

### Phenotypic characterization and genotypic antimicrobial resistance profile of enterococci from poultry

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Enterococci are associated with nosocomial infections worldwide. We investigated the occurrence and antimicrobial resistance of enterococci in Egyptian poultry. A total of 117 cloacal swabs were collected. Bacterial isolates were identified by (MALDI-TOF MS). The antibiotic susceptibility testing against 22 antibiotics was performed with the MICRONAUT system. The presence of resistance-associated genes (tetK, tetL, tetM, tetS, tetO, erm(B), msrC, aac6-aph2, vanA, vanB, vanC1 and mecA) was investigated using PCR assays.

28 *Enterococcus faecium*, 16 *Enterococcus faecalis* and 9 *Enterococcus gallinarum* were identified. All *Enterococcus faecium* and *Enterococcus gallinarum* isolates were multidrug-resistant. More than 15% of *Enterococcus faecium* isolates were resistant to vancomycin. Resistance rates to other antibiotics were between 31.8% and 86.4%. The most frequently identified resistance genes were msrC, erm(B), aac6-aph2 and mecA. The vanB gene was identified in 2 *Enterococcus faecium*, whereas vanC1 was detected in 6 *Enterococcus faecium* and 6 *Enterococcus gallinarum* isolates. Tetracycline resistance-associated genes were found in 25 isolates whereas mecA was detected in nine isolates.

The development of resistance of bacteria to antibiotics in poultry. Our data corroborate that prudent use of antibiotics is essential in poultry production and should be applied in all countries.

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