MICROBIOLOGICAL DIAGNOSIS AND ANTIMICROBIAL RESISTANCE PROFILES OF RESPIRATORY INFECTIONS IN EUROPEAN HEDGEHOGS ADMITTED AT A WILDLIFE REHABILITATION CENTER

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INTRODUCTION AND OBJECTIVES

The wildlife rehabilitation center of Torreferrussa, located in Barcelona, admits more than 10,000 wild animals with wounds, sick, orphans or who present abnormal behaviour. The aim of this study is to carry out al **microbiological diagnosis** and to perform **antimicrobial resistance profiles** of the wild hedgehogs with respiratory infections admitted at the WRC of Torreferrussa in order to suggest a correct antibiotic treatment and reduce the selection of resistant strains.

MATERIALS AND METHODS

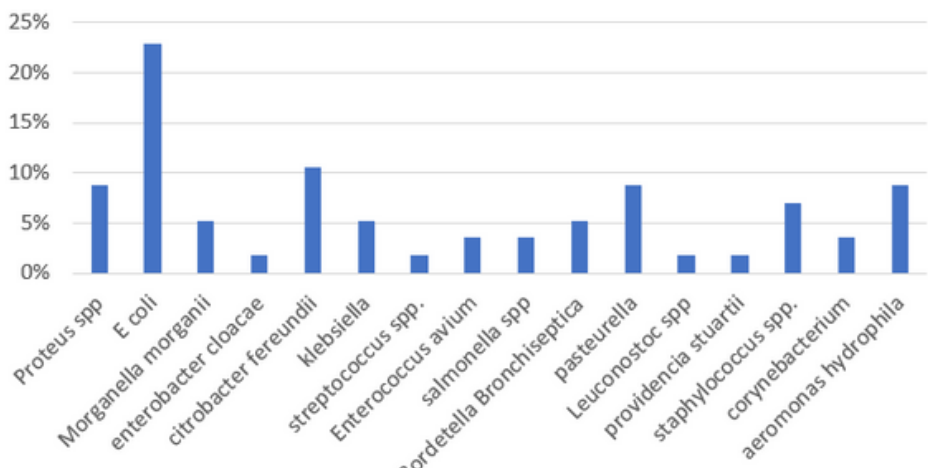
The WRC realized the necropsy and the recollection of samples of the hedgehogs, and later submitted them at the UAB, where they were processed. Microbiological identification consisted on spreding the sample on **Columbia blood agar** and **MacConkey agar** and wait for 24 hours. The bacteria was then identified using c**onventional biochemistry tests and API methods**. Finally, a **Kirby-Bauer disk difussion** was used in order to determine the phenotypic antimicrobial susceptibility of the bacteria isolated. The bacteria was then classified as S (susceptible), I (Intermediate) or R (resistant) based on the breackpoints explained by CLSI. Another classification made finally is if the bacteria is non resistant (NR), antimicrobial resistant (AMR), multidrug resistant (MDR) or extended resistant (XDR).

CONCLUSION

Enterobacteria was the most common family isolated (63%), with ***E coli*** as the main representant. ***Pasteurella*** and ***Aeromonas*** were also found. **Aminopenicillins** and **Cefalexin** were the antibiotics with the highest resistance levels, so its use should be minimmum without previous tests of susceptibility. *E coli* had a lot of MDR strains, but the most important finding is a XDR strain detected in *Citrobacter freundii*, which can compromise the efficency of the antibiotic therapy.

RESULTS

The family mostly found was Enterobacteriaceas, with a high prevalence of ***E coli*** **(23%)** and ***citrobacter freundii*** **(11%)**; *Pasteurella* spp. (9%) and *Aeromonas* spp. (9%) were also found.



The majority of the microorganisms had MDR strains, and *C freundii* presented a XDR strain, which can compromise antibiotic therapy.

Microorganism	Antimicrobial resistance pattern	Total isolates (n)	% AMR MDR NR
Bordetella Bronchiseptica	AMP+CL+CRO+LS+E+ENRO+XNL (n=1) CL+CRO+LS+E+ENRO+XNL (n=1)	2	MDR→100%
Pasteurella	CL+TE+ENRO (n=1) NR (n=1) AMP+AMC+TE+LS+E+C+AMX+ATM (n=1) TE+LS+E+C+AMX+ATM (n=1)	4	NR→25% MDR→75%
Providencia stuartii	AMP+AMC+CL+TE+LS+E+AMX+FEP+ATM (n=1)	1	MDR→100%
Staphylococcus	CIP+ATM (n=1) NR (n=1) CIP (n=1)	3	NR→33,3% AMR→66,6 %
Corynebacterium	NR (n=1) AMP+E (n=1)	2	NR→50% AMR→50%
Aeromonas hydrophila	AMP+AMC+E+ATM (n=1) E+AMC (n=1) AMP+AMC+CL+E+ENRO+AMX (n=2)	4	AMR→25% MDR→75%

Microorganism	Antimicrobial resistance pattern	Total isolates (n)	% of AMR, MDR, NR
E Coli	AMC (n=1) AMC+CL (n=1) CL+CRO+LS+ENRO+XNL+ATM (n=1) AMX+E (n=2) AMP+E+N+ENRO+AMX+ATM (n=1) CIP+E+N+GM+ENRO+AMX (n=1) AMC+CL+TE+E (n=2) CL+LS+E+N (n=3) AMP+AMC+TE+LS+E+C+AMX+ATM (n=1)	12	AMR→33,3 % MDR→66,6 %
Proteus	AMC+CL (n=1) CL (n=1) AMC+CL+E+AMX+ATM (n=2)	4	AMR→50% MDR→50%
Morganella morganii	AMP+AMC+CL+TE+LS+E (n=1) AMP+AMC+CL+E+AMX (n=2)	3	MDR→100%
Salmonella	E+AMX+ATM (n=1) E (n=1)	2	AMR→50% MDR→50%
Enterococcus	AMP+E+AMX (n=1) CIP+TE+LS+SXT+ENRO+ATM (n=1)	2	MDR→100%
Streptococcus	CL+CRO+CIP+TE+SXT (n=1)	1	MDR→100%
Klebsiella	AMP+E+AMX+ATM (n=1) AMP+AMC+LS+E+N+AMX (n=1) AMP+AMC+LS+E+N+AMX+ATM (n=1)	3	MDR→100%
Citrobacter freundii	N (n=2) AMP+AMC+CL+CRO+CIP+TE+LS+E+N+ENRO+AMX (r E (n=1) TE+E+ATM (n=1) TE (n=1)	6	AMR→66,6 % MDR→16,6 % XDR→16,6%
Enterobacter spp.	AMP+AMC+CL+E+N+AMX (n=1)	1	MDR→100%