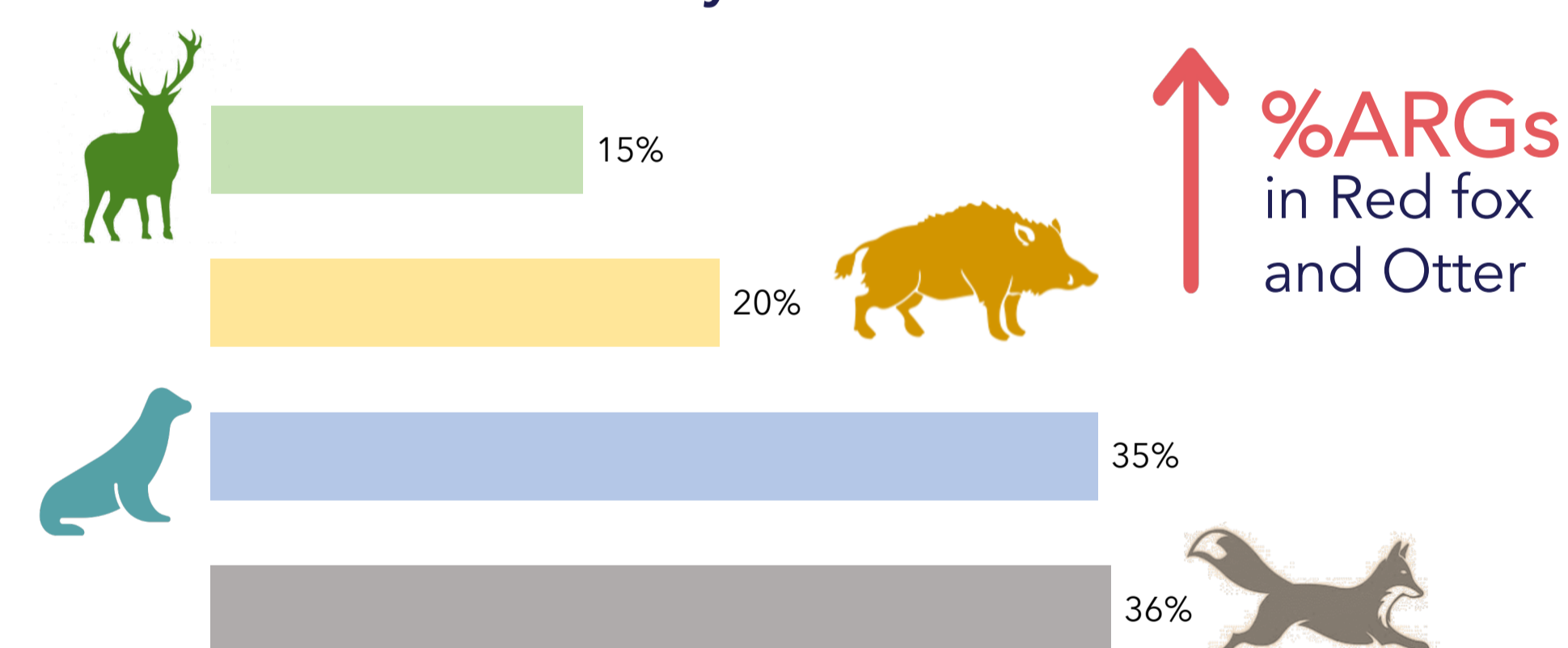


CULTURE-INDEPENDENT APPROACH:
Screening of antibiotic resistance genes by PCR

% ARGs detected by antibiotic class

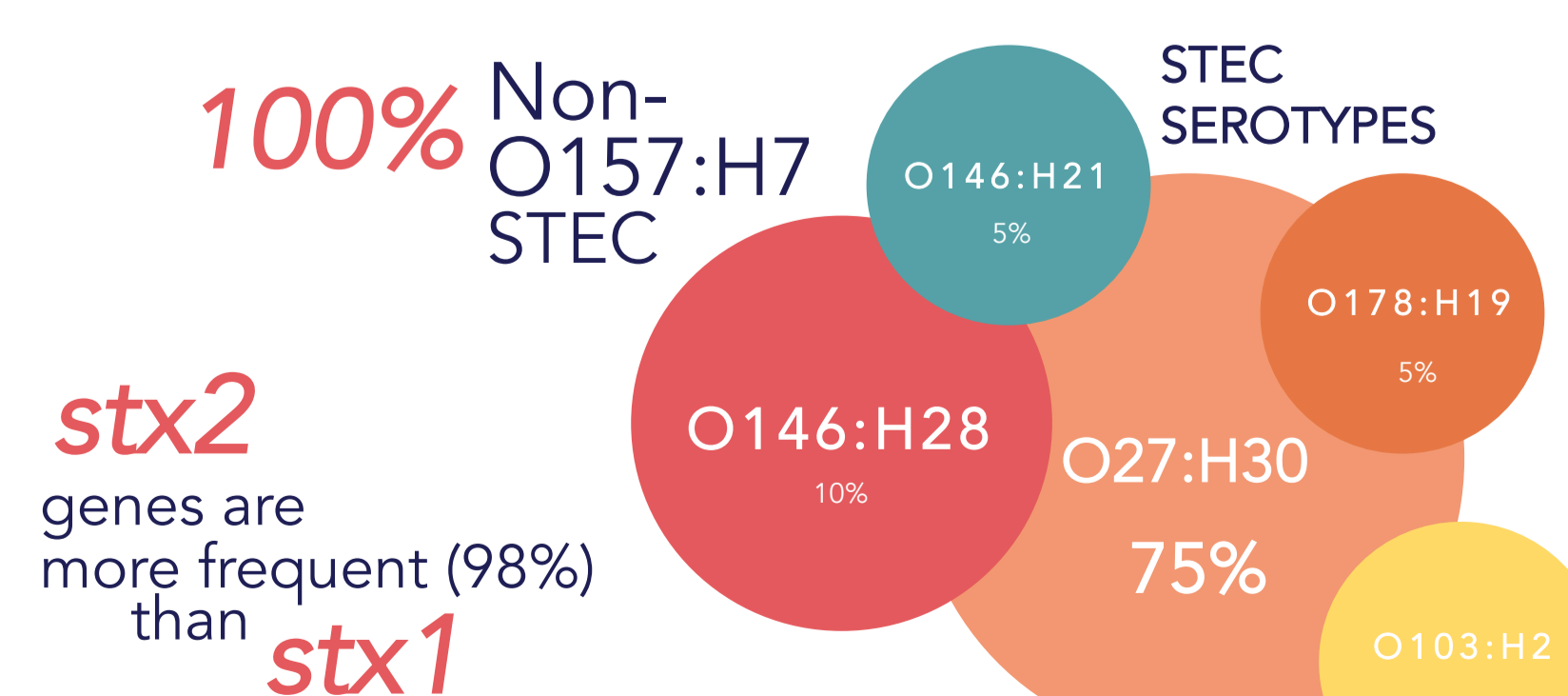
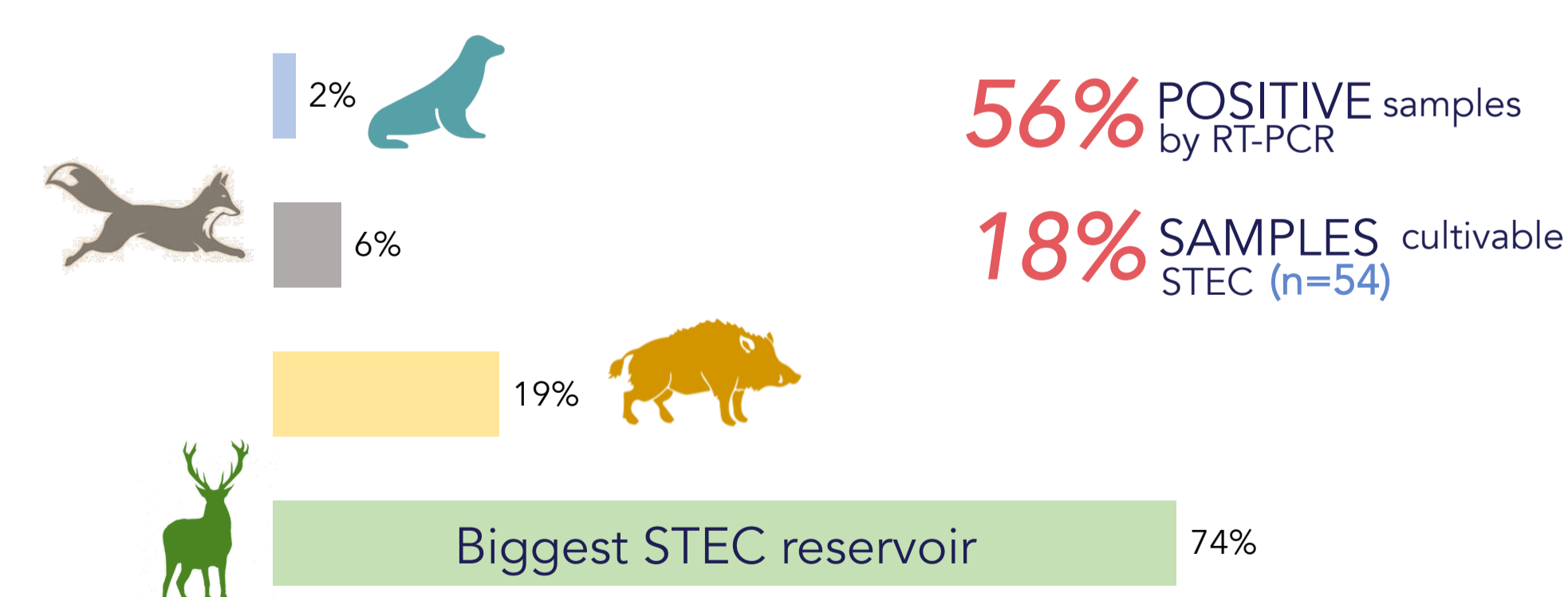


% ARGs detected by animal



POTENTIAL PATHOGENS

STEC (Shiga toxin-producing E. coli)



Salmonella spp.

