

# Wild animals as health indicators: pathogens monitoring and their antimicrobial resistance



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## Introduction

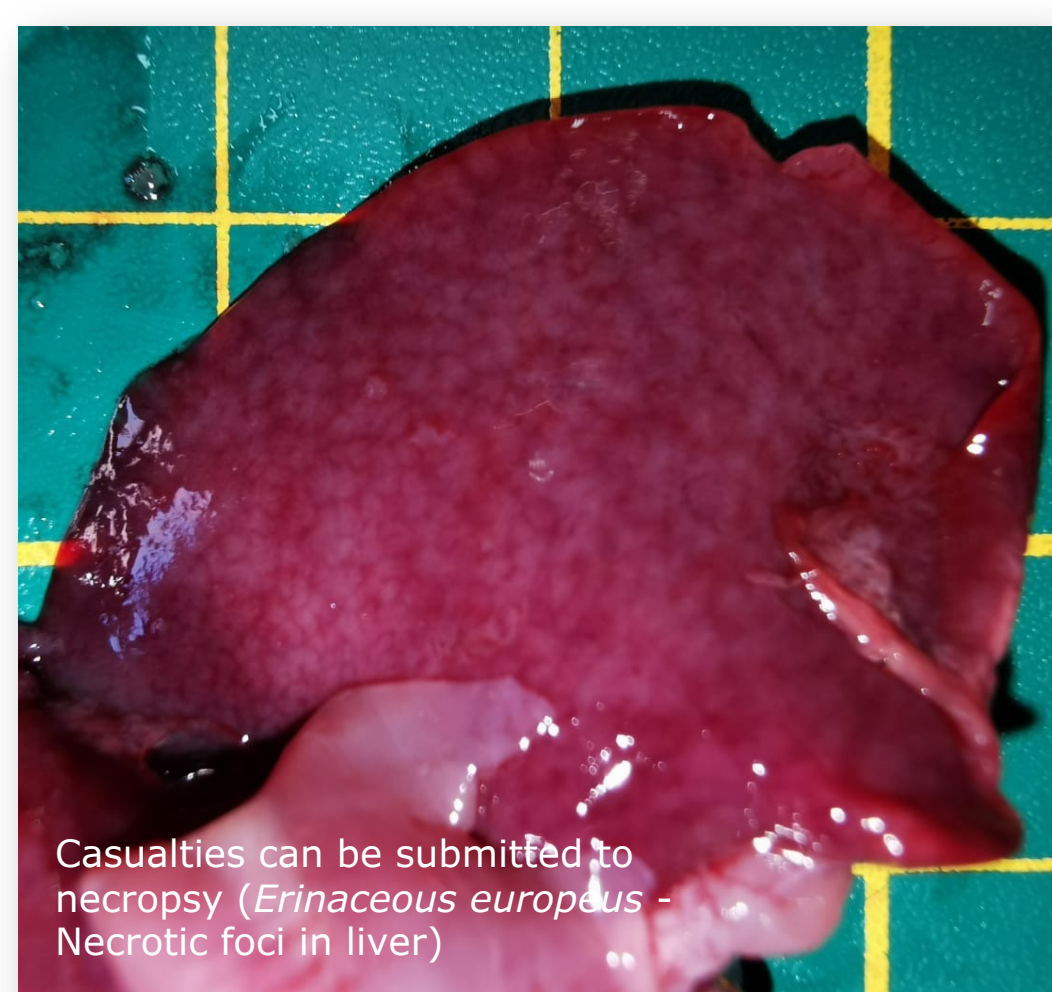
The presence of bacteria carrying antimicrobial resistance (AMR) genes is an increasingly serious and complex threat affecting public health worldwide [1,2]. Wildlife does not naturally meet antimicrobial molecules except in special cases of rescued and injured animals. However, wildlife can be infected by antibiotic-resistant bacteria present in the environment. Therefore, there are many ways allowing the resistance genes to flow into the environment: areas of intensive agriculture, industrial districts, intensive livestock systems, sewage drains [3]. Once infected, animals can act as reservoirs, vectors and bioindicators of AMR in the environment [4]. However, biological and health monitoring activities in wild animals are difficult to carry out due to various factors: legislative provisions, characteristics linked to the species and the environment and the discovery of deceased animals in an advanced state of decomposition, which makes difficult to carry out correct diagnostic investigations.

## Aim of the work

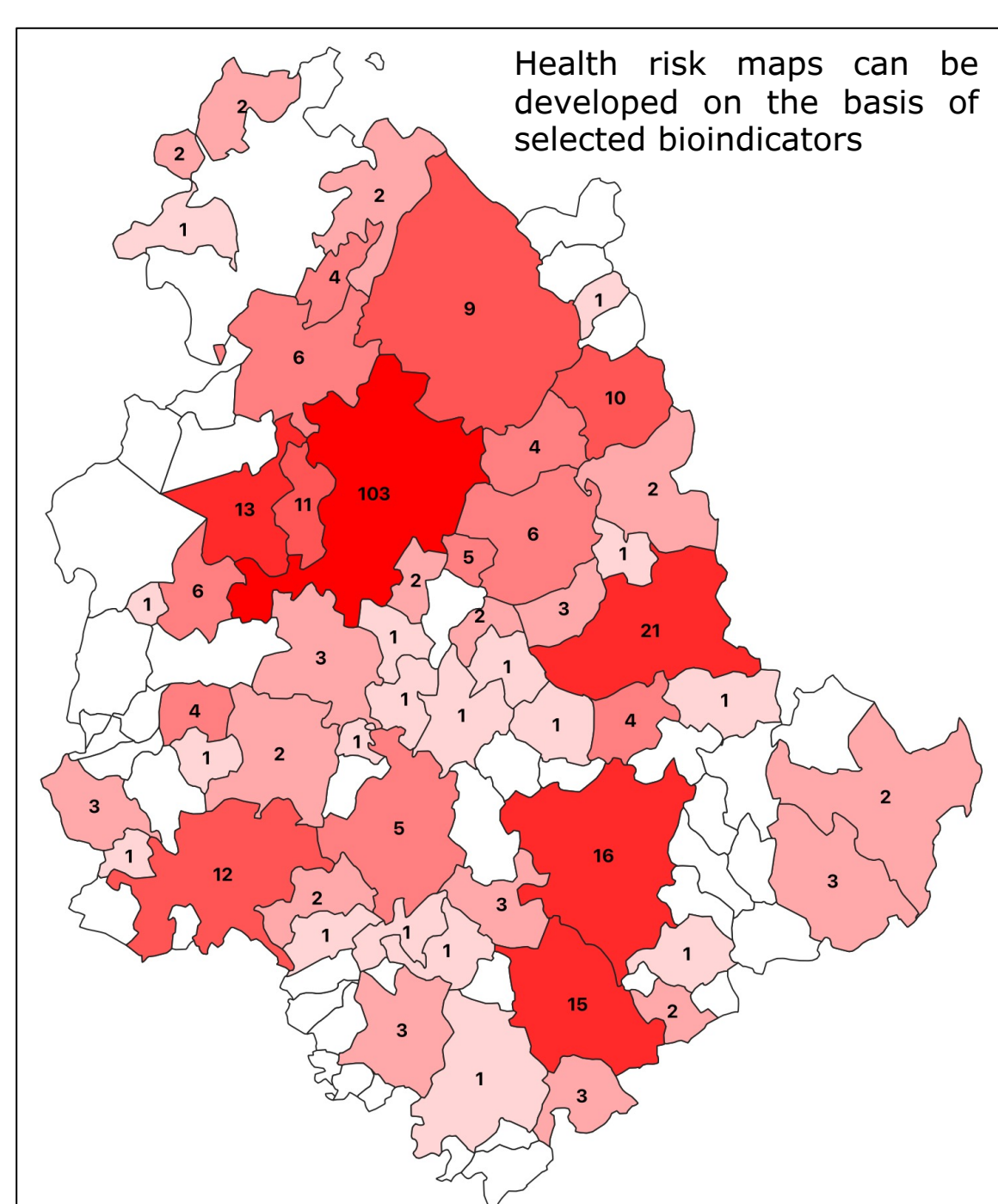
this project aims to explore and increase the know-how in AMR and pathogens shared between wild animals and humans, in collaboration with the WildUmbria Wildlife Rescue Center. The specific objective is to develop a monitoring system for the AMR on bacteria isolated in the wild species acting as bioindicators.



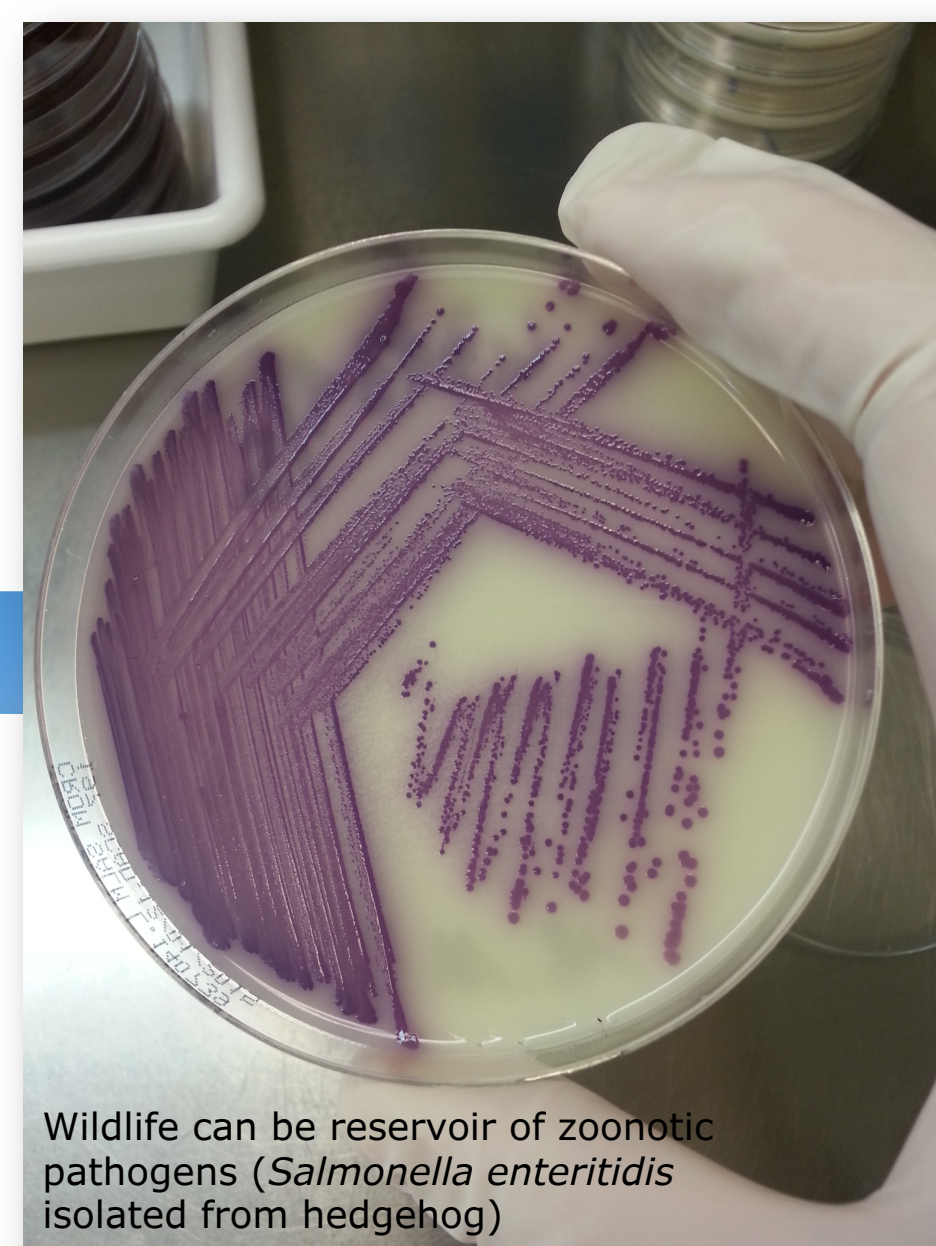
Injured wildlife is often in critical clinical condition



Casualties can be submitted to necropsy (*Erinaceus europaeus* - Necrotic foci in liver)



Health risk maps can be developed on the basis of selected bioindicators



Wildlife can be reservoir of zoonotic pathogens (*Salmonella enteritidis* isolated from hedgehog)



Examples of rescued wildlife:  
Common owl (*Asio otus*);  
European hedgehog (*Erinaceus europaeus*);  
Eurasian hobby (*Falco subbuteo*);  
Roe deer (*Capreolus capreolus*).

## Materials and Methods

We will work on wild animals rescued by the WildUmbria Wildlife Rescue Center on the Umbria region. In case of death or euthanasia, the animals were examined at the laboratories of the Experimental Institute of Zooprophyllaxis of Umbria and Marche. The considered species will be the European hedgehog (*Erinaceus europaeus*), the roe deer (*Capreolus capreolus*) and other species of nocturnal and diurnal birds of prey. In addition to the detection of any pathological lesions, samples will be taken for carrying out bacteriological and biomolecular investigations for diagnostic purposes and to evaluate the possible presence of zoonotic agents. The phenotypic and genotypic characterization of AMR genes of *E. coli* and *Salmonella* spp. will be also evaluated taking into consideration antimicrobials used in human and veterinary medicine. In hedgehogs (*Erinaceus europaeus*), *Escherichia coli* resistant to third generation cephalosporins and carbapenems in the wild considered species will be evaluated, as well as the prevalence and genomic characterization study of *Salmonella*.

## Expected results

- Georeferentiation of the rescued animals and production of descriptive maps;
- Collection of samples and related diagnostic investigations on the specimens identified;
- Development of wildlife health monitoring protocols;
- Description of the presence of pathogens with zoonotic and zootechnical interest relating to the wild considered species;
- Description of AMR bacteria in wild species on the Umbria region;
- Phenotypic and molecular characterization of *Escherichia coli* resistant to third generation cephalosporins and carbapenems in *Erinaceus europaeus* rescued in urban and non-urban areas;
- *Salmonella* spp. prevalence and genomic characterization investigation in *Erinaceus europaeus*.

## REFERENCES

[1] WHO(2014). Antimicrobial Resistance: Global Report on Surveillance. Geneva: World Health Organization. [2] Lammie SL, Hughes JM. Antimicrobial resistance, food safety, and one health: the need for convergence. Annu. Rev. Food Sci. Technol. (2016) 7:287–312. doi: 10.1146/annurev-food-041715-033251 [3] Hendriksen RS, Munk P, Njage P, van Bunnik B, McNally L, Lukjancenko O, et al. Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nat. Commun. (2019) 10:1124. doi: 10.1038/s41467-019-08853-3. [4] Holt, E. A. & Miller, S. W. (2010) Bioindicators: Using Organisms to Measure Environmental Impacts. Nature Education Knowledge 3(10):8

