CORRECTION

Correction: Clinical Impact of MALDI-TOF MS Identification and Rapid Susceptibility Testing on Adequate Antimicrobial Treatment in Sepsis with Positive Blood Cultures

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There are numerical errors in the first and penultimate sentences of the second paragraph of the Results under the subheading "Rapid identification and susceptibility test performances." The correct paragraph is: βLT performed on 164 BSI (P1 and P2 combined) yielded 24 positive, 139 negative and 1 uninterpretable test result due to an incoherent color change of the chromogenic test. All positive βLT results were found in non-natural AmpC EB isolates displaying third generation cephalosporin resistance by complete AST results and subsequently confirmed as ESBL producers. In 7 cases, βLT yielded false-negative results since complete AST and molecular testing identified 6 AmpC producing *Escherichia coli* and 1 VIM metallo-beta-lactamase-producing *P. aeruginosa*, all resistant to third generation cephalosporin. Globally, sensitivity and specificity of βLT were respectively 77.4% and 100%. No erroneous or uninterpretable results were observed with PBP2a testing. Performed on 25 *S. aureus* BSI in P1 and P2, PBP2a was able to detect all 3 MRSA strains (sensitivity and specificity of 100%). Ultimately, 8 BSI (6 in P1 and 2 in P2) were discarded from outcome analysis due to erroneous/uninterpretable rapid test results.

Tables 1 and 2 appear incorrectly in the published article. Please see the correct Tables 1 and 2 and their captions here.

Table 1. Distribution of microorganisms and main resistances of all bloodstream infections across the three study periods. 3GC, third generation cephalosporin (cefotaxime, ceftriaxone, ceftazidime); AST, antimicrobial susceptibility testing; BSI, bloodstream infection; carbapenem (imipenem, meropenem); ID, identification; P0, pre-intervention period; P1, intervention period 1; P2, intervention period 2. Natural AmpC producers identified during the study periods: *Citrobacter freundii, Enterobacter aerogenes, Enterobacter cloacae, Hafnia alvei, Serratia marcescens.* Non-natural AmpC producers identified during the study periods: *Citrobacter koseri, Escherichia coli, Klebsiella oxytoca, Klebsiella pneumoniae, Proteus mirabilis, Proteus vulgaris, Salmonella spp.*

Microorganism Resistance	P0	P1			P2		
	n BSI (%)	n BSI (%)	n BSI	n BSI	n BSI (%)	n BSI	n BSI
	final outcome analysis	final outcome analysis	with failed ID	with failed partial AST	final outcome analysis	with failed ID	with failed partial AST
Gram-positive bacteria	**50 (37.3)**	**40 (35.7)**	**8**	**0**	**44 (28.6)**	**7**	**0**
Staphylococci	25	22	3	0	24	2	0
Staphylococcus aureus	14	11	1	0	14	0	0
methicillin	1	1	0	-	2	-	-
Coagulase negative *Staphylococci*	11	11	2	0	10	2	0
Enterococci	12	11	1	0	9	1	0
Streptococci	9	7	2	0	10	4	0
Other Gram-positive bacteria	4	0	2	0	1	0	0
Gram-negative bacteria	**77 (57.5)**	**71 (63.4)**	**1**	**6**	**107 (69.5)**	**2**	**2**
Enterobacteriaceae	71	63	0	5	103	1	2
natural AmpC producers	5	6	0	0	11	0	0
3GC	2	1	-	-	4	-	-
carbapenem	0	0	-	-	0	-	-
non-natural AmpC producers	66	57	0	5	92	1	2
3GC	10	6	-	5	18	0	2
carbapenem	0	0	-	0	0	0	0
Non fermenters	6	6	1	1	4	1	0
Pseudomonas aeruginosa	3	4	0	1	3	1	0
3GC	0	0	-	1	0	0	-
carbapenem	0	0	-	1	0	0	-
Other non fermenters	3	2	1	0	**1**	0	0
Other Gram-negative bacteria	0	2	-	0	**0**	0	0
Anaerobes	**6 (4.5)**	**0 (0.0)**	**6**	**0**	**2 (1.3)**	**6**	**0**
Yeast	**1 (0.7)**	**1 (0.9)**	**2**	**0**	**1 (0.6)**	**3**	**0**
TOTAL	**134 (100)**	**112 (100)**	**17**	**6**	**154 (100)**	**18**	**2**

Table 2. Time to identification and time to partial/complete susceptibility results of all bloodstream infections during pre-intervention and intervention period 1 and 2.

Time to identification			
Phase	Method	BSI (n)	Mean time to ID (hours)
P0	**TOTAL**	**134**	**28.3**
	Subculture MALDI-TOF MS	134	28.3
	Early MALDI-TOF MS	-	-
	Direct MALDI-TOF MS	-	-
P1	**TOTAL**	**112**	**10.2**
	Subculture MALDI-TOF MS	23	15.9
	Early MALDI-TOF MS	65	10.6
	Direct MALDI-TOF MS	24	3.6
P2	**TOTAL**	**154**	**10.8**
	Subculture MALDI-TOF MS	32	17.1
	Early MALDI-TOF MS	96	10.7
	Direct MALDI-TOF MS	26	4.0
Time to complete susceptibility result			
Phase	Method	BSI (n)	Mean time to complete AST result (hours)
P0	**TOTAL**	**134**	**44.7**
	Phoenix from subculture	58	46.9
	Phoenix from young subculture	-	-
	Direct Phoenix	48	28.3
	Manual testing from subculture	28	68.3
	Manuel testing from young subculture	-	-
P1	**TOTAL**	**112**	**32.4**
	Phoenix from subculture	28	41.2
	Phoenix from young subculture	23	32.2
	Direct Phoenix	45	25.6
	Manual testing from subculture	7	49.1
	Manuel testing from young subculture	9	27.3
P2	**TOTAL**	**154**	**32.6**
	Phoenix from subculture	34	41.6
	Phoenix from young subculture	81	29.9
	Direct Phoenix	22	22.2
	Manual testing from subculture	8	52.2
	Manuel testing from young subculture	9	30.9
Time to partial susceptibility result			
Phase	Method	BSI (n)	Mean time to partial susceptibility testing result (hours)
P1	**TOTAL**	**72**	**11.8**
	Culture βLT	20	17.9
	Young subculture βLT	29	11.2
	Direct βLT	12	3.7
	Culture PBP2a	3	15.3
	Young subculture PBP2a	6	12
	Direct PBP2a	2	2

(*Continued*)

Table 2. (*Continued*)

P2			
	TOTAL	**109**	**11.7**
	Culture βLT	29	16.8
	Young subculture βLT	51	11.1
	Direct βLT	15	3.6
	Culture PBP2a	4	20.2
	Young subculture PBP2a	9	8.8
	Direct PBP2a	1	6

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Reference

1. Verroken A, Defourny L, le Polain de Waroux O, Belkhir L, Laterre P-F, Delmée M, et al. (2016) Clinical Impact of MALDI-TOF MS Identification and Rapid Susceptibility Testing on Adequate Antimicrobial Treatment in Sepsis with Positive Blood Cultures. PLoS ONE 11(5): e0156299. doi: 10.1371/journal.pone.0156299 PMID: 27228001