AMENDED ABSTRACT

Background: JNJ-Q2 is a broad-spectrum bactericidal fluoroquinolone (FQ) with potent activity against Grampositive pathogens including methicillin-resistant (MR) S. aureus (SA), Gram-negative pathogens, atypical respiratory pathogens, and anaerobic pathogens and is in clinical development for the treatment of acute bacterial skin and skin structure infection (ABSSSI) and communityacquired bacterial pneumonia. In this study, the in vitro activity of JNJ-Q2 and other FQ agents was evaluated against a panel of genetically defined strains representative of global MRSA clones.

Methods: A collection of 111 genetically defined SA strains (predominantly MRSA [103/111, 92.8%]) representative of the major circulating global clones were evaluated. Along with the groups specified in the table (below), USA PFGE types 100 to 1100 (not 900), SCCmec types I to IV (and IVa), agr types I to IV, and PVL-positive strains were all represented. Isolates were tested against JNJ-Q2, moxifloxacin (MOX), levofloxacin (LEV), and other comparator agents per the CLSI broth microdilution method (M07-A8; M100-S21).

Results: Overall, JNJ-Q2 inhibited all 111 major circulating S. aureus clones at $\leq 1 \mu g/ml$. MOX and LEV demonstrated high levels of resistance (R) to these strains (69.4 and 73.9%, respectively). JNJ-Q2 inhibited all ten VRSA strains at a MIC of $\leq 1 \mu g/ml$ and all ten were R to MOX and LEV. JNJ-Q2 was also very active against strains R to comparator agents (n strains): daptomycin (7), linezolid (5), tetracycline (32), trimethoprim-sulfamethoxazole (13), erythromycin (86) and clindamycin (41).

Conclusion: JNJ-Q2 retained activity against these subsets of challenging strains regardless of antimicrobial resistance phenotype, ST or PFGE clonal types, PVL positivity, and agr or SCCmec type. These JNJ-Q2 in vitro results against major global MRSA clones are very promising and support further clinical development of this new FQ for treatment of ABSSSI.

Abstract Table							
	JNJ-	·Q2	Levo	ofloxacin	Moxifloxacin		
Group or clone (n)	MIC _{50/90}	Range	MIC _{50/90}	Range	MIC _{50/90}	Range	
All strains (111)	0.12/0.25	≤0.06 – 1	8/32	0.12->128	2/8	≤0.06 - >128	
ST239ª (12)	0.25/0.25	0.12-0.25	16/32	4-32	4/8	1->128	
ST8 USA300 (23)	≤0.06/0.12	≤0.06-1	0.25/4	0.12-4	1/2	≤0.06-2	
ST22 [♭] (15)	0.12/0.25	≤0.06-0.5	8/32	0.12-32	2/8	≤0.06-8	
ST5° (5)	0.12/-	0.12-1	8/-	8-16	2/-	2-4	
ST5 USA100 (6)	0.25/-	0.25-1	32/-	32->128	8/-	4-32	
VRSA (10)	0.25/0.25	0.12-1	16/64	16->128	8/8	4-32	
 a. ST239 Hungarian/Brazilian. b. ST22 EMRSA-15. 							

INTRODUCTION

JNJ-Q2 is a novel fluorinated 4-quinolone with potent activity against Gram-positive (including MRSA) and Gram-negative pathogens that has been demonstrated to have balanced potency against DNA gyrase and topoisomerase IV. JNJ-Q2 is in clinical development for the treatment of acute bacterial skin and skin structure infections (ABSSSI's) and community-acquired bacterial pneumonia (CABP).

Previously, JNJ-Q2 was shown to be active against 511 selected S. aureus isolates (including 308 fluoroquinoloneresistant MRSA) collected between 2008 to 2009, with levofloxacin/JNJ-Q2 MIC₅₀ values, MIC₉₀ values, and MIC ranges of 8/0.12, >16/0.5 and 0.12 - >16/≤0.008 - 4 µg/ml, respectively.

The objective of this study was to determine the in vitro activity of JNJ-Q2 tested against a panel of genetically defined strains representative of global MRSA clones.

MATERIALS AND METHODS

Susceptibility testing. MIC values were determined using the reference CLSI broth microdilution method as described in M07-A8 [2009]. For the four tested fluoroquinolones: 96well, frozen-form panels were produced by JMI Laboratories (North Liberty, Iowa, USA) consisting of one media type e.g. cation-adjusted Mueller-Hinton broth. For the comparator agents, the MIC data was obtained from the SENTRY Antimicrobial Surveillance Program database.

Quality Control (QC) was performed daily during the testing period and inoculum density was monitored by colony counts. QC ranges and interpretive criteria for the comparator compounds were as published in CLSI M100-S21 [2011]; tested QC strains included S. aureus ATCC 29213 and Enterococcus faecalis ATCC 29212. All QC values were within specified ranges.

Bacterial isolates. A collection of 111 genetically defined S. aureus strains (predominantly MRSA [103/111, 92.8%]) representative of the major circulating global clones were evaluated. These strains were from two sources: 1) clinical isolates from the JMI Laboratories bacterial strain collection; and 2) the Network on Antimicrobial Resistance in Staphylococcus aureus (NARSA), funded by the National Institute of Allergy and Infectious Diseases.

The following strains were tested:

• NARSA strains (30) included USA100 to 1100 clones (except for USA900), linezolid- and tigecycline-resistant strains, vancomycin-intermediate strains (VISA), strains positive for several toxin genes including Panton-Valentine Leukocidin (PVL).

c. ST5 Cordobes/Chilian.

Activity of JNJ-Q2 and Comparators against Genetically Defined MRSA Clones

D.J. FARRELL¹, L.C. LIVERMAN², R.E. MENDES¹, D.J. BIEDENBACH¹, R.N. JONES¹ ¹JMI Laboratories, North Liberty, Iowa, USA and ²Furiex Pharmaceuticals Inc., Morrisville, North Carolina, USA

- NARSA vancomycin-resistant S. aureus strains (VRSA,
- ST239; Hungarian/Brazilian clone; SCCmec III (12 strains from 5 different countries)
- ST8; USA300; SCCmec IV; PVL-positive (23 clinical strains from the USA)
- ST22; EMRSA-15; European clone; SCCmec IV; PVLnegative (15 strains from 4 countries).
- ST5; Cordobes/Chilean clone; SCCmec I (5 strains from 4 countries)
- ST5; USA100 (6)
- Others (10)

RESULTS

- All strains combined (111 strains, Tables 1 and 2). The MIC distributions of JNJ-Q2 and comparison fluoroquinolones against all 111 strains are summarized in Table 1. JNJ-Q2 displayed very high potency (MIC_{50/90}, 0.12/0.25 µg/ml) against this panel of strains inhibiting all 111 strains at a MIC of $\leq 1 \mu g/ml$. Using MIC₅₀, JNJ-Q2 demonstrated 16-, 64-, and 256-fold greater activity than moxifloxacin (69.4% resistant), levofloxacin (73.9% resistant) and ciprofloxacin (74.8% [75.7% by EUCAST criteria] resistant), respectively (Tables 1 and 2). Overall, 92.8% of strains were oxacillin resistant and resistance was high against erythromycin (77.5%), clindamycin (36.9 - 38.9%), tetracycline (28.8 -30.6%) and trimethoprim/sulphamethoxazole (18.9%).
- NARSA strains (30 strains; Table 3). Against this reference panel of strains representing the major worldwide clones of MRSA, JNJ-Q2 inhibited all strains at $\leq 1 \mu g/ml$ and with a MIC_{50/90} of 0.12/0.25 µg/ml that was 16-, 64- and 128-fold more active than moxifloxacin, levofloxacin and ciprofloxacin using MIC₅₀ values, respectively.
- <u>VRSA (10 strains; Table 3)</u>. JNJ-Q2 was the most active fluoroquinolone tested against VRSA (MIC_{50/90}, 0.25/0.25 µg/ml, Table 3). Significantly, all ten VRSA strains were resistant to moxifloxacin (MIC₅₀, 8 μ g/ml), levofloxacin (MIC₅₀, 16 μ g/ml) and ciprofloxacin (MIC₅₀, 64 μ g/ml)
- ST239 Hungarian/Brazilian clone (12 strains; Table 3). This MRSA clone is prevalent in Europe and Latin America and increasing in prevalence in North America. JNJ-Q2 was also the most active fluoroquinolone tested against the ST239 Hungarian/Brazilian clone (MIC_{50/90}, 0.25/0.25 µg/ml, Table 3). The highest JNJ-Q2 MIC observed was only 0.25 µg/ml.
- ST8 USA300 (23 strains; Table 3). ST8 USA300 is the clone responsible for the majority of cases of communityacquired (CA-) MRSA in the USA and displayed the lowest fluoroquinolone MIC₅₀ results among all groups analyzed (ranging from ≤0.06 [for JNJ-Q2] to 8 µg/ml [for ciprofloxacin]; Table 3).

- µg/ml)
- with all MIC values $\leq 1 \mu g/ml$.

Table 1. MI all 111 S. au	•	icy and c	umulativ	e percent	t inhibitec	l distribut	ions of JI	NJ-463 a	nd comp	arator flu	oroquino	lone antii	microbial	agents a	gainst
Antimicrobial				Ν	lo. (cumulativ	/e %) of strair	ns inhibited a	t antimicrobia	al MIC (µg/ml):					
agent	≤0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	>128	MIC ₅₀	MIC ₉₀
JNJ-463	31 (27.9)	32 (56.8)	41 (93.7)	1 (94.6)	6 (100.0)									0.12	0.25
Ciprofloxacin	_a	1 (0.9)	14 (13.5)	11 (23.4)	1 (24.3)	1 (25.2)	0 (25.2)	7 (31.5)	14 (44.1)	13 (55.9)	24 (77.5)	15 (91.0)	10(100.0)	32	128
Levofloxacin	0 (0.0)	11 (9.9)	16 (24.3)	1 (25.2)	0 (25.2)	1 (26.1)	13 (37.8)	25 (60.4)	23 (81.1)	12 (91.9)	3 (94.6)	0(94.6)	6(100.0)	8	32
Moxifloxacin	25 (22.5)	3 (25.2)	0 (25.2)	0 (25.2)	6 (30.6)	37 (64.0)	19 (81.1)	14 (93.7)	0 (93.7)	6 (99.1)	0 (99.1)	0(99.1)	1(100.0)	2	8
a. Ciprofloxacin w	as not tested a	t this concentr	ation and hence	ce the isolate a	at 0.12 µg/ml is	actually ≤0.12	2 μg/ml.								

Table 2. Activity	of JNJ-G	2 and c	omparator ar	ntimicrobial	agents whe	en tested against all 111	S. aureu	s strains.			
Antimicrobial agent	MIC ₅₀	MIC ₉₀	Range	CLSIª %S / %R	EUCASTª %S / %R	Antimicrobial agent	MIC ₅₀	MIC ₉₀	Range	CLSIª %S / %R	EUCASTª %S / %R
JNJ-Q2	0.12	0.25	≤0.06 – 1	- / -	- / -	Clindamycin	≤0.25	>2	≤0.25 - >2	61.3 / 36.9	59.5 / 38.7
Ciprofloxacin	32	128	≤0.12 – >128	24.3/74.8	24.3 / 75.7	Daptomycin	0.5	1	0.12 – >8	93.7 / -	93.7 / 6.3
Levofloxacin	8	32	0.12 – >128	25.2 / 73.9	25.2 / 73.9	Vancomycin	1	8	≤0.12 – >16	83.8 / 9.0	83.8 / 16.2
Moxifloxacin	2	8	≤0.06 – >128	25.2 / 69.4	25.2 / 69.4	Linezolid	1	2	0.5 ->8	95.5 / 4.5	95.5 / 4.5
Oxacillin	>2	>2	≤0.25 - >2	7.2/92.8	7.2/92.8	Tetracycline	≤2	>8	≤2 – >8	71.2 / 28.8	68.5 / 30.6
Erythromycin	>2	>2	≤0.25 – >2	22.5 / 77.5	22.5 / 77.5	Trimethoprim/sulfamethoxazole	≤0.5	>2	≤0.5−>2	81.1 / 18.9	81.1 / 18.9
a. Criteria as published	by the CLSI (C	LSI, 2011) ar	IN EUCAST (EUCAS	ST, 2011).							

Group or clone (n) NARSA strains (30) VRSA (10) ST239 Hungarian/Brazilian (12) ST8 USA300 (23) ST22 EMRSA-15 (15) ST5 Cordobes/Chilian (5) ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> I (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42) SCCmec type IV-A (3)	
VRSA (10) ST239 Hungarian/Brazilian (12) ST8 USA300 (23) ST22 EMRSA-15 (15) ST5 Cordobes/Chilian (5) ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) pvl positive (8) agrl (4) agrl (2) agrl (2) agrl (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	Group or clone (n)
ST239 Hungarian/Brazilian (12) ST8 USA300 (23) ST22 EMRSA-15 (15) ST5 Cordobes/Chilian (5) ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA600 (1) USA500 (2) USA600 (1) USA700 (1) USA1000 (1) USA1000 (1) Other genetic markers (n) pvl positive (8) agrl (4) agrl (2) agrl (2) agrl (2) agrl (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	NARSA strains (30)
ST8 USA300 (23) ST22 EMRSA-15 (15) ST5 Cordobes/Chilian (5) ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	VRSA (10)
ST22 EMRSA-15 (15) ST5 Cordobes/Chilian (5) ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA300 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	ST239 Hungarian/Brazilian (12)
ST5 Cordobes/Chilian (5) ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	ST8 USA300 (23)
ST5 USA100 (6) USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>s</i> CCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	ST22 EMRSA-15 (15)
USA PFGE types (n) USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	ST5 Cordobes/Chilian (5)
USA100 (7) USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	ST5 USA100 (6)
USA200 (1) USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	USA PFGE types (n)
USA300 (24) USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
USA400 (2) USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
USA500 (2) USA600 (1) USA700 (1) USA700 (1) USA1000 (1) USA1000 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (1) SCCmec type I (11) SCCmec type II (3) SCCmec type IV (42)	
USA600 (1) USA700 (1) USA800 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
USA700 (1) USA800 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
USA800 (1) USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (2) <i>agr</i> l (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
USA1000 (1) USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> lI (2) <i>agr</i> lI (2) <i>agr</i> lV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	()
USA1100 (1) Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> l (4) <i>agr</i> ll (2) <i>agr</i> ll (2) <i>agr</i> lV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
Other genetic markers (n) <i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> III (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
<i>pvl</i> positive (8) <i>agr</i> I (4) <i>agr</i> II (2) <i>agr</i> IV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	()
agrl (4) agrll (2) agrll (2) agrlV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	U
agrII (2) agrIII (2) agrIV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
agrIII (2) agrIV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	
agrIV (1) SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	2 ()
SCCmec type I (11) SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	U ()
SCCmec type II (3) SCCmec type III (12) SCCmec type IV (42)	S ()
SCCmec type III (12) SCCmec type IV (42)	
SCCmec type IV (42)	
, , , ,	
SCCmec type IV-A (3)	
	SCCmec type IV-A (3)

 <u>ST22 EMRSA-15 clone (15 strains; Tables 3)</u>. This clone is the predominant clone causing hospital infection in the United Kingdom. JNJ-Q2 was very active ($MIC_{50/90}$, 0.12/0.25 µg/ml, Table 3) against this clone and demonstrated much greater activities than the fluoroquinolone comparators (MIC₅₀ values of 2 - 64

 ST5 – USA100 (6 strains) and Cordobes/Chilian clone (5 strains; Table 3). Again, JNJ-Q2 was the most active fluoroquinolone agent against these clones with all strains being inhibited at a MIC $\leq 1 \mu g/ml$ compared to MIC values as high as >128 μ g/ml for comparator fluoroquinolones.

• <u>USA PFGE types (Table 3)</u>. JNJ-Q2 demonstrated high activity against the known USA PFGE types 100 to 1100

• <u>PVL positive strains (8 strains; Table 3)</u>. All eight PVLpositive strains tested were inhibited by both JNJ-Q2 and moxifloxacin MIC values of $\leq 0.06 \mu g/ml$.

- agr and SCCmec types (Table 3). JNJ-Q2 demonstrated high activity against all strains tested with known agr and SCCmec types. The highest JNJ-Q2 MIC₉₀ for any subgroup of strains tested was 1 µg/ml against strains with SCC*mec* type I; corresponding MIC₉₀ values for moxifloxacin, levofloxacin and ciprofloxacin were manyfold higher.
- <u>Daptomycin-resistant strains</u>. Seven strains were resistant to daptomycin and the JNJ-Q2 MIC values for these strains were $\leq 0.06 \ \mu g/ml$ (2 strains), 0.12 $\mu g/ml$ (2 strains) and 0.25 μ g/ml (3 strains).
- Vancomycin non-susceptible strains. Two strains were vancomycin-intermediate and the JNJ-Q2 MIC value for both strains was 0.25 µg/ml. Ten strains were VRSA and the JNJ-463 MIC values for these strains were 0.12 µg/ml (2 strains), 0.25 μ g/ml (7 strains) and 1 μ g/ml (1 strain).
- Linezolid-resistant strains. Five strains were resistant to linezolid and the JNJ-Q2 MIC values for these strains were $\leq 0.06 \ \mu g/ml$ (1 strain) and 0.25 $\mu g/ml$ (4 strains).

Table 3. Activities of JNJ-Q2, ciprofloxacin, levofloxacin and moxifloxacin by reference group, clonal group, and other genetic markers. JNJ-Q2 Ciprofloxacin Moxifloxacin evofloxaci MIC_{50/90} 0.12/0.25 MIC_{50/90} 16/128 MIC_{50/90} 8/16 Range ≤0.06-32 Range ≤0.06->128 Range 0.12->128 Range ≤0.06-1 0.25/0.25 0.12-1 64/128 16/64 16->128 32->128 4-32 0.25/0.25 0.12-0.25 64/128 8-128 16/32 4-32 1->128 ≤0.06/0.12 ≤0.06-1 0.25-32 0.25/4 0.12-4 ≤0.06-2 8/16 1/20.12/0.25 ≤0.06-0.5 8/32 0.12-32 ≤0.06-8 64/>128 025->128 0.12/-0.12-1 32/-16-64 8-16 2-4 0.25/-0.25-1 >128/-32->128 4-32 128->128 ≤0.06-1 8->128 2-32 0.25/-16->128 >128/-0.25 64 16 4 ≤0.06/0.12 ≤0.06-0.25 0.25/16 0.25-32 0.5/4 0.12-8 0.12/2 ≤0.06-2 ≤0.06 0.12-0.25 ≤0.06 -/-0.25 2-4 0.25 ≤0.06 0.5 0.25 ≤0.06 ≤0.06 0.5 0.25 ≤0.06 ≤0.06 0.25 ≤0.06 -/-0.25 ≤0.06 ≤0.06 ≤0.06 0.25-1 0.12-0.25 ≤0.06/-0.25/-0.12/-≤0.06/-≤0.06-0.25 0.5-64 0.25-16 ≤0.06-4 ≤0.06-0.12 0.5-16 0.25-8 ≤0.06-2 ≤0.06-0.25 0.25-64 0.25-16 ≤0.06-4 ≤0.06 0.25 ≤0.06 1 128/>128 32/>128 0.12/1 0.12-1 16->128 8->128 4/32 2-32 0.12-0.25 16-64 8-16 2-4 -/-0.25/0.25 64/128 16/32 1->128 8-128 4-32 0.12-0.25 4/8 0.12-32 ≤0.06-8 0.12/0.25 ≤0.06-0.5 8/64 0.25->128 4/16 0.25-0.5 ≤0.06-0.12 ≤0.06 0.25-2

IDSA 2011

JMI Laboratories North Liberty, IA, USA www.jmilabs.com 319.665.3370, fax 319.665.3371 david-farrell@jmilabs.com

CONCLUSIONS

- Overall, JNJ-Q2 inhibited a panel of 111 major circulating S. aureus clones (92.8% MRSA) at MIC values of $\leq 1 \mu g/ml$ (MIC_{50/90}, 0.12/0.25) µg/ml). These strains demonstrated high levels of resistance to comparator fluoroquinolones (69.4 to 74.8%) using contemporary CLSI and EUCAST breakpoints.
- JNJ-Q2 inhibited all ten VRSA strains at a MIC of ≤1 µg/ml (MIC_{50/90}, 0.25/0.25 µg/ml). All ten strains were resistant to moxifloxacin. levofloxacin and ciprofloxacin.
- JNJ-Q2 retained activity (MIC₉₀, 0.12 to 1 μ g/ml) against these sub-sets of challenging strains regardless of antimicrobial resistance phenotype, ST or PFGE clonal types, PVL positivity, and agr or SCC*mec* type.

ACKNOWLEDGEMENTS

This study was funded by a research grant from Furiex Pharmaceuticals Inc., Morrisville, North Carolina, USA

REFERENCES

- Clinical and Laboratory Standards Institute (2009). M07-A8. Methods for dilution antimicrobial susceptibility tests for bacteria that grow aerobically; approved standard: eighth edition. Wayne, PA: CLSI.
- Clinical and Laboratory Standards Institute (2011). M100-S21. Performance standards for antimicrobial susceptibility testing: 21st informational supplement. Wayne, PA: CLSI.
- 3. EUCAST (2011). Breakpoint tables for interpretation of MICs and zone diameters. Version 1.3, January 2011. Available at http://www.eucast.org/clinical_breakpoints/
- 4. Farrell, DJ, Liverman, LC, Biedenbach, DJ, & Jones, RN (2011) JNJ-Q2, a new fluoroquinolone with potent in vitro activity against Staphylococcus aureus, including methicillin- and fluoroquinolone-resistant strains. Antimicrob Agents Chemother, 55, 3631-3634.
- 5. Morrow, BJ, He, W, Amsler, KM, Foleno, BD, Macielag, MJ, Lynch, AS, & Bush, K (2010) In vitro antibacterial activities of JNJ-Q2, a new broad-spectrum fluoroquinolone. Antimicrob Agents Chemother, 54, 1955-1964.