## FEMS7-1891 Environmental Microbiology/Microbial Ecology /Microbial Communities - Part II

# ANTIMICROBIAL RESISTANCE PROFILES AFTER CONJUGATIVE EVENTS WITH AN ESCHERICHIA COLI ISOLATE FROM HOSPITAL EFFLUENT

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### Backgrounds

The dissemination of antibiotic resistance in the environment is an issue of growing concern in which the selection and horizontal gene transfer have important roles. While bacteria of human origin released into sewage already harbour plasmids encoding for antibiotic resistance, further contact with other sewage contaminants may promote the conjugative transfer of resistance traits.

### Objectives

This study aims at understanding the influence of candidate stressors on the rate of conjugation as well as characterising the conjugative plasmidome.

#### Methods

The isolate *Escherichia coli* H1FC54 from hospital effluent was used as donor and the azide resistant *Escherichia coli* J53 as recipient strain. The nucleotide sequence of the conjugative plasmidome obtained with these strains in the presence of ceftazidime was determined. Conjugation assays were carried out in the presence of ceftazidime (10 mg/L), tellurite (0.5-5  $\mu$ M), or arsenite (0.5-15 $\mu$  M), and the resistance phenotypes, genotypes and plasmids profiles were determined.

## Conclusions

Stressors did not lead to significant increase in the conjugation rates. Transconjugants acquired resistance to amoxicillin, ticarcillin, sulfamethoxazole and tetracycline. Distinct conjugative plasmidomes and variations in the acquired phenotypes were detected in different conjugation assays.

The nucleotide sequence of the conjugative plasmidome revealed the presence of an HI2 plasmid backbone with determinants of resistance to antibiotics (beta-lactams, (fluoro)quinolones, sulfonamides), tellurite and arsenite.

The variable composition of the conjugative plasmidome and the formation of cointegrates during conjugation are novel findings, which may bring interesting insights into the comprehension of the molecular and physiological mechanisms that underlie antibiotic resistance propagation in the environment.