

Multidrug-resistant methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from quails

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Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a worrisome microorganism resistant to almost all beta-lactams and it frequently carries resistance to other major antibiotic classes. In addition to humans, it has been reported that MRSA also colonizes and infects domestic animals, farm animals, wild, captive or free-living species. The increased prevalence of this microorganism in animals for consumption has been a concern, due to the high zoonotic risk. Thus, we isolated MRSA from quails and aimed to characterize their antimicrobial resistance.

Methods

One-hundred mouth and cloaca swabs were collected from quails at a slaughterhouse in Portugal. The swabs were incubated in BHI broth with 6.5% of NaCl for 24h at 37° C. The inoculum was seeded onto oxacillin resistance screening agar (ORSAB) plates supplemented with 2 mg/L of oxacillin and incubated at 37° C for 24-48h for MRSA isolation. One colony per plate was collected. The staphylococci specie and the presence of *mecA* genes were confirmed by maldi-tof and PCR, respectively. The antimicrobial resistance phenotype was evaluated by the Kirby Bauer disc diffusion method against 14 antibiotics.

Results

From the 100 samples, 29 MRSA were recovered. All isolates were classified as multidrug-resistant since they were resistance to at least 3 different classes of antibiotics. All isolates were resistant to penicillin, cefoxitin, ciprofloxacin, erythromycin and clindamycin. All isolates except one presented resistance to tetracycline and resistance to aminoglycosides (n=9), chloramphenicol (n=3) and fusidic acid (n=5) was also detected.

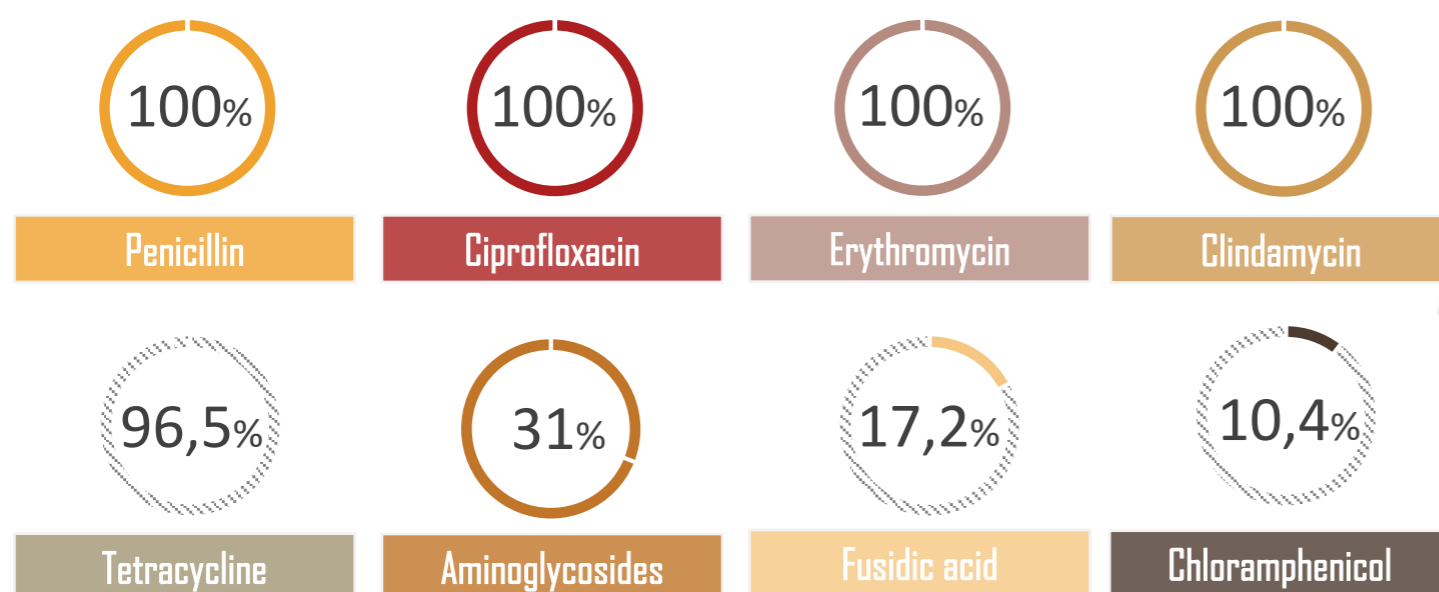


Figure 1. Percentages of the most prevalent resistances found among the MRSA isolates.

Conclusions

The indiscriminate use of antimicrobial agents in animal production and other agricultural activities has largely contributed to the distribution of MRSA among animals. Further studies will be carried out to investigate the antimicrobial resistance genes and clonal lineages of these isolates.

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