

Supplementary tables

***Helicobacter pylori* infections in the Bronx, New York: Surveying Antibiotic Susceptibility and Strain Lineage by Whole-genome Sequencing**

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Supplementary Table 1: Amino acid substitutions in PBPs among amoxicillin resistant isolates and loci of nearby putative amoxicillin binding motifs

Sl no	Isolate ID	Amino acid substitutions in PBPs – exclusively		
		observed in resistant isolates		Nearby motifs'
		Protein name	Amino acid changes	
1	MHP11	Pbp1A	I259T	SSN ₂₃₆₋₂₃₈
		Pbp2	None	-
		Pbp3	D2N	-
			A50S	-
			F490Y	SARK ₄₉₇₋₅₀₀
A541T	KTG ₅₂₇₋₅₂₉ , SYN ₅₄₃₋₅₄₅ , SHGK ₅₆₈₋₅₇₂			
2	MHP12	Pbp1A	None	-
		Pbp2	T498S	KTG ₅₁₃₋₅₁₅
		Pbp3	None	-
3	MHP22	Pbp1A	N107R	-
			A201V	-
			V250I	SSN ₂₃₆₋₂₃₈
			S543T	SSN ₅₆₀₋₅₆₂
		Pbp2	None	-
		Pbp3	V374I	SSN ₃₈₂₋₃₈₄ , SKN ₃₉₁₋₃₉₃

		frxA mutations																									
26695		V	V	A	Q	A	P	1	G	R	A	F	G	A	T	N	R	I	M	N	S	A	E	E	N	C	Nonsense mutation
Isolate ID	MIC	6	7	16	27	32	41	44	45	58	70	72	73	85	110	111	113	117	126	129	130	154	169	176	182	193	
MHP08	>256				V								S										K				
MHP09	>256	I	I	T	E	V						S	S			H					T	D			D	S	109 stop
MHP10	>256		I	T		V		V				S	S	V		D											S
MHP13	>256	I	I	T	E	V					G	S	S			H					T	D		K		S	
MHP16	>256		I													I	G										109 stop
MHP17	>256	I	I	T	E	V					G	S	S			H					T	D				S	
MHP18	>256		I		E	V						S	S														
MHP20	>256		I																				K				
MHP28	>256	I	I	T	E	V					G	S	S			H					T	D				S	74 stop
MHP32	>256	I	I	T	E	V					G	S	S			H					T	D				S	74 stop
MHP34	>256	I	I	T	E	V					G	S	S			H					T	D		K		S	74 stop
MHP36	>256		I								C			V													
MHP37	>256	I	I	T																							
MHP40	>256	I	I	T	E	V					G	S	S		S						T	D			D	S	74 stop
MHP44	>256	I	I	T	E	V					G	S	S			H			I							S	74 stop
MHP47	>256	I	I	T	E	V					G	S	S			H					T	D		K		S	74 stop
MHP50	>256	I	I	T	E	V					G	S	S		S				I							S	74 stop
MHP52	>256	I	I	T	E	V					G	S	S		S					I							S
MHP54	>256	I	I	T	E	V					G	S	S			H					T	D				S	74 stop
MHP01	0.38	I	I	T	E	V					G	S	S			H					T	D			D	S	74 stop
MHP02	0.047	I	I	T	E	V					G	S	S			H					T	D				S	
MHP03	0.5		I	T		V							S			D											
MHP04	0.19		I		E	V							S														39 stop
MHP05	0.032	I	I	T	E	V					G	S	S			H					T	D		K	D	S	
MHP06	0.25	I	I	T	E	V					G	S	S			H					T	D		K	D	S	74 stop
MHP11	0.75	I	I	T	E	V							S														
MHP12	0.75	I	I	T	E	V					G	S	S			H					T	D		K		S	39 stop
MHP15	0.19	I	I	T	E	V					G	S	S			H					T	D		K		S	
MHP19	0.5	I	I	T																		V					
MHP22	0.125	I	I	T	E	V					G	S	S								T	D			D	S	74 stop
MHP23	0.016	I	I	T	E	V					G	S	S			H					T	D				S	
MHP29	0.064	I	I	T											S							T	D			D	S
MHP30	0.125																										
MHP31	0.38	I	I	T	E	V					G	S	S			H					T	D				S	74 stop
MHP33	0.032	I	I	T	E	V					G	S	S			H					T	D		K		S	74 stop
MHP35	0.125	I	I	T	E	V					G	S	S			H					T	D				S	74 stop
MHP38	0.094	I	I	T																							
MHP39	0.38	I	I	T	E	V					G	S	S			H					T	D				S	
MHP41	0.016	I	I	T	E	V						S	S			H				I	T	D	T	K	D	S	
MHP42	0.032	I	I	T	E	V					G	S	S		S	H				I					K	D	S
MHP43	0.016	I	I	T	E	V				R	G	S	S			H					T	D		K		S	
MHP51	0.19						T										M		F								

* Amino acid substitutions in *rdxA* and *frxA*, which are exclusively noticed in resistant isolates were highlighted in green

‡ Isolates with truncations in *rdxA* and *frxA* (nonsense codon substitutions) are highlighted in orange