

# Vancomycin and ciprofloxacin resistance in enterococci from a Hospital effluent and in the receiving Municipal Wastewater Treatment Plant

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## Scope and objectives

•Hospital effluents can be discharged to municipal wastewater treatment plants (MWWTP) without previous treatment;

•Enterococci are indicators of faecal contamination and recognized harbours of clinically relevant resistance phenotypes;

The major objectives in this study were:

•Assess if hospital effluents may be a source of ciprofloxacin and vancomycin resistant enterococci;

• Compare the enterococci loads and respective resistance rates in the untreated hospital effluent and in the raw inflow of the receiving municipal wastewater treatment plant (MWWTP);

• Characterize the most relevant enterococci species and antibiotic resistance patterns observed in hospital effluents and in municipal wastewater.

## Approach

Water samples:  
Hospital – MWWTP (raw & treated)  
Comparison of:  
Cultivable counts  
Antibiotic resistance prevalence  
Species diversity

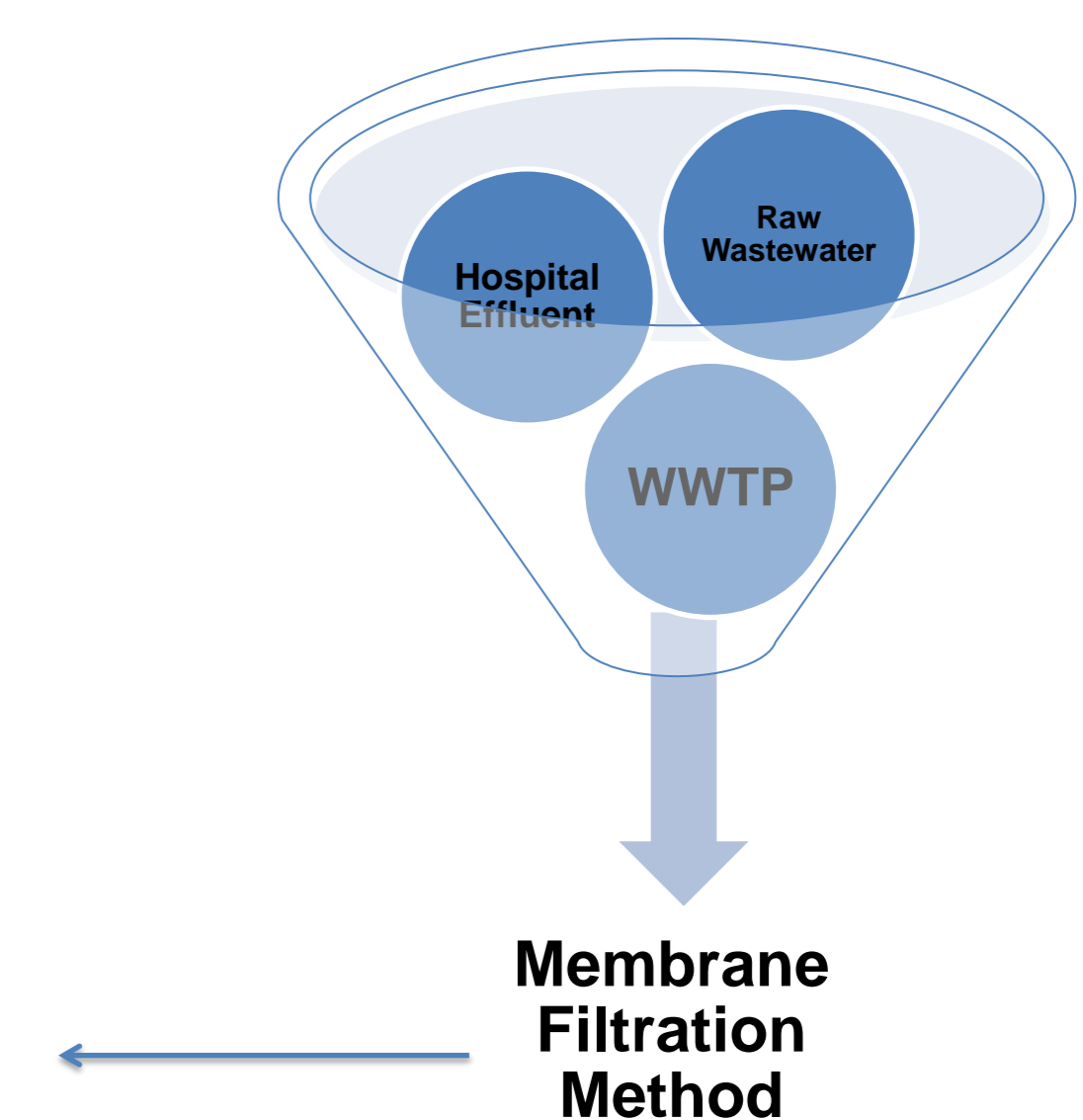
-Isolation on mEnterococcus agar and on mEnterococcus agar supplemented with vancomycin or ciprofloxacin

-CFU/mL and percentage of resistance

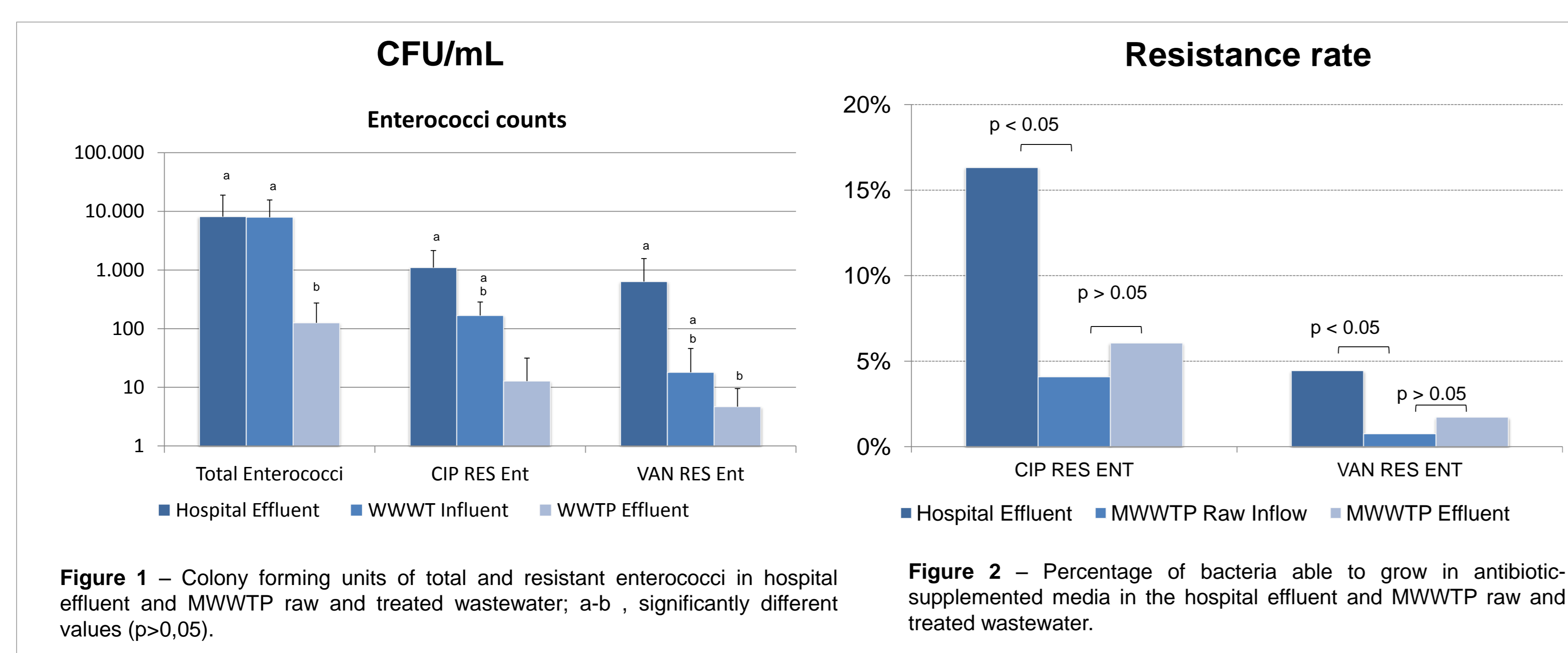
-16S rRNA gene sequence analysis

-Antibiotic resistance phenotypes - disk diffusion method

-- Detection of vancomycin-resistance associated genes



## Results



## General comments

•Strong temporal variations of cultivable counts, mainly in the untreated hospital effluent;

• Enterococci counts, including the ciprofloxacin and vancomycin resistant, were not significantly different in the hospital effluent and in the MWWTP raw inflow;

Nevertheless,

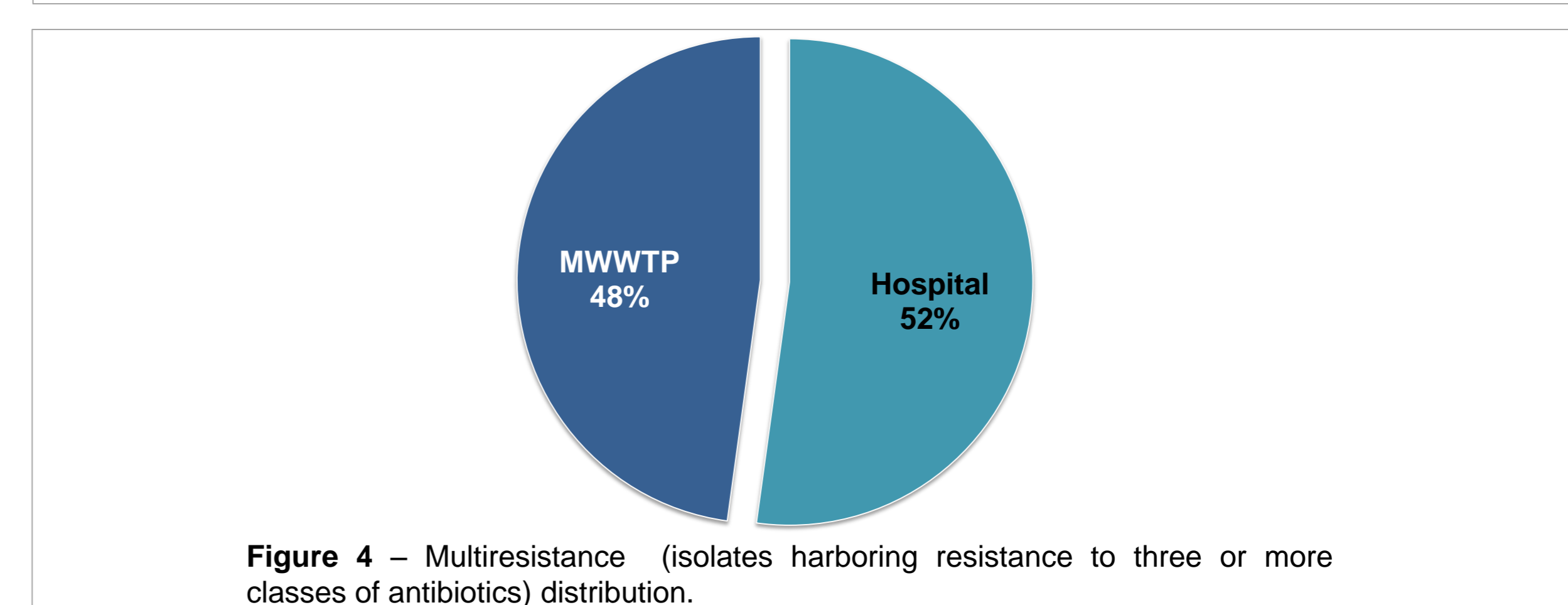
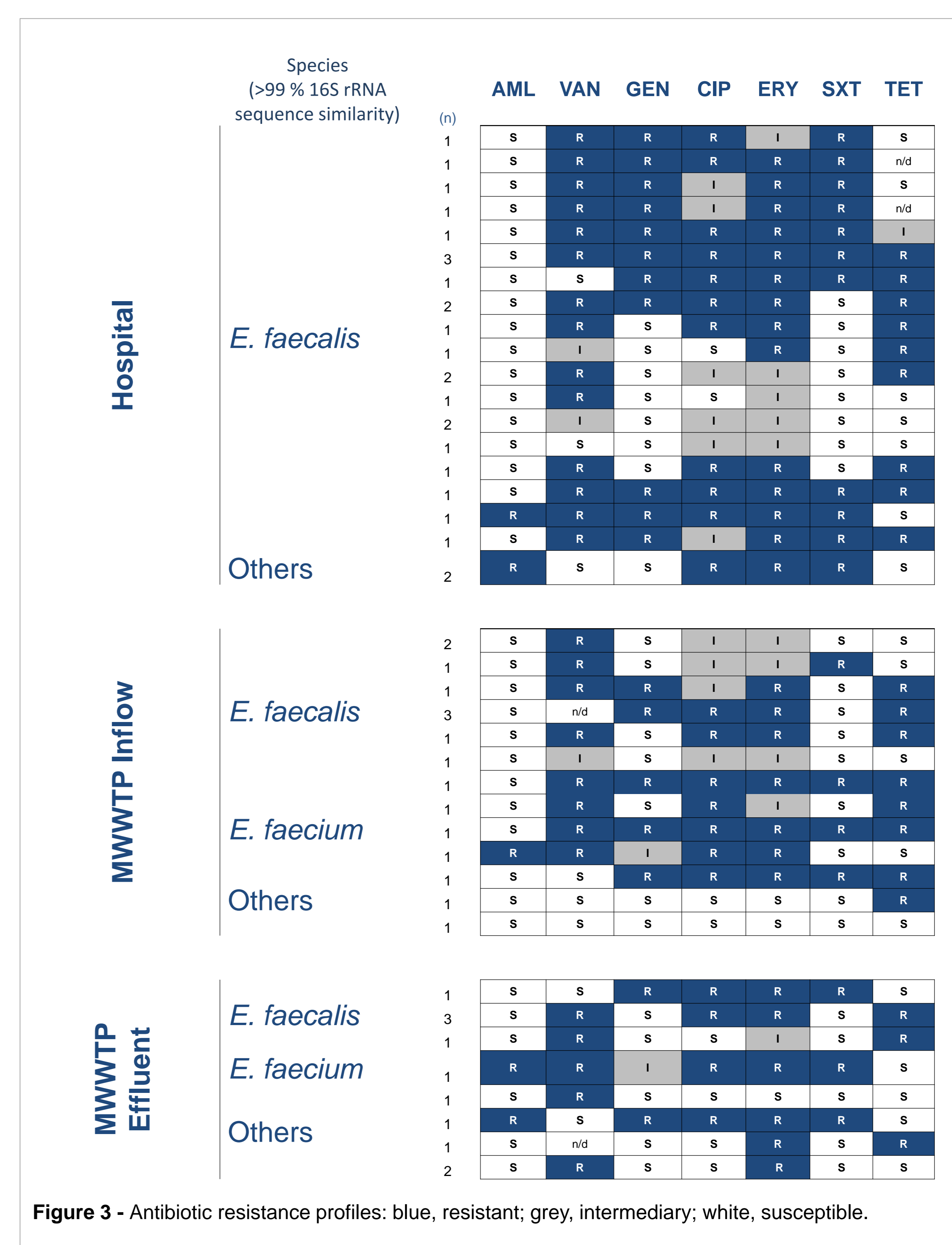
• The mean percentage of antibiotic resistant enterococci was at least three times higher in the hospital effluent than in the raw inflow;

• The prevalence of resistance in the raw and treated wastewater was not significantly different;

• The final treated effluent had lower resistance rates than the hospital effluent.

However,

•The *vanA* gene was found in samples from the three types of water analysed, in 40% of the total isolates.



## Acknowledgements

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