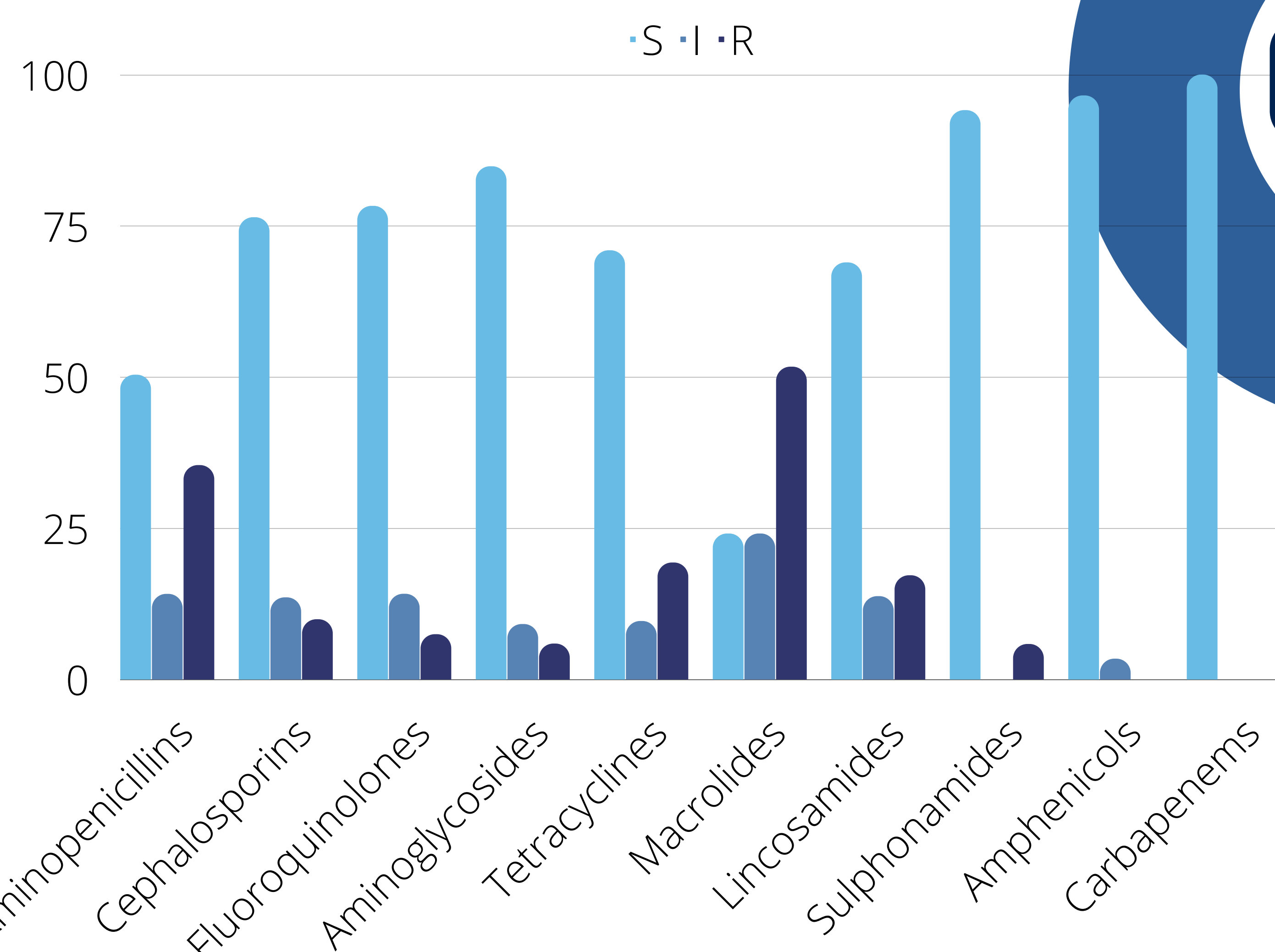
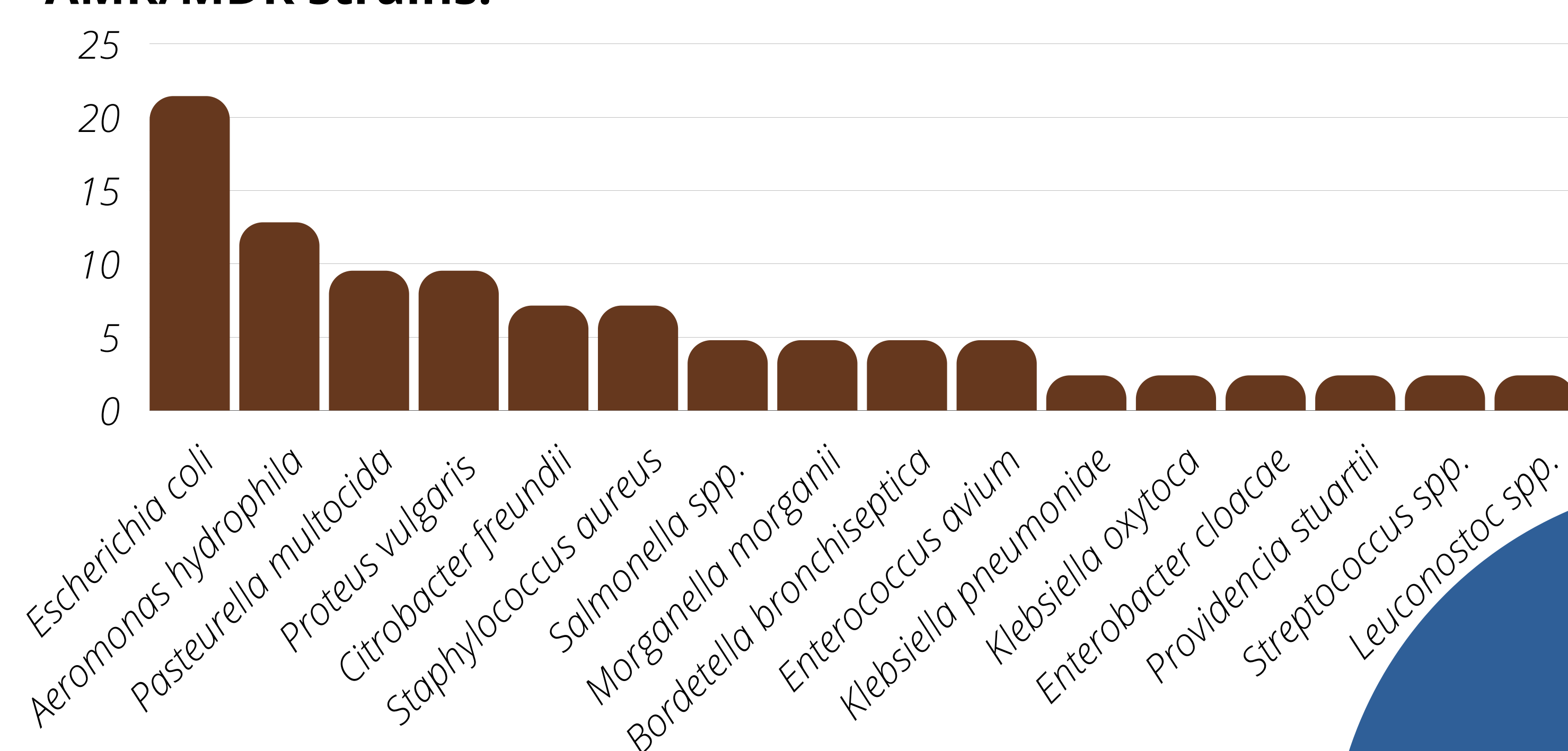


INTRODUCTION AND OBJECTIVES

In 32% of the cases, wild hedgehogs admitted at the WRC of Torreferrusa (Catalonia) die from respiratory injuries. This study was aimed to assess the **microbiological etiology** and **phenotypical antimicrobial resistance profile** of respiratory infections in wild European hedgehogs admitted at the WRC of Torreferrusa to **detect** the existence of antimicrobial resistance (**AMR**) and multi-drug resistance (**MDR strains**), in order to propose adequate treatment and **preventive protocols to reduce the selection of AMR/MDR strains**.



CONCLUSIONS

Enterobacteriaceas (principally E.coli) was the most prevalent family (57%) isolated from respiratory samples of Hedgehogs at the WRC of Torreferrusa, followed by **Aeromonas** spp. (13%) and **Pasteurella** spp. (10%). **Macrolides** and **aminopenicillins** were the antimicrobials with the highest levels of resistance. **MDR** strains were basically detected in Enterobacteria strains such as **E.coli (62%)**, and other **nosocomial infections by K.pneumoniae, E.cloacae, M.morganii, P.stuartii**, and a extended drug resistance (**XDR**) **C. freundii** strain, compromising the efficacy of conventional antimicrobial therapy. It is of concern the high prevalence of **Pasteurella** spp. MDR strains found in this study. Empiric treatment with conventional antibiotics (macrolides, aminopenicillins) is not recommended without a prior **culture and AST diagnosis** to all patients admitted with an infectious process whenever is possible in order to **reduce the selection of MDR strains**.

MATERIALS AND METHODS

Necropsy and sampling collection were centralized at the WRC and submitted at the UAB where they were processed for microbiological identification streaked on Columbia blood agar and MacConkey agar. Bacteria were identified analyzed by **biochemistry** (conventional tests and API ® methods). A **Kirby-Bauer disk diffusion** was used to determine phenotypic antimicrobial susceptibility of isolates against **16 antimicrobials**. The susceptibility of bacteria was interpreted based on the breakpoints provided by CLSI¹as **S (susceptible), I (intermediate) or R (resistant)**.

Own source, based on Yudhanto et al. (2022) adapted to this study data.²

Gram-negative Enterobacteria	Antimicrobial resistance patterns ^a	Number of antimicrobial classes in pattern	N (%) of NR, AMR and MDR
<i>Escherichia coli</i> (n=8) ^b	AMX AMC AMC/CL CL/CRO/XNL/LS/ENR AMX/AM/E/N/ENR AMX/N/GM/E/ENR/CIP AMC/CL/TE/E CL/LS/N/E	1 1 1 3 4 4 3 4	3 (37.5%) AMR 5 (62.5%) MDR
<i>Proteus vulgaris</i> (n=3) ^b	CL AMC/CL AMX/AMC/CL/E	1 1 2	3 (100%) AMR
<i>Citrobacter freundii</i> (n=3)	E TE AM/AMX/AMC/CL/CRO/ CIP/ENR/TE/LS/E/N	1 1 7	2 (66.6%) AMR 1 (33.3%) XDR
<i>Klebsiella</i> spp (n=2) <i>K. oxytoca</i>	AM/AMX/E	2	1 (50%) AMR 1 (50%) MDR
<i>K. pneumoniae</i>	AM/AMX/AMC/LS/E/N	4	
<i>Morganella morganii</i> (n=2)	AM/AMX/AMC/CL/E AM/AMC/CL/TE/LS/E	2 4	1 (50%) AMR 1 (50%) MDR
<i>Salmonella</i> spp. (n=2)	E AMX/E	1 2	2 (100%) AMR
<i>Enterobacter cloacae</i> (n=1)	AM/AMX/AMC/CL/E/N	3	MDR
<i>Providencia stuartii</i> (n=1)	AM/AMX/AMC/CL/TE/LS/E/	4	MDR
Gram-negative non enterobacteria	Antimicrobial resistance patterns ^a	Number of antimicrobial classes in pattern	N (%) of NR, AMR and MDR
<i>Aeromonas hydrophila</i> (n=4) ^b	AM/AMC/E AMC/E AM/AMX/CL/E/ENR AM/AMX/AMC/CL/E	2 2 4 3	2 (50%) AMR 2 (50%) MDR
<i>Pasteurella multocida</i> (n=3) ^b	CL/TE/ENR No resistant (NR) AM/AMX/AMC/TE/LS/E/C	3 1 5	2 (66.6%) MDR 1 (33.3%) NR
<i>Bordetella bronchiseptica</i> (n=1) ^b	AM/CL/CRO/XNL/LS/E/ENR	5	MDR
Gram-positive bacteria	Antimicrobial resistance patterns ^a	Number of antimicrobial classes in pattern	N (%) of AMR and MDR
<i>Staphylococcus aureus</i> (n=2)	CIP No resistant (NR)	1 1	1 (50%) AMR 1 (50%) NR
<i>Enterococcus</i> spp (n=2)	AM/AMX/E CIP/ENR/TE/LS/SXT	2 4	1 (50%) AMR 1 (50%) MDR
<i>Streptococcus</i> spp (n=1)	CL/CRO/CIP/TE/SXT	4	MDR

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