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Letter to the Editor

Off-site versus on-site clinical microbiology laboratory: a 2-year comparison study of blood culture result reporting

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To the Editor,

In recent years, the 'medical care consolidation' phenomenon has resulted in centralized clinical microbiology laboratories capable of providing services to patients who receive care in remote locations [1]. In some cases, a 'core' microbiology laboratory is within a large tertiary care hospital that serves smaller hospitals, whereas in other cases it acts as a commercial reference laboratory for hospitals outside of the parent organization [1]. However, microbiology tests such as blood cultures (BCs)—in which the turnaround time (TAT) from patient's blood collection to organism identification (and susceptibility testing) results is critical to patient care—should to be kept at the referring hospital site, especially if the laboratory is open 24 h/day [1]. As centralized hospital or free-standing service laboratories may be distant hours from patient care locations [1], sample transportation times often exceed the time-to-positivity of BCs, that is, the time from the start of

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incubation (in a dedicated BC instrument) to a positive signal (by the dedicated BC instrument).

We analysed reporting of BC results at a 230-bed general hospital (namely, the Ospedale San Carlo GVM in Rome, Italy) by comparing on-site (year 2018) and off-site (year 2017) microbiology laboratory testing statuses. Starting from 2018, the hospital laboratory collects and processes clinical samples for any microbiological tests (including BCs) around the clock. Before 2018, all the BCs were collected daily in the on-site (hospital) laboratory, and transported by courier to an off-site (core) laboratory at either 2:30 p.m. (Monday through Friday) or 13:30 a.m. (Saturday). On Sundays/holidays, BCs were collected and stored at room temperature in the hospital laboratory until the courier service was in operation. The times between BC collection and bottle loading (i.e., time to load) ranged from ≤ 8 h to ≥ 48 h, which included the time between the BC storage at, and delivery from, the hospital laboratory plus the transportation time from the hospital laboratory to the core laboratory. The latter was within the SYNLAB Group (www.synlab. com) network of laboratories open 8 h/day from Monday to Friday and 6 h/day on Saturday. Upon receipt at both the on-site and offsite laboratories, BC bottles were immediately loaded into a BC automated instrument (i.e. BACT/ALERT® 3D system, bioMérieux, Marcy l'Étoile, France, or BACTEC™ FX system, Becton Dickinson, Sparks, MD, USA) and incubated for up to 5 days or until they signalled positive. At the time bottles gave a positive signal, the BC broth's aliquots were Gram-stained and cultured on standard agar plates to confirm true-positive detection results (any organism, potential contaminants included). At the end of the incubation period (i.e., 5 days), bottles were discarded as negative. BC results from the core laboratory were released online as soon as available to the hospital laboratory.

Table 1 shows the distribution of the positive BCs, documenting single-patient bloodstream infection episodes, as well the aetiology of the episodes in the 2 years (2017 and 2018) under comparison. We observed a difference of 3.1-fold in the number of BCs requested

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Table 1Distribution of positive blood cultures (BCs) by hospital wards and aetiology of single-patient bloodstream infection episodes in 2 calendar year

	2017 n (%)	2018 n (%)
Number of positive BCs/no. of demands ^a 1	from:	
Medical wards	6/61 (9.8)	43/148 (29.0)
Surgical wards	2/18 (11.1)	18/87 (25.3)
Orthopaedic wards	1/3 (33.3)	12/22 (68.2)
Total wards	9/82 (10.9)	73/257 (28.4)
Number of isolates from positive BCs ^b	9 (100)	49 (100)
Gram-negative species	6 (66.7)	30 (61.2)
Gram-positive species	3 (33.3)	13 (26.6)
Yeast species	0 (0.0)	6 (12.2)
Number of infectious episodes	9 (100)	37 (100)
Single infections	9 (100)	25 (67.6)
Mixed infections	0 (0.0)	12 (32.4)

^a One demand is equivalent to at least one pair of bottles (aerobic and anaerobic) required per single episode of bloodstream infection.

by the wards' physicians between 2018 (n = 257) and 2017 (n = 82). as well as an increase in the rate of BC positivity in 2018 compared to 2017: 73/257 (28.4%) versus 9/82 (11.0%) (p 0.001). Interestingly, the mean (±SD) TAT for positive BCs was 4.0 (±1.5) days in 2018 versus 6.4 (\pm 1.5) days in 2017 (p <0.001), whereas the TAT for negative BCs was $5.4 (\pm 0.9)$ in 2018 versus $7.3 (\pm 1.0)$ days in 2017 (p 0.01). Consistently, the overall number of bloodstream infection episodes was 37 in 2018 and nine in 2017. Only in 2018, 12 episodes had a multiple-species aetiology (i.e., were caused by more than one bacterial species or by both bacterial and yeast species). Therefore, there were 49 organisms (30 Gram-positives, 13 Gramnegatives and six yeasts) identified in that year, compared to nine organisms (six Gram-negatives and three Gram-positives) identified in 2017 (Table 1). In 2018, the most prevalent organisms were coagulase-negative staphylococci (18/49, 36.7%), followed by members of the Enterobacteriales (11/49, 22.4%), enterococci (9/49, 18.4%) and yeasts (6/49, 12.2%). In 2017, the number of BC demands equated the number of organisms detected from positive BCs. We feel that knowing by the wards' physicians that the patients' BCs were processed in an off-site laboratory may have influenced their disposition in ordering BCs during that year. However, we cannot exclude that a different case mix between 2017 and 2018 may have been a potential bias leading to the differences observed between the two periods of time.

We did not know the exact operational hours of the off-site laboratory, but it is plausible that the longer TATs to both positive and negative results of the BCs collected in 2017 resulted from a delayed entry of BC bottles into the instrument. However, it is certain that there was no courier service either in the weekday evenings or during nightshifts, weekends, and holidays. It is also certain that the bottle loading always occurred during the off-site laboratory's work hours. As the gold standard for bloodstream infection diagnosis [2], BCs should be processed and reported in a timely fashion to maximize the benefits for patient care. Because the BC performance relies mainly on the quality of its pre-analytical phase [3], delay in bottle loading is an important influencer of the BC TAT but is overlooked in routine laboratory practice [4]. Thus, suboptimal pre-analytical conditions, including delayed BC processing, may have negatively affected the BC outcomes in 2017.

In conclusion, our findings support the concept that BC diagnostics may often suffer from an insufficient service coverage by the clinical microbiology laboratories [5]. Therefore, more effort is necessary to render BC diagnostics more compliant with the requirements for the optimal management of bloodstream infections.

Transparency declaration

The authors report no conflicts of interest relevant to this letter. No external funding was received for this study.

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b In 2017, isolates belonged to seven microbial species as follows: Escherichia coli (n = 2), Klebsiella pneumoniae (n = 2), Citrobacter koseri (n = 1), Staphylococcus aureus (n = 1), Staphylococcus epidermidis (n = 1), Bacteroides fragilis (n = 1) and Micrococcus sp. (n = 1). One E. coli isolate was an extended-spectrum β -lactamase-(ESBL-)producing organism and the S. aureus isolate was a methicillin-resistant S. aureus (MRSA) organism. In 2018, isolates belonged to 19 microbial species as follows: Acinetobacter baumannii (n = 2), Cryptococcus neoformans (n = 1), Candida albicans (n = 2), Candida glabrata (n = 1), Candida parapsilosis (n = 2), Enterobacter aerogenes (n = 1), Enterococcus faecalis (n = 5), Enterococcus faecium (n = 4), Escherichia coli (n = 4), Klebsiella pneumoniae (n = 4), Proteus mirabilis (n = 2), Staphylococcus aureus (n = 3), Staphylococcus epidermidis (n = 6), Staphylococcus capitis (n = 5), Staphylococcus caprae (n = 1), Staphylococcus haemolyticus (n = 2), Staphylococcus hominis (n = 2), Staphylococcus warneri (n = 1) and Streptococcus mitis (n = 1). Both A. baumannii isolates were multidrug-resistant organisms, one S. aureus isolate was an MRSA, and three E. coli isolates and two K. pneumoniae isolates were ESBLs.