Diagnosis and Management of Polymicrobial Blood Stream Infections using Multiplex PCR in Hospitalized Children

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Background: Patients with polymicrobial bloodstream infections (PBSIs) are known to have increased severity of illness, prolonged ICU and hospital stays, increased mortality, and are more likely to receive inadequate empirical antibiotics compared to monomicrobial infections. Prolonged unnecessary broad-spectrum therapy can lead to antibiotic resistance and adverse events. Multiplex PCR (mPCR) can lead to faster species identification in bloodstream infections. Prior studies in monomicrobial infections have shown a reduction in broad spectrum antibiotic use, less treatment of contaminant infections, and quicker escalation and de-escalation of therapy using mPCR.

Objectives: To describe the impact of mPCR on the management of patients with PBSIs after the introduction of mPCR at Lurie Children's Hospital (LCH).

Design/Methods: A single-center, retrospective cohort study was conducted of patients with PBSIs at LCH between October 2014-July 2018. PBSIs were defined as isolation of 2 or more organisms (bacterial or fungal) from one bottle or >1 bottle drawn within an hour of each other. Patients were excluded if they died prior to culture speciation or if mPCR was not performed. The cohort was divided into those whose final cultures consisted of pathogen-only PBSIs (pPBSIs), contaminant-only PBSIs (cPBSIs), or mixed pathogen-contaminant PBSIs (mPBSIs). A contaminant was considered a coagulase-negative staphylococci (CONS), an alpha hemolytic streptococcus, or a gram-positive rod organism, with the exception of CONS infections in the NICU. Chart review was performed to identify clinical characteristics of patients and antibiotic adjustments attributable to mPCR results. Statistical analyses were performed using chi-square test for independence and Fisher exact probability test.

Results: A total of 134 polymicrobial infections were identified in 116 patients, including 63 pPBSIs, 41 cPBSIs, and 30 mPBSIs. Patients with pPBSI were more likely to receive initial empiric antibiotics than those with cPBSIs (95.2% v 65.9%; $p<0.0005$). They had a significant decrease in bug/drug mismatch after mPCR results (27.0% v 11.1%; $p<0.03$). Bug/drug mismatch did not significantly decrease after mPCR in patients with mPBSIs (10% v 6.7%; $p=0.6$), though overall decrease in mismatch from empiric therapy to after mPCR was significant (26.7% v 6.7%; $p=0.03$). Those with cPBSIs were less likely to broaden antibiotics after mPCR compared to pPBSIs and mPBSIs (14.6% v 41.3%; $p<0.005$; 14.6% v 40.0%; <0.05 respectively), but remained on higher rates of Vancomycin and Linezolid after mPCR compared to the empiric regimen (63.4% v 29.3%; $p<0.005$). Missed opportunities to modify therapy included missed opportunities to correct bug/drug mismatch (6.3% of pPBSIs; 0% of mPBSIs) and missed opportunities to discontinue or narrow antibiotics in all groups (36.5% of pPBSIs, 58.5% of cPBSIs, and 56.7% of mPBSIs)

Conclusion: mPCR is an important and potentially life-saving tool for patients with pathogenic PBSIs given their high rates of bug/drug mismatch on empiric therapy. There were missed opportunities to narrow and discontinue agents after mPCR. While providers are less likely to broaden therapy after contaminant-only mPCR results, discontinuation and narrowing of antibiotics, including Vancomycin and Linezolid, remain low.