

Q2 2018 Urine Culture



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Specimen 1 - 78 year old Female, Nursing home, incontinent

Organisms	Extent	1	2	3	4	5	Total
943 - Aerobe found; but referred for ID		9	0	1	0	0	10
799 - Escherichia coli		0	0	4	0	1	5
993 - Growth of gram-negative organisms		2	2	1	0	0	5
987 - E.coli; Citrobacter or Enterobacter		1	0	3	0	0	4
942 - Primary culture only, refer for ID		0	2	0	0	0	2
798 - Escherichia sp.; NOS		0	0	1	0	0	1
	TOTAL PARTICIPANTS						27

Flagging appears for failure to report 798, 799, 942, 943, 983, 987 or 993.

In addition to the required organism, participants in all extents may report (No additional codes)

This sample contained *Escherichia coli*.

Strong urges to urinate, and sometimes urinary incontinence can be symptoms of a urinary tract infection (UTI), as seen in this case. Quantitative urine culture of a clean-catch urine specimen obtained from this patient grew $>10^5$ CFU/ml *Escherichia coli*. *E. coli* is an organism that, in contrast to the vast majority of organisms encountered in the clinical bacteriology laboratory, can be tested and reported with minimal work-up. That is, oxidase-negative and gram-negative organisms that are spot indole-positive and β -hemolytic on blood agar can be identified as *E. coli*. Alternatively, indole-positive colonies that are nonhemolytic and lactose positive (e.g., MAC, EMB) can be identified as *E. coli* with a negative Pyrrolidonyl Arylamidase (PYR) test.

Specimen 2 Urine - 58 year old Female, Dysuria

Organisms	Extent	1	2	3	4	5	Total
943 - Aerobe found; but referred for ID		7	0	0	0	0	7
993 - Growth of gram-negative organisms		4	0	0	0	0	4
834 - Proteus sp.; NOS		0	0	3	0	0	3
835 - Proteus mirabilis		0	0	2	0	0	2
777 - Corynebacterium sp.; NOS		0	0	2	0	0	2
949 - No aerobic growth		1	0	0	0	0	1
942 - Primary culture only, refer for ID		1	0	0	0	0	1
	TOTAL PARTICIPANTS						20

Flagging appears for failure to report 834, 835, 942, 943, 990 or 993.

In addition to the required organism, participants in all extents may report 777

This sample contained *Proteus mirabilis* and *Corynebacterium spp.*

This patient's (noninvasive) urine specimen grew $>10^5$ CFU/ml gram-negative rods (GNR) and $<10^4$ CFU/ml of catalase-positive gram-positive rods (GPR). Most work-up recommendations/guidelines, in general, would suggest work-up for only the GNR and a minimal morphologic identification (MMI) for the GPR (i.e., based on colony/Gram stain morphology, hemolysis, and rapid same-day biochemical or serological tests). The GNR was presumptively identified as *Proteus spp.* with swarming growth on blood agar and a clear colony on MAC (nonlactose fermenter) and later confirmed as *Proteus mirabilis* on a semi-automated ID system. While the coryneform GPR was worked-up by MMI (according to the local protocol) and reported as "Urogenital Microbiota", it can be important in some cases (i.e., especially for high-risk patients) to rule-out uropathogenic *Corynebacterium urealyticum*, if clinically indicated (*C. urealyticum* tests urease-positive; whereas, most other *Corynebacterium spp.* test negative for urease).

Q2 2018 Urine Culture

Specimen 3 Urine - 74 year old Male, Foley catheter

Organisms	Extent	1	2	3	4	5	Total
949 - No aerobic growth		10	0	5	0	0	15
943 - Aerobe found; but referred for ID		1	0	0	0	0	1
948 - No pathogens isolated		1	0	0	0	0	1
		TOTAL PARTICIPANTS					17

Flagging appears for failure to report [no codes].

In addition to the required organism, participants in all extents may report 720, 948 and 949

All inoculated media was negative for culture of this urine specimen. Such culture results are typically reported as "Urine culture negative" or "No growth of uropathogens". While infectious syndromes such as cystitis or, more commonly, acute pyelonephritis can be associated with flank pain, other noninfectious causes are possible, as well (e.g., kidney stones, muscle spasm, Crohn's disease).

Specimen 4 - 48 year old Male, Flank pain

Organisms	Extent	1	2	3	4	5	Total
943 - Aerobe found; but referred for ID		9	0	1	0	0	10
993 - Growth of gram-negative organisms		2	2	1	0	0	5
838 - Pseudomonas sp.; NOS		0	0	3	0	1	4
990 - Proteus or Pseudomonas		1	0	3	0	0	4
841 - Pseudomonas aeruginosa		0	0	2	0	0	2
942 - Primary culture only, refer for ID		0	2	0	0	0	2
		TOTAL PARTICIPANTS					27

Flagging appears for failure to report 838, 841, 942, 943, 990 or 993.

In addition to the required organism, participants in all extents may report (No additional codes)

This sample contained *Pseudomonas aeruginosa* and *Neisseria spp.*

The urine culture (obtained from indwelling Foley catheter) for this hospitalized patient with symptoms of pyelonephritis (fever and flank pain) grew a clinically significant ($>10^5$ CFU/ml) quantity of gram-negative rods (GNR) and few ($<10^4$ CFU/ml) gram-negative diplococci. The GNR appeared β -hemolytic on blood agar, and subsequent biochemical testing identified this organism as *Pseudomonas aeruginosa*. *P. aeruginosa* is a common cause of hospital-acquired infections and can be presumptively identified by its fruity odor of grapes combined with its characteristic colony morphology (green pigment) and oxidase^{pos} and indole^{neg} biochemical reactions. This organism should not be confused with β -hemolytic *E. coli* as *P. aeruginosa* is a nonfermenter (i.e., clear-to-dark on MAC). Insignificant numbers of gram-negative diplococci were also associated with this patient's urine culture, described by minimal morphologic identification criteria and reported as "Urogenital Microbiota". Commensal *Neisseria spp.* are more often considered microbiota of the upper respiratory tract, but can colonize the urogenital tract as well.

Specimen 5 - 72 year old Female, Pelvic pain

Organisms	Extent	1	2	3	4	5	Total
943 - Aerobe found; but referred for ID		9	0	1	0	0	10
799 - Escherichia coli		0	0	4	0	1	5
993 - Growth of gram-negative organisms		2	2	1	0	0	5
987 - E.coli; Citrobacter or Enterobacter		1	0	3	0	0	4
942 - Primary culture only, refer for ID		0	2	0	0	0	2
798 - Escherichia sp.; NOS		0	0	1	0	0	1
994 - Growth of gram-positive organisms		0	0	1	0	0	1
874 - Staphylococcus sp.; coagulase-negative; NOS		0	0	1	0	0	1
		TOTAL PARTICIPANTS					29

Q2 2018 Urine Culture

Flagging appears for failure to report 798, 799, 942, 943, 987 or 993.

In addition to the required organism, participants in all extents may report 718, and 994.

This sample contained *Escherichia coli* and *Staphylococcus epidermidis*.

A voided clean-catch urine specimen was obtained from the 72 year-old female outpatient for urine culture and urinalysis (UA). The UA was positive for nitrites and leukocyte esterase, suggestive of true infection. Subsequently, the culture results grew significant numbers of GNRs ($>10^5$ CFU/ml) and scant ($<10^4$ CFU/ml) gram-positive cocci (GPC) in clusters. The GNR organism was presumptively identified as *Escherichia coli* with its characteristic pink colonies on MAC and oxidase^{neg}, spot indole^{pos}, and PYR^{neg} biochemical reactions. *Staphylococcus epidermidis* was also associated with the patient's culture, and given its low predominance (>10 -fold less numerous than predominant organism) was described by minimal morphologic identification criteria and reported as "Urogenital Microbiota".