# Molecular Analysis of Vancomycin Resistant *Enteroccocus* Isolates from Pediatric Population

Thesis

Submitted for partial fulfillment of MD degree in Medical Microbiology and Immunology

Presented by

***Yasmin Mahmoud Zedan Ragab***

M.B.B.Ch, M.SC

Faculty of Medicine

Fayoum University

**Under supervision of**

***Dr. Rasha Hamed Ahmed Bassyouni***

Professor of Medical Microbiology and Immunology Department

Faculty of Medicine

Fayoum University

***Dr. Enas Mamdough Hefzy***

Professor of Medical Microbiology and Immunology

Faculty of medicine

Fayoum University

***Dr. Fatma Abo elnaga Ahmed***

Assisstant Professor of Medical Microbiology and Immunology

Faculty of Medicine

Fayoum University

***Dr. Eslam Rabie Abdel Alaziz***

Lecturer of pediatrics Medicine

Faculty of Medicine

Fayoum University

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# Summary

This cross sectional study aimed to detect the prevalence of rectal colonization by vancomycin resistant *Enterococci* among pediatrics admitted to Fayoum University Pediatrics Hospital and to detect its molecular characters.

Rectal swabs were collected from a representative sample of inpatient of the pediatric department, Each patient was screened for vancomycin resistant *Enterococci* colonization on the day of admission.

The study included 80 patients, out of 80 rectal swabs only 63 rectal swabs showed growth of *Enterococci* by cultured on bile esclin agar and isolates that to be *Enterococci* were confirmed by housekeeping genes.

Isolates that identified as *Enterococci* were cultured on VRE based agar (chromogenic agar) and those appeared as blue to green colonies were identified as VRE.

Species level of *Enterococci* was identified by detection of unique housekeeping genes using monoplex PCR. Our results showed that *Enterococcus faecium* was the predominant isolate 43/63 (68.3%), *E. casselifavus* species and *E. gallinarum* had the same prevalence of 7/63 (11.1%), while *E. faecalis* species was the least frequently isolated bacteria 6/63 (9.5%).

We studied the virulence traits among *Enterococcus* isolates isolated from rectal swabs of hospitalized patients .The enterococcal surface protein (*esp)* and hyalouronidase *(hyl*) genes were studied. The prevelance of both genes was nearly the same 30/63(47.6%) for *hyl* , 31/63(49.2%) for *esp* and eighteen(28.8%) for both.

By studying MIC of vancomycin and teicoplanin among different *Enterococcus* species identified in our study (*E. casselifavus*, *E. faecium*, *E. faecalis* and *E. gallinarum*), *E. faecalis* had the highest MIC for vancomycin and *E. casselifavus* for teicoplanin.

The study investigated the prevelance of van genes (*vanA, vanB, vanC, vanD, vanE and vanG*) among glycopeptide resistance *Enterococcus* isolates, *vanD* had the highest prevelance 36/58 (60.1%) while *vanE* had the lowest prevelance 17/58 (29.3%).

We have studied genes encoding linezolid resistance among *Enterococci*, *optrA* and *poxtA*. Our results showed that 20/58 isolates had *optrA* genes and only one isolate had *poxtA* gene.

By analysis of the relation between *Enterococcus* species and the prevelance of resistance and virulance genes, we found a significant relation between *E. faecalis* bacteria and absence *hyl* gene.

As regards the prevelance of *esp*, *hyl* and *optrA* genes a significant relation was noted between the presence of *optrA* gene and ciprofloxacin resistance.

The study suggests that VRE harboring *van A* generally exhibit higher resistance to antibiotics than those with *van B*, with specific resistance patterns varying depending on the antibiotic and regional factors. The presence of vancomycin resistance genes (*van C and van D*) is associated with resistance to common antibiotics used to treat enterococcal infections, raising concerns about antimicrobial therapy choices

The study emphasizes the significance of considering vancomycin susceptibility and specific *Enterococcus* phenotypes when selecting antibiotics for optimal patient outcomes and reducing treatment failure and resistance emergence.