

Supplementary Data

Genomic analysis of multidrug-resistant clinical *Enterococcus faecalis* isolates for antimicrobial resistance genes and virulence factors from the western region of Saudi Arabia

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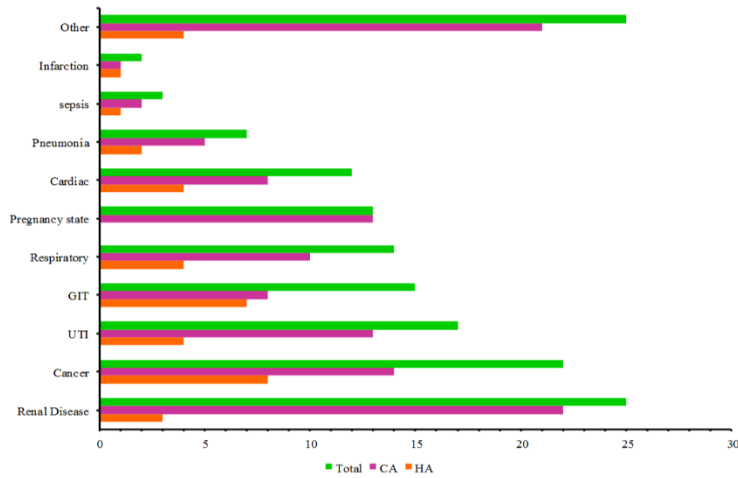


Figure S1. Percentage distribution of hospital-acquired infection (HA), and community-acquired infection (CA) infections of *E. faecalis* in different disease patients.

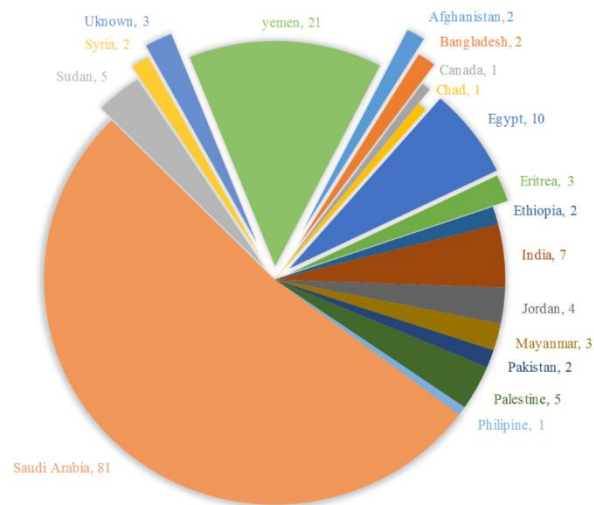


Figure S2. Distribution of the *E. faecalis* isolates analyzed in this study based on nationalities. The number of isolates is mentioned with the country name.

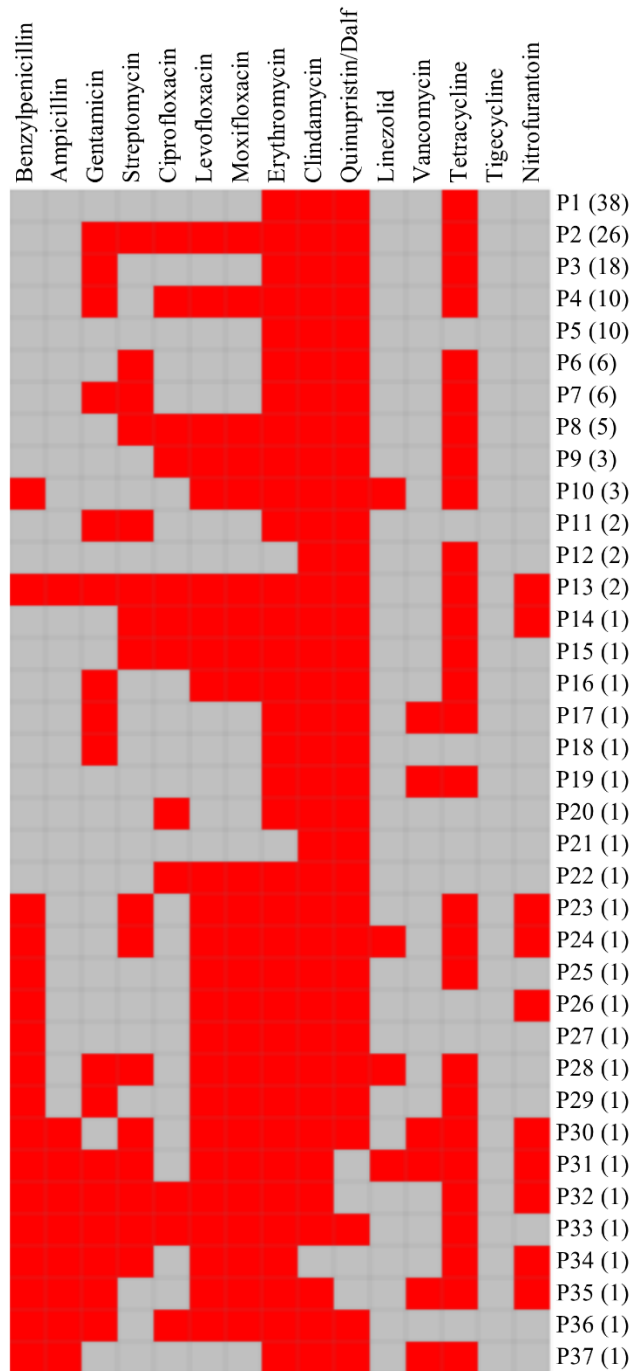


Figure S3. Heat map of antimicrobial resistance and susceptibility patterns among the 155 *E. faecalis* isolates.

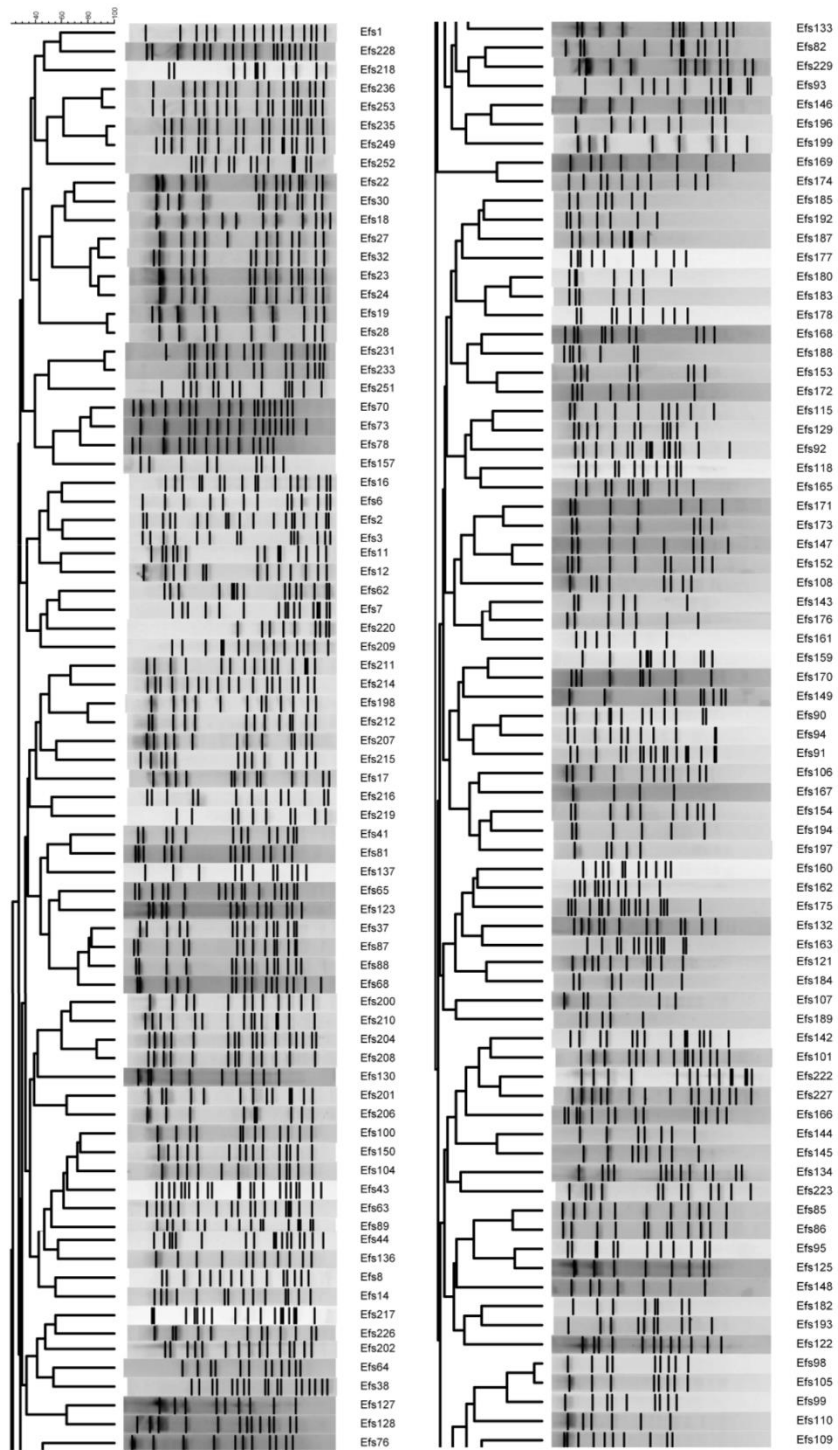


Figure S4. UPGMA dendrogram of pulsed-field gel electrophoresis (PFGE) bands patterns from the clinical isolates of *E. faecalis*.

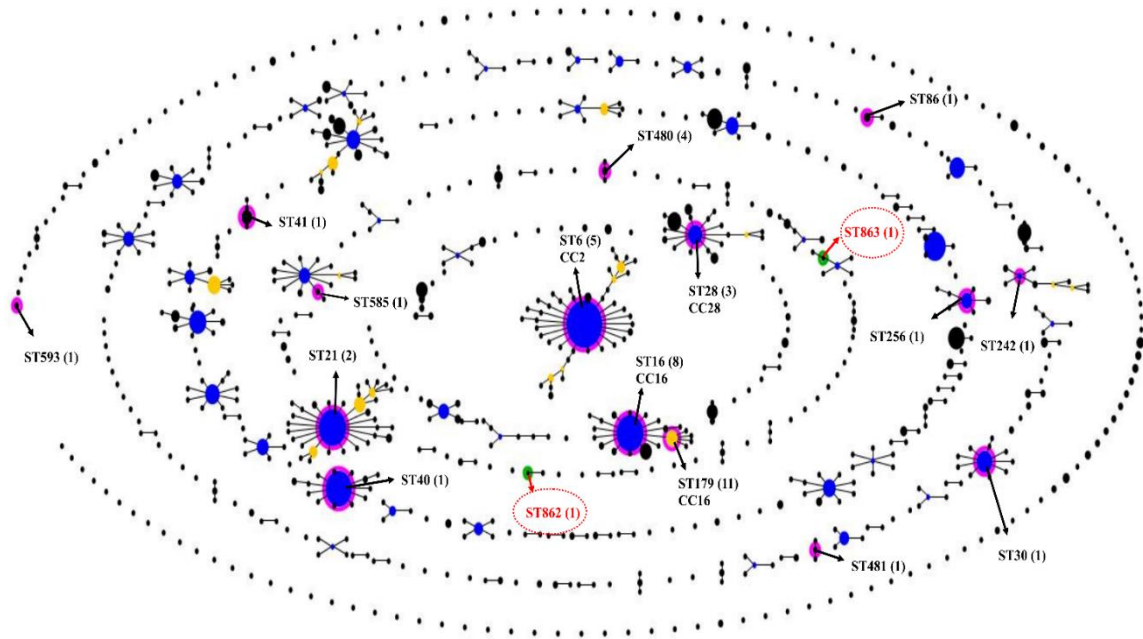


Figure S5. eBURST analysis of the STs from *E. faecalis* isolates. The pink nodes indicate the STs detected in this study that were present in the MLST database. Green nodes indicate the novel STs detected in this study and red circled.

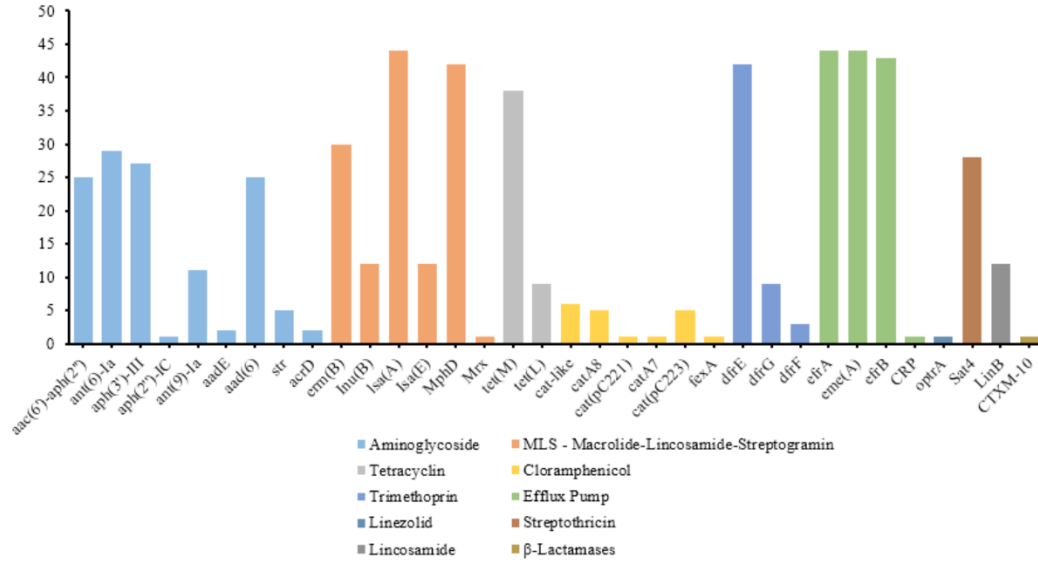


Figure S6. Distribution of antimicrobial resistance genes among clinical *E. faecalis* isolates. Total 34 ARGs and variants were retrieved from the genomes sequence of the 44 isolates. The y-axis values are expressed in number.

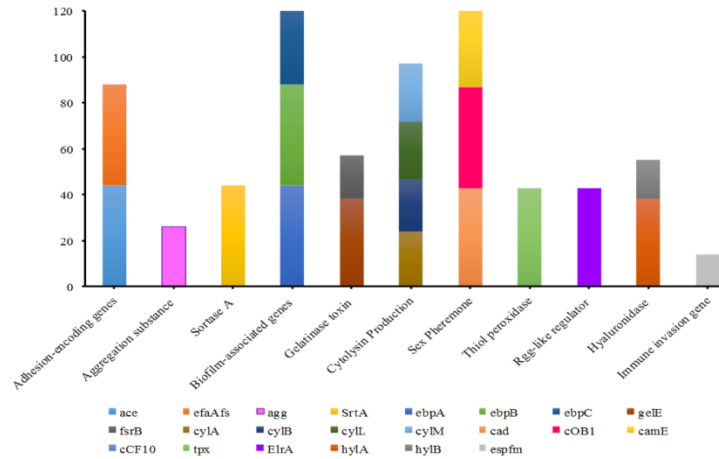


Figure S7. Distribution of virulence genes retrieved from the genomes sequence of *E. faecalis* isolates. Total 22 virulence-associated genes were identified in this study, and among them, six genes (*cOB1*, *SrtA*, *ebpB*, *ebpA*, *efaAfs*, and *ace*) were commonly found in the 44 isolates. The y-axis values are expressed in number.

Table S1. Distribution of *E. faecalis* isolates according to demographic and clinical data.

	Source	Total (155)	Inp n = 102 (65.8%)	Outp n = 53 (34.2%)	P-value	HA n = 38 (24.5%)	CA n = 117 (75.5%)	P-value
Gender	Male	83 (53.5)	62 (60.7)	21 (39.6)	0.01	24 (63.2)	59 (50.4)	0.17
	Female	72 (46.4)	40 (39.2)	32 (60.3)		14 (36.9)	58 (49.5)	
Age	≤ 1	23 (14.8)	19 (5.8)	4 (7.5)	0.07	7 (18.4)	16 (13.6)	0.61
	2-11	13 (8.3)	8 (7.8)	5 (9.4)		5 (13.5)	21 (17.9)	
	12-18	3 (1.9)	2 (1.9)	1 (1.9)		1 (2.6)	2 (1.8)	
	19-50	49 (31.6)	25 (24.5)	24 (45.2)		9 (23.6)	40 (34.1)	
	>50	67 (43.2)	48 (47)	19 (35.8)		19 (50)	48 (41.1)	
Nationality	Saudis	81 (52.2)	48 (47)	33 (62.2)	0.17	17 (44.7)	64 (54.7)	0.04
	Yemini	21 (13.5)	16 (15.6)	5 (9.4)		3 (7.9)	18 (15.3)	
	Egyptian	10 (6.4)	6 (5.8)	4 (7.5)		3 (7.9)	7 (6)	
	Indian	7 (4.5)	7 (6.8)	0		3 (7.9)	4 (3.4)	
	Palestinian	5 (3.2)	3 (2.9)	2 (3.8)		3 (7.9)	2 (1.8)	
	Eritrean	3 (1.9)	2 (1.9)	1 (1.9)		1 (2.6)	2 (1.8)	
	Bangladeshi	2 (1.2)	1 (0.9)	1 (1.9)		2 (5.2)	0	
	Others	26 (16.7)	19 (18.6)	7 (13.2)		6 (15.7)	20 (17.1)	
Specimens Type	Urine-midstream	58 (37.4)	35 (34.3)	23 (43.3)	0.03	9 (23.6)	49 (41.8)	0.05
	Urine-catheter	49 (31.6)	35 (34.3)	14 (26.4)		14 (36.9)	35 (29.9)	
	Wound swab	13 (8.3)	5 (4.9)	8 (15.1)		4 (10.5)	9 (7.7)	
	Blood	11 (7.1)	10 (9.8)	1 (1.9)		6 (15.7)	5 (4.3)	
	Others	24 (15.4)	17 (16.6)	7 (13.2)		5 (13.5)	19 (16.2)	

Inp, Inpatient; Outp, Outpatient; HA, Hospital-acquired; CA, Community-acquired.

Table S2. Distribution of insertion sequences (ISs) in the *E. faecalis* genomes.

Isolate Number	STs	Insertion sequences	IS Families
Efs6	ST480	<i>ISEf1</i>	IS256
Efs7	ST481	No hits found	-
Efs14	ST21	<i>IS6770</i>	IS30
Efs16	ST30	<i>IS6770</i>	IS30
Efs24	ST593	<i>IS16</i>	IS256
Efs30	ST41	<i>IS1062</i>	IS30
Efs41	ST21	<i>IS6770</i>	IS30
Efs44	ST16	<i>ISEf1</i>	IS256
Efs62	ST179	<i>IS6770</i>	IS30
Efs76	ST179	<i>IS6770</i>	IS30
Efs88	ST480	<i>ISEf1</i>	IS256
Efs93	ST480	<i>ISEf1</i>	IS256
Efs107	ST179	<i>IS6770</i>	IS30
Efs110	ST16	<i>ISEf1</i>	IS256
Efs122	ST179	<i>IS6770</i>	IS30
Efs128	ST16	<i>ISEf1</i>	IS256
Efs133	ST40	<i>IS6770</i>	IS30
Efs136	ST179	<i>IS6770</i>	IS30
Efs142	ST28	<i>ISEnfa2</i>	IS1182
Efs144	ST86	<i>ISEnfa364</i>	IS30
Efs145	ST28	<i>ISEnfa2</i>	IS1182
Efs149	ST179	<i>IS6770</i>	IS30
Efs153	ST6	<i>IS6770</i>	IS30
Efs154	ST179	<i>IS6770</i>	IS30
Efs162	ST862	<i>IS6770</i>	IS30
Efs163	ST16	<i>ISEf1</i>	IS256
Efs165	ST179	<i>IS6770</i>	IS30
Efs166	ST6	<i>IS6770</i>	IS30
Efs171	ST28	<i>ISEnfa2</i>	IS1182
Efs173	ST863	<i>ISEf1</i>	IS256
Efs175	ST16	<i>ISEf1</i>	IS256
Efs178	ST16	<i>ISEf1</i>	IS256
Efs180	ST179	<i>IS6770</i>	IS30

Efs183	ST585	<i>ISEf1</i>	IS256
Efs185	ST16	<i>ISEf1</i>	IS256
Efs187	ST179	<i>IS6770</i>	IS30
Efs189	ST179	<i>IS6770</i>	IS30
Efs196	ST6	<i>ISEf1</i>	IS256
Efs197	ST6	<i>IS6770</i>	IS30
Efs208	ST480	<i>ISEf1</i>	IS256
Efs210	ST16	<i>ISEf1</i>	IS256
Efs212	ST6	<i>IS6770</i>	IS30
Efs215	ST256	<i>IS1062</i>	IS30
Efs216	ST242	<i>ISEnfa364</i>	IS30