

Effect of Carbapenem Exposure On The Fitness of

Extended Spectrum Beta-Lactamase (ESBL)-Producing

Escherichia coli Strains Isolated From Migrant



Communities Working in the Klang Valley, Malaysia **RES-256**

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Introduction

Silent carriage of Extended Spectrum Beta-Lactamase (ESBL)producing Escherichia coli (ESBLEC) is a risk factor for onward dissemination of the bacteria and host future infections. We investigated the effect of carbapenem exposure on the fitness of ESBLEC strains isolated from economic migrants of the Klang Valley, Malaysia.

Results

Figure 1 : ESBLEC carriage and AST results of tested strains

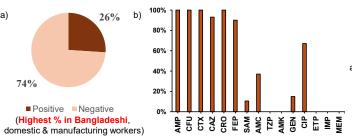


Table 1: Common AST profiles of tested strains

| Most common AST profiles | No. of strains (%) |
|---|-----------------------|
| Ampicillin+ Cefuroxime + Cefotaxime + Ceftazidime + Ceftriaxone + Cefepime + Ciprofloxacin | 14 (20.9) |
| Ampicillin+ Cefuroxime + Cefotaxime + Ceftazidime + Ceftriaxone + Cefepime | 13 (19.4) |
| Ampicillin+ Cefuroxime + Cefotaxime + Ceftazidime + Ceftriaxone + Cefepime + Ampicillin/Sulbactam + Ciprofloxacin | 12 (17.9) |

Table 2: ESBL genotyping of tested strains

| ESBL gene / genotype | N (%) |
|--------------------------------|------------------------------------|
| blaTEM | 27 (40.3) |
| blaCTX-M-1 | 61 (91.0) Most prevalent ESBL gene |
| blaCTX-M-9 | 5 (7.4) among our study strains |
| blaOXA-1 | 15 (22.4) |
| ESBL genotype | |
| blaTEM | 1 (1.5) |
| blaCTX-M-1 | 33 (49.3) |
| blaCTX-M-9 | 1 (1.5) |
| blaTEM + blaCTX-M-1 | 14 (20.9) |
| blaTEM + blaCTX-M-9 | 3 (4.5) |
| blaCTX-M-1 + blaOXA-1 | 7 (10.4) |
| blaCTX-M-9 + blaOXA-1 | 1 (1.5) |
| blaTEM + blaCTX-M-1 + blaOXA-1 | 7 (10.4) |

Figure 2: ERIC-PCR analysis of strains with the most common AST profiles to select

Carried blaCTX-M

fingerprint in each

ESBLEC MG 32 ESBLEC MG 48 **ESBLEC MG 57**

Dominant ERIC

cluster

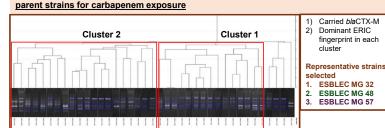


Table 3: Number of strains that survived carbapenem exposure

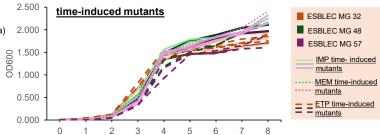
| | Time based induction | | | Concentration based induction | | |
|------------------|----------------------|----|----|-------------------------------|----|----|
| ESBLEC MG | 32 | 48 | 57 | 32 | 48 | 57 |
| IMP Induction | 3 | 2 | 3 | 2 | 3 | 3 |
| MEM Induction | 0 | 1 | 1 | 0 | 0 | 0 |
| ETP Induction | 3 | 2 | 2 | 3 | 0 | 1 |
| Total strains | 6 | 5 | 6 | 5 | 3 | 4 |

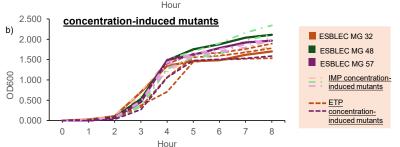
ESBLEC identification (CHROMagar) and Participant recruitment antibiotic susceptibility testing (AST) Antibiotic exposure : and Enterobacterial Repetitive (IMP), meropenem (MEM) and ertapenem (ETP)) Intergenic Consensus Polymerase Chain Reaction (ERIC-PCR) Genotyping Time based induction (24, 48 and 72 h with 1/2x MIC of representative strain selection tested strains) Concentration based induction Fitness test (1x. 2x and 1/2x MIC of tested Growth curve analysis strains in 24 hour)

Desiccation assay (24, 48 and 72 h)

Methodology

Figure 3: Growth curve analysis

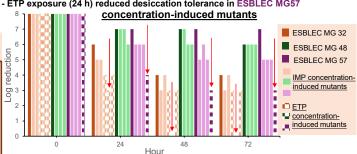




-Similar growth trends for parent and mutants under both exposure conditions

Figure 4 : Desiccation assay analysis time-induced mutants ESBLEC MG 32 ESBLEC MG 48 ESBLEC MG 57 reduction IMP time-induced MEM time-induced Log <u>mutants</u> ETP time- induced mutants

- ETP exposure (24 h) reduced desiccation tolerance in ESBLEC MG57



- ETP exposure (1/2× MIC) reduced tolerance in ESBLEC MG57;

- ETP exposure (2× MIC) reduced tolerance in ESBLEC MG32

Conclusion

Our findings show the presence of ESBLEC in migrant communities and their phenotypic stability post-carbapenem exposure, posing a risk for forward antimicrobial resistance dissemination.

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