

International Spread of Tet(X4)-Producing *Escherichia coli* Isolates

Zengfeng Zhang, Zeqiang Zhan and Chunlei Shi *

MOST-USDA Joint Research Center for Food Safety, School of Agriculture and Biology, and State Key Laboratory of Microbial Metabolism, Shanghai Jiao Tong University, Shanghai 200240, China; zhanzengfeng118@163.com (Z.Z.); zhanzeqiang@sjtu.edu.cn (Z.Z.)

* Correspondence: clshi@sjtu.edu.cn

Table S1. AMR genotypes in *tet(X4)*-producing *Escherichia coli* isolates.

Antibiotic resistance determinants		Numbers	Ratio/%
Carbapenems	<i>bla</i> _{NDM-5}	8	1.3
	<i>bla</i> _{NDM-1}	1	0.2
Colistin	<i>mcr</i> -1.1	77	12.6
	<i>mcr</i> -3.1	3	0.5
Tigecycline	<i>tmexC-tmexD-toprJ1</i>	7	1.1
Aminoglycosides	<i>df</i> rA12	325	53.0
	<i>df</i> rA14	110	17.9
	<i>df</i> rA17	66	10.8
	<i>df</i> rA5	52	8.5
	<i>df</i> rA1	17	2.8
	<i>aph</i> (6)-Id	314	51.2
	<i>aph</i> (3'')-Ib	288	47.0
	<i>aph</i> (3')-Ia	173	28.2
	<i>aph</i> (4)-Ia	65	10.6
	<i>aad</i> A2	331	54.0
	<i>aad</i> A1	292	47.6
	<i>aad</i> A22	92	15.0
	<i>aad</i> A5	45	7.3
	<i>aac</i> (6')-IIc	1	0.2
	<i>aac</i> (6')-Ib-cr5	22	3.6
	<i>aac</i> (3)-IIId	108	17.6
	<i>aac</i> (3)-IVa	65	10.6
	<i>aac</i> (3)-IIe	5	0.8
	<i>aac</i> (3)-IIg	1	0.2
β-Lactamase	<i>bla</i> _{CTX-M-14}	50	8.2
	<i>bla</i> _{CTX-M-55}	49	8.0
	<i>bla</i> _{CTX-M-65}	44	7.2
	<i>bla</i> _{CTX-M-15}	4	0.7
	<i>bla</i> _{CTX-M-3}	3	0.5
	<i>bla</i> _{CTX-M-24}	3	0.5
	<i>bla</i> _{CMY-2}	18	2.9
	<i>bla</i> _{TEM}	545	88.9
	<i>bla</i> _{SHV-12}	51	8.3
	<i>bla</i> _{DHA-1}	4	0.7
	<i>bla</i> _{OXA-1}	12	2.0
	<i>bla</i> _{OXA-10}	14	2.3
	<i>bla</i> _{OXA-232}	3	0.5
Rifampicin	<i>arr</i> -3	18	2.9
Chloramphenicol	<i>cml</i> A1	239	39.0
	<i>cat</i> B3	22	3.6

	<i>catA2</i>	14	2.3
Macrolides	<i>mph(A)</i>	168	27.4
	<i>mef(B)</i>	118	19.2
	<i>erm(B)</i>	70	11.4
	<i>erm(42)</i>	59	9.6
Fosfomycin	<i>fosA3</i>	49	8.0
	<i>fosA4</i>	35	5.7
Florfenicol	<i>floR</i>	584	95.3
Lincomycin	<i>lnu(F)</i>	142	23.2
	<i>lnu(G)</i>	148	24.1
Sulfonamide	<i>sul3</i>	417	68.0
	<i>sul2</i>	340	55.5
	<i>sul1</i>	101	16.5
Tetracyclines	<i>tet(A)</i>	501	81.7
	<i>tet(M)</i>	226	36.9
	<i>tet(B)</i>	127	20.7
Quinolones	<i>qnrS1</i>	381	62.2
	<i>oqxA</i>	42	6.9
	<i>oqxB</i>	42	6.9
	<i>qnrS2</i>	19	3.1
	<i>qnrB4</i>	4	0.7
	<i>qepA1</i>	3	0.5
	<i>qnrB19</i>	2	0.3
	<i>qnrB2</i>	1	0.2
AMR Mutations	<i>glpT_E448K</i>	351	57.3
	<i>gyrA_S83L</i>	242	39.5
	<i>parC_S80I</i>	163	26.6
	<i>gyrA_D87N</i>	139	22.7
	<i>uhpT_E350Q</i>	46	7.5
	<i>parE_S458A</i>	37	6.0
	<i>cyaA_S352T</i>	31	5.1
	<i>parC_A56T</i>	20	3.3
	<i>nfsA_G131D</i>	14	2.3
	<i>soxS_A12S</i>	9	1.5
	<i>nfsA_R15C</i>	7	1.1
	<i>parE_L416F</i>	4	0.7
	<i>parE_I355T</i>	2	0.3
	<i>nfsA_Q44STOP</i>	2	0.3
	<i>marR_S3N</i>	1	0.2



Figure S1. Phylogenetic subtree of Lineage IV isolates extracted from the tree in Figure 5. Column ① depicts isolate isolation countries; ② denotes the distribution of years; ③ denotes sample sources. The detailed information in ①-③ is shown in the key using various colors.