Supplementary data

Table S1: Distribution of linezolid resistance genetic determinants among the collected enterococcal isolates regarding linezolid susceptibility

linezolid resistance genetic determinants (n=39)		
Linezolid-resistant isolates (n=12) (30.8%)	**Linezolid-susceptible isolates (n=27) (69.2%)**	
E. faecium (OptrA)	***E. faecium (PoxtA)***	***E. faecium (OptrA)***
E. faecium (23s r RNA mutation)	***E. faecium (PoxtA)***	***E. faecium (OptrA)***
E. faecium (23s r RNA mutation)	***E. faecium (PoxtA)***	***E. faecium (PoxtA+OptrA)***
E. faecium (23s r RNA mutation)	***E. faecium (PoxtA)***	***E. faecalis (OptrA)***
E.faecium (PoxtA+OptrA)	***E. faecium (PoxtA)***	***E. faecalis (OptrA)***
E.faecium (PoxtA+OptrA)	***E. faecium (PoxtA)***	***E. faecalis (OptrA)***
E.faecium(PoxtA+OptrA)	***E. faecium (PoxtA)***	***E. faecalis (OptrA)***
E. faecium (PoxtA, OptrA)	***E. faecium (PoxtA)***	***E. faecalis (OptrA)***
E.faecalis (OptrA+ poxtA+ mutation)	***E. faecium (OptrA)***	***E. faecalis (PoxtA)***
E.faecalis(optrA)	***E. faecium (OptrA)***	***E. faecalis (PoxtA)***
E.faecalis(OptrA)	***E. faecium (OptrA)***	***E. faecalis (PoxtA)***
E.faecalis (PoxtA)	***E. faecium (OptrA)***	***E. faecalis (PoxtA)***
optrA +poxtA+ 23S r RNA mutation=1 (8.3 %) *PoxtA+ optrA*=4 (33.3%) 23S r RNA mutation= 3 (25%) *PoxtA* alone = 1 (8.3%) *optrA* alone=3 (25%)	***E. faecium (OptrA)***	***E. faecalis (PoxtA)***
	E. faecium with poxtA=8 (29.6) *E.faecium with optrA=7 (25.9)* *E. faecium with PoxtA +OptrA =1(3.7)*	***E. faecalis (PoxtA)***
		E. faecalis with optrA=5 (18.5) *E. faecalis with poxtA=6 (22.2)*

Table S2: Genotypic Analysis of *E. faecalis* and *E. faecium* Isolates: Transferable Linezolid Resistance Genes and 23S rRNA Mutations (Sample Size: 100)

Variables	*E. faecalis* (n=56)		*E. faecium* (n=44)		Total (n=100)		Test of significance	p-value
	No.	%	No.	%	No.	%		
PoxtA								
Present	7	12.5	8	18.2	15	15	$\chi 2$=0.62	>0.05
Absent	49	87.5	36	81.8	85	85		(NS)
OptrA								
Present	7	12.5	8	18.2	15	15	$\chi 2$=0.62	>0.05
Absent	49	87.5	36	81.8	85	85		(NS)
Co-existence of *OptrA* +*PoxtA*								
Present	1	1.8	5	11.4	6	6	$\chi 2$= 4.01	<0.05
Absent	55	98.2	39	88.6	94	94		
23 S rRNA mutation (G2505A)								
Variable	*E. faecalis* (n=4)		*E. faecium* (n =8)		Total (n=12)		Test of significance	p-value
	No.	%	No.	%	No.	%		
Present	1	25	3	37.5	4	33.3	FE	>0.05
Absent	3	75	5	62.5	8	66.6		(NS)

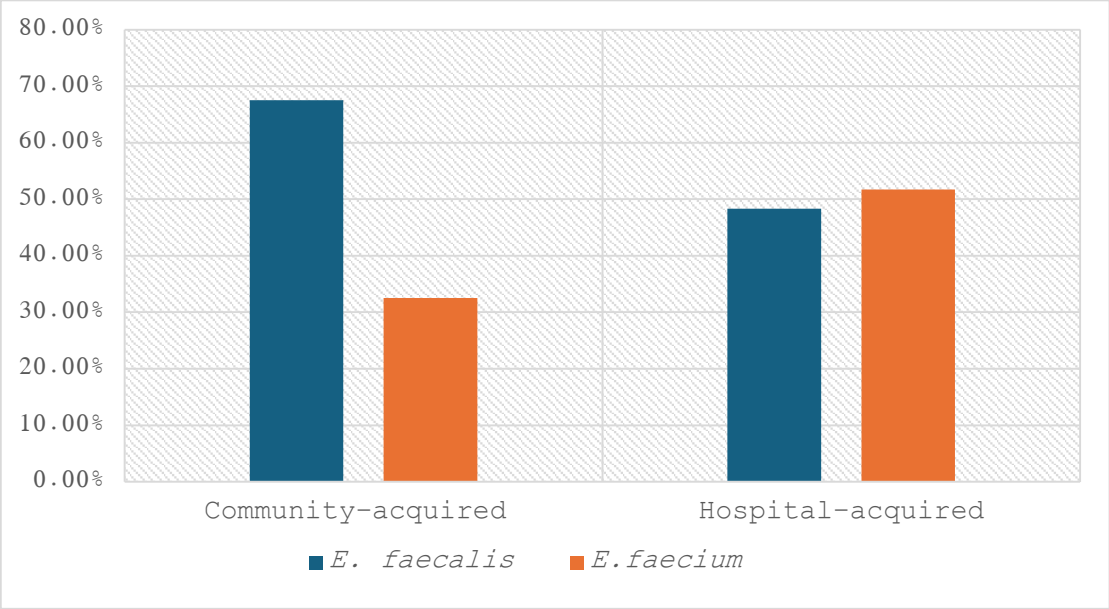

Figure (S1): Distribution of *Enterococcus* spp. isolates according to the source of infection