ERRATUM

Molecular Analysis of Antimicrobial Resistance Mechanisms in *Neisseria gonorrhoeae* Isolates from Ontario, Canada

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Volume 55, no. 2, p 703–712, 2011. Page 707: the “PBP 2 pattern” column of Table 4 is incorrect and should appear as shown below.

TABLE 4 *N. gonorrhoeae* isolates with reduced susceptibility to CFM and CRO ($n = 14$)^a

MIC (μg/ml)									
PEN	CFM	CRO	Porin PIB (<i>porB</i>)	PBP 1 (<i>ponA</i>)	PBP 2 pattern	<i>mtrR</i> promoter	MtrR	ST	No. of isolates
2	0.25	0.125	G120K, A121D	L421P	XXXVI	Deletion A	WT	225	1
2	0.25	0.125	WT	L421P	XXXV	Deletion A	G45D	299	1
1	0.25	0.125	G120K, A121N	WT	XXXIV	Deletion A	WT	3158	3
1	0.125	0.125	WT	WT	XXXVII	Deletion A	WT	546	1
0.5	0.125	0.125	G120K, A121N	WT	XXXVIII	Deletion A	WT	3596	1
1	0.125	0.063	G120K, A121N	L421P	XXXIV	Insertion T	WT	3158	1
1	0.125	0.063	G120K, A121N	L421P	XXXIV	Deletion A	WT	3158	1
2	0.125	0.063	G120K, A121N	L421P	XXXIV	Deletion A	WT	3570	1
2	0.125	0.063	A121S	L421P	XXXIV	Deletion A	WT	3116	1
1	0.125	0.063	G120K, A121N	L421P	XXXIV	Deletion A	WT	3563	1
1	0.125	0.063	WT	WT	XXXVI	WT	WT	51	1
0.5	0.125	0.032	WT	WT	XXXIV	Deletion A	WT	3553	1

^a Classified by β-lactam MICs, amino acid alterations in porin PIB, PBP 1 and 2, repressor MtrR and mutations in the *mtrR* promoter.

Page 706, right column, line 24: “The most common PBP 2 type found in this study was the sequence pattern XXXVIII (9/13 isolates, 5 of them belonging to ST3158)” should read “The most common PBP 2 type found in this study was the sequence pattern XXXIV (9/14 isolates, 5 of them belonging to ST3158).”

Page 708, Figure 2: in the upper left portion of the figure, the PBP 2 patterns and numbers of isolates should be XXXIV (9), XXXV (1), XXXVI (2), XXXVII (1), and XXXVIII (1).