

Please read this bit first

This CPD/ CEU exercise is designed to take approximately two hours as a small group exercise within your laboratory. The Thistle QA CPD No is: **MT00025**.

Please keep a register of those taking part in the exercise. When the exercise is completed, please ask using the above email address, and we will send you a sheet showing the correct responses to each question.

Each attendee should claim two CPD points for completing the questions correctly, by retaining a copy of the relevant Thistle QA Participation Certificate as proof of registration on a Thistle QA EQA.

Cycle 19 Organism 7

The causative organism was *Enterococcus gallinarum*.

The variety of infections in which the enterococci are involved, include urinary tract infections, which are the most common. They are implicated in about 10% of all such infections and in 16% of nosocomial urinary tract infections. Intra-abdominal or pelvic wound infections are the next most commonly encountered infections. Bacteraemia is the third most common type of infection, and enterococci are the third leading cause of nosocomial bacteraemia^{1, 2, 3, 4}.

Enterococcus gallinarum is classified under group 11. The enterococci species are separated into five groups based on acid formation in mannitol and sorbose broths and hydrolysis of arginine⁵. *E. gallinarum* differs from *Enterococcus faecalis* by acid formation in arabinose and with regard to *Enterococcus faecium* by being motile.

The three most common phenotypes of vancomycin resistance among the enterococci are (i) high-level vancomycin (MICs, >64µg/ml) with accompanying teicoplanin resistance (>16µg/ml) (VanA phenotype); (ii) low- to high-level vancomycin resistance (MICs, 16 to 512µg/ml) most commonly without teicoplanin resistance (VanB phenotype); and (iii) intrinsic low-level resistance associated with *E. gallinarum*, *Enterococcus casseliflavus*, and *E. flavescens* (MICs, 2 – 32µg/ml) (VanC phenotype)^{6, 7}.

Vancomycin resistant enterococci (VRE) have emerged as nosocomial pathogens over the last decade, but little is known about their epidemiology. A prevalence study of VRE from rectal swabs was conducted on hospitalised as well as non-hospitalised patients in France. A total of 37% of the hospitalised patients and 11.8% of subjects from the community were found to be VRE carriers. A total of 65 VRE strains were isolated: 12(18.5%) *E. faecium*, 46 (70.7%) *E. gallinarum*, and 7 (10.8%) *E. casseliflavus* strains. The patients and subjects were recruited from a predominantly agricultural area where vancomycin-related antibiotics had recently been used in animal husbandry and which could have contributed to the high levels of VRE patients and subjects alike⁸.

References

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3. Nichols, RL., and Muzik, AC. 1992. Enterococcal infections in surgical patients: the mystery continues. *Clin. Infect. Dis.* **15**:72-76.
4. Gullberg, RM. *et al.* 1989. Enterococcal bacteraemia: analysis of 75 episodes. *Rev. Infect. Dis.* **11**:74-85.

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5. Teixeira, LM. *et al.* 1997. Recent approaches on the taxonomy of the enterococci and some related microorganisms. *Adv. Exp. Med. Biol.* **418**:397-400.
6. Leclercq, R., and Courvalin, P. 1997. Resistance to glycopeptides in enterococci. *Clin. Infect. Dis.* **24**:545-556.
7. Leclercq, R. *et al.* 1992. Vancomycin resistant gene vanC is specific to *Enterococcus gallinarum*. *Antimicrob. Agents. Chemother.* **36**:2005-2008.
8. Gambarotto, K 2000. Prevalence of vancomycin-resistant enterococci in fecal samples from hospitalised patients and non-hospitalised controls in a cattle- rearing area of France. *J. Clin. Microbiol.* **B38(2)**:620-624.

CPD Questions ?

1. How would you differentiate between *E. gallinarum* and other species of the genus *Enterococcus*?
2. What phenotypic vancomycin resistance is found with *E. gallinarum*?

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