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Dispersion of the Vancomycin Resistance Genes *van*A and *van*C of *Enterococcus* Isolated from Nile Tilapia on Retail Sale: A Public Health Hazard

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Abstract:

Although normally regarded harmless commensals, enterococci may cause a range ofdifferent infections in humans, including urinary tract infections, sepsis, and endocarditis.The acquisition of vancomycin resistance by enterococci (VRE) has seriously affectedthe treatment and infection control of these organisms. VRE are frequently resistantto all antibiotics that are effective treatment for vancomycin-susceptible enterococci,which leaves clinicians treating VRE infections with limited therapeutic options. With VREemerging as a global threat to public health, we aimed to isolate, identify enterococcispecies from tilapia and their resistance to van-mediated glycopeptide (*vanA* and*vanC*) as well as the presence of enterococcal surface protein (*esp*) using conventionaland molecular methods. The cultural, biochemical (Vitek2 system) and polymerasechain reaction results revealed eight Enterococcus isolates from the 80 fish samples(10%) to be further identified as *E. faecalis* (6/8, 75%) and *E. gallinarum* (2/8, 25%).Intraperitoneal injection of healthy Nile tilapia with the eight Enterococcus isolatescaused significant morbidity (70%) within 3 days and 100% mortality at 6 days post-injection with general signs of septicemia. All of the eight Enterococcus isolates werefound to be resistant to tetracycline. The 6/6 *E. faecalis* isolates were susceptible forpenicillin, nitrofurantoin, gentamicin, and streptomycin. On the other hand 5/6 weresusceptible for ampicillin, vancomycin, chloramphenicol, and ciprofloxacin. The twoisolates of *E. gallinarum* were sensitive to rifampicin and ciprofloxacin and resistantto vancomycin, chloramphenicol, and erythromycin. Molecular characterization provedthat they all presented the prototypic *vanC* element. On the whole, one of the twovancomycin resistance gene was present in 3/8 of the enterococci isolates, whilethe *esp* virulence gene was present in 1/8 of the enterococci isolates. The resultsin this study emphasize the potential role that aquatic environments are correlated toproximity to anthropogenic activities in determining the antimicrobial resistance patternsof *Enterococcus* spp. recovered from fish in the river Nile in Giza, Elmounib, Egyptas a continuation of our larger study on the reservoirs of antibiotic resistance in theenvironment.