American Association of Bioanalysts

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Q2 2018 Throat Culture

Specimen 1 - 12 year old Male, Swollen lymph nodes

Organisms	Extent	1	2	3	4	5	Total
923 - Pos for Grp A strep screen by culture		20	17	8	1	1	47
976 - Pos for strep Group A antigen		1	3	2	0	0	6
921 - Pos for beta-hemolytic strep screen		1	1	0	0	0	2
886 - Streptococcus sp.; beta-hemolytic Grp A (S. pyogenes)		0	1	0	0	0	1
922 - Neg for Grp A strep screen by culture		0	1	0	0	0	1
				TOTAL PARTICIPANTS			57

Flagging appears for failure to report 886, 921, 923 or 976.
In addition to the required organism, participants in all extents may report (No additional codes)
This sample contained *Streptococcus pyogenes,* Group A.

Culture of this patient's throat swab displayed abundant growth of *Streptococcus pyogenes* also referred to as Group A -hemolytic streptococcus (GABHS; based on the Lancefield classification for grouping streptococci according to their carbohydrate cell wall antigens) and few *Neisseria* spp. (i.e., limited to the growth in the first quadrant). Cervical lymphadenopathy and age 3 to 14 are two criteria used in GABHS clinical prediction scoring systems, and therefore, serves as clinical validation of laboratory findings in this scenario. The presence of any -hemolytic streptococcus grown in a throat culture should be evaluated for possible clinical significance. Accordingly, any -hemolytic, catalase^{neg}, gram-positive cocci in pairs or chains can be confirmed as *S. pyogenes* by either: 1) positive PYR test; 2) positive result for GABHS antigen with immunological grouping test; or 3) positive DNA probe test. Lastly, the presence of few *Neisseria* spp. in this culture reflects the presence of commensal organisms in the oropharynx and should be reported as such (e.g., "Usual upper respiratory microbiota").

Specimen 2 - 20 year old Male, Fever, cough

Organisms	Extent	1	2	3	4	5	Total
922 - Neg for Grp A strep screen by culture		19	18	8	0	1	46
975 - Neg for strep Group A antigen		1	3	1	0	0	5
919 - Neg for beta-hemolytic strep screen		1	1	0	0	0	2
947 - No aerobic growth on blood agar		0	0	1	0	0	1
923 - Pos for Grp A strep screen by culture		1	0	0	0	0	1
976 - Pos for strep Group A antigen		0	0	1	0	0	1
				TOTAL PARTICIPANTS			56

Flagging appears for failure to report 838, 841, 842, 919, 922, 925, 927, 943, 975 or 983.
In addition to the required organism, participants in all extents may report (No additional codes).
This sample contained *Pseudomonas aeruginosa* and *Neisseria spp.*

Abundant (i.e., third and fourth quadrant growth) *Pseudomonas aeruginosa* and few *Neisseria* spp. colonies were isolated from this patient's throat culture obtained upon hospital admission. Specimens obtained from the upper respiratory tract in general (e.g., throat, nasopharyngeal swabs, nasal discharges), while easily obtained, are typically contaminated with resident microbiota that are present in both the disease and carrier states. While both organisms recovered are not typically associated with acute pharyngitis and should not be reported from such cultures, abundant growth of *P. aeruginosa* from the initial throat culture correlated with subsequent pure growth of this organism observed from a lower respiratory specimen that confirmed this patient's hospital-acquired pneumonia. *P. aeruginosa* is an opportunistic pathogen most often associated with nosocomial pneumonia. Colonies on blood agar plates (BAP) are -hemolytic, but can be distinguished from pathogenic -hemolytic streptococci by their dark color on BAP (from green pigment produced) and Gram stain reaction/morphology.

Specimen 3 - 8 year old Female, Sore throat

Organisms	Extent	1	2	3	4	5	Total
922 - Neg for Grp A strep screen by culture		17	16	6	0	1	40
923 - Pos for Grp A strep screen by culture		3	2	2	0	0	7
975 - Neg for strep Group A antigen		1	2	1	0	0	4
919 - Neg for beta-hemolytic strep screen		1	1	1	0	0	3
976 - Pos for strep Group A antigen		0	1	1	0	0	2
		TOTAL PARTICIPANTS					56

Flagging appears for failure to report (No Codes).
In addition to the required organism, participants in all extents may report 919, 922, and 975.

This inoculated blood agar plate utilized for this patient's throat culture was negative for pathogenic organisms, typically reported as "No pathogenic streptococci isolated". However, few -hemolytic streptococci and *Neisseria* spp. (i.e., first quadrant growth only) were identified. Such organisms from a throat culture can be added to a throat culture report (as above) as "Normal upper respiratory microbiota" or "Mixed flora", for example. That is, reporting the presence or the absence of pathogenic bacteria without description of other organisms (*by name*) that may be commensals provides the clearest message for directing patient management, and is consistent with antimicrobial stewardship principles and practices.

Specimen 4 - 3 year old Male, Fever

Organisms	Extent	1	2	3	4	5	Total
922 - Neg for Grp A strep screen by culture		20	18	8	0	1	47
975 - Neg for strep Group A antigen		1	3	1	0	0	5
919 - Neg for beta-hemolytic strep screen		1	1	0	0	0	2
947 - No aerobic growth on blood agar		0	0	1	0	0	1
886 - Streptococcus sp.; beta-hemolytic Grp A (S. pyogenes)		0	1	0	0	0	1
976 - Pos for strep Group A antigen		0	0	1	0	0	1
		TOTAL PARTICIPANTS					57

Flagging appears for failure to report 919, 922, 947 or 975.
In addition to the required organism, participants in all extents may report (No additional codes).
This specimen contained *Escherichia coli* and *Neisseria spp.*

Abundant (4+) growth of *Escherichia coli* and few *Neisseria* spp. colonies were isolated from this patient's throat culture. While the *Neisseria* spp. should be considered (and reported) as resident microbiota, enteric organisms (such as *Escherichia coli*, in this case) are infrequent as colonizers of the upper respiratory tract, but also not considered to have a pathogenic role in pharyngitis. However, this case involved a hospitalized 3 year-old boy that also had lower respiratory specimen that was growing the same organism, and therefore, the likely reason for the observed result. While viruses (i.e., predominantly RSV) are the most common cause of pediatric nosocomial respiratory tract infections, gram-negative bacteria (*E. coli*, *K. pneumoniae*, and *P. aeruginosa*) are the predominant bacterial pathogens, and are associated with a high mortality rate. Therefore, while adherence to reporting protocols is paramount, unusual results such as this should be communicated to clinical laboratory leadership to be investigated further.

Specimen 5 - 68 year old Female, Cough, fever, sore throat

Organisms	Extent	1	2	3	4	5	Total
923 - Pos for Grp A strep screen by culture		20	17	9	0	1	47
976 - Pos for strep Group A antigen		1	3	2	0	0	6
921 - Pos for beta-hemolytic strep screen		1	1	0	0	0	2
886 - Streptococcus sp.; beta-hemolytic Grp A (S. pyogenes)		0	1	0	0	0	1
922 - Neg for Grp A strep screen by culture		0	1	0	0	0	1
		TOTAL PARTICIPANTS					57

Q2 2018 Throat Culture

Flagging appears for failure to report 886, 921, 923 or 976.
In addition to the required organism, participants in all extents may report (No additional codes).
This sample contained *Streptococcus pyogenes,* Group A.

Culture demonstrated abundant growth of *Streptococcus pyogenes* for this patient. *S. pyogenes* or Group A β-hemolytic streptococcus (GABHA) accounts for 30% of pharyngitis cases in children (ages 5 to 15), but only 10% of adult cases. So, while a rare case of acute pharyngitis for this demographic, it can and does occur. Other bacterial causes of pharyngitis include group C and G β-hemolytic streptococci, *Neisseria gonorrhoeae*, *Corynebacterium diphtheria*, and *Arcanobacterium haemolyticum*. However, most cases have a viral etiology (e.g., rhinovirus, coronavirus). Given the emergence of commercial rapid diagnostic tests (RDTs; antigen- and nucleic acid-based) for GABHA and their comparable performance to that of culture, most guidelines are no longer recommending routine culture to back-up negative RDTs (especially, in this age category), but rather leave the decision to the physician to order when indicated (e.g., outbreak investigations, monitoring the spread of antimicrobial resistance, examination for pathogens other than GABHS).