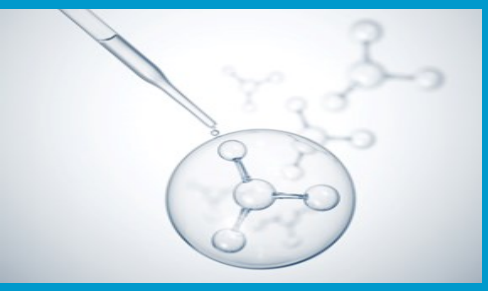
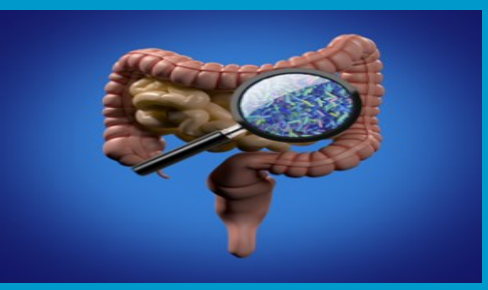
September 22-24 2022, The Royal Hotel, Hammamet, Tunisia

Book of abstracts





THIRD INTERNATIONAL SYMPOSIUM ON NATURAL ANTIMICROBIALS:

Current status, challenges and perspectives

ANTIMIC 2022

3rd INTERNATIONAL SYMPOSIUM ON NATURAL ANTIMICROBIALS: CURRENT STATUS, CHALLENGES AND FUTURE PERSPECTIVES

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DETECTION OF LINEZOLID AND VANCOMYCIN RESISTANT *ENTEROCOCCUS* STRAINS ISOLATED FROM AVIAN CECUM IN TUNISIA

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Background: *Enterococcus* has become a potentially high risk zoonotic opportunistic pathogen that can cause critical public health problems. The ability of these bacteria to acquire antibiotic resistance genes poses a major global threat. The aim of this investigation was to detect and characterize vancomycin and linezolid resistance acquired by enterococci isolated from avian cecum samples in Tunisia.

Materials/Methods: Cæcum chicken samples (n=294) were collected from 49 different Tunisian farms during December 2019 to March 2020. Six caeca per each farm were collected and then mixed in sterile spittoons, constituting a composite sample. More than one colony per sample was taken. A total of 167 isolates were recovered on Slanetz– Bartley agar supplemented or not with vancomycin. All the isolates were identified by MALDI-TOF. Phenotypic antimicrobial susceptibility testing, resistance genotyping and molecular typing by pulsed-field gel electrophoresis (PFGE) were performed.

Results: The identification results showed the predominance *E. faecium* (n=112), followed by *E. faecalis* (n=34), *E. durans* (n=08), *E. hirae* (n=10), *E. gallinarum* (n=2) and *E. avium* (n=1). Linezolid-resistance was detected in five *Enterococcus* isolates. After PCR and sequencing, our results showed that four *E. faecalis* harbored the *optr*A gene and one *E. faecium* harbored the *poxt*A gene. Acquired-vancomycin-resistance was detected in two *E. faecalis* isolates. This resistance was mediated by the *vanA* gene. High rates of resistance to tetracycline, erythromycin and chloramphenicol were also observed. After molecular characterization of the collected *Enterococcus* isolates, our results highlighted that the *tet(M)*, *tet(L)*, *erm(B)*, *msr* and *fexA* genes were detected in most tetracycline, erythromycin, and chloramphenicol resistant enterococci. The molecular typing of linezolid- and vancomycin-resistant isolates, performed by PFGE, showed a high genetic diversity.

Conclusion: This investigation provides insights that avian sector can be a reservoir of vancomycin and linezolid resistant enterococci and could be a potential vector of MDR enterococci transmission. Consequently, the implementation of specific control systems in regional and national surveillance of antibiotic resistant bacteria is becoming mandatory.