Date of Search: 05 Dec 16

Sources Searched: Medline, Embase, DynaMed, NHS Evidence.

Mixed Growth and Mid-Stream Samples

Summary:

Evaluating urine culture findings has long been dominated by Kass's criteria for significant bacteriuria. Kass found that 95% of women with pyelonephritis had $\geq 10^8$ CFB/L ($\geq 10^5$ CFU/mL) or one bacterial species in a clean-catch mid-stream urine, and that such a finding in two consecutive mid-stream urine specimens in asymptomatic women would, with 95% probability, give the same result in a third mid-stream urine specimen (Kass EH. Trans Assoc Am Phys 1956; 69: 56-63; Kass EH. In: Quinn Biology of pyelonephritis. Boston: Little & Brown; 1960. p. 399-412.). Kass also showed that $<10^7$ CFB/L indicated contamination during sample collection, whereas bacterial concentration in the interval of 10^7 - $<10^8$ CFB/L was difficult to interpret. Despite the fact that the criteria were developed for acute pyelonephritis and asymptomatic bacteriuria in women, they began to be used generally, even for symptomatic lower urinary tract infection.

Source: Health Protection Agency: Diagnosis of UTI

URL: https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/345784/UTI_quick_ref_guidelines.pdf

The significance of polymicrobial growth in urine: Contamination or true infection

Author(s): Siegman-Igra Y.; Kulka T.; Schwartz D.; Konforti N.

Source: Scandinavian Journal of Infectious Diseases; 1993; vol. 25 (no. 1); p. 85-91

Publication Date: 1993

Abstract: Urine growing more than one organism is usually considered contaminated. During 1980-1984, among 198 episodes of urosepsis with at least one identical organism in blood and urine, there were 62 with polymicrobial growth from urine. The significance of the multiple growth from urine was confirmed in 12 episodes by the growth of more than one identical organism in blood and urine and in 21 episodes by repeated growth of the same mixture of organisms in multiple urine specimens. Escherichia coli had a higher tendency to invade blood stream than other Gram-negative organisms, such as pseudomonas and proteus. In specific populations with high risk of polymicrobial infection, multiple growth in urine should be carefully evaluated with appropriate colony count and identification of each isolate.

Database: EMBASE

The significance of urine culture with mixed flora.

Author(s): Siegman-Igra, Y

Source: Current opinion in nephrology and hypertension; Nov 1994; vol. 3 (no. 6); p. 656-659

Publication Date: Nov 1994

Abstract:Urine cultures that contain more than one organism are usually considered contaminated. The frequency with which such growth truly represents mixed infection is unknown. Surprisingly few studies have evaluated the clinical significance of polymicrobial growth from urine. Such significance was demonstrated in these studies either by recovering the same combination of microorganisms from blood and urine, in cases of urosepsis, or by the reproducibility of the same mixture of bacteria from sequential urine cultures. In certain clinical settings, polymicrobial bacteriuria is not only

frequently significant but its overall clinical impact seems to be substantial. Bacteriuria associated with long-term catheterization, the most common nosocomial infection in American medical care facilities, is predominantly polymicrobial. Symptomatic urinary tract infection is a common outcome of such bacteriuria and has been associated with increased risk for bloodstream infections and excess mortality. Early species identification and antimicrobial susceptibility testing of each urinary isolate may be of paramount benefit to the care of these patients. We believe that in properly collected urine samples, multiple growth often represents true mixed infection and should therefore be completely evaluated.

Database: Medline

Urine culture contamination.

Author(s): Washington, J A

Source: Archives of pathology & laboratory medicine; Feb 1998; vol. 122 (no. 2); p. 120-122

Publication Date: Feb 1998

Available in full text at Archives of Pathology and Laboratory Medicine - from ProQuest

Database: Medline

Urine specimen contamination: How dirty is too dirty?

Author(s): Metzger G.D.

Source: Clinical Laboratory Science; 1994; vol. 7 (no. 2); p. 78-79

Publication Date: 1994

Database: EMBASE

Revisiting urine culture contamination.

Author(s): Fuchs PC

Source: MLO: Medical Laboratory Observer; Jul 1994; vol. 26 (no. 7); p. 13-14

Publication Date: Jul 1994

Database: CINAHL

Defining urine culture contamination.

Author(s): Fuchs PC

Source: MLO: Medical Laboratory Observer; Feb 1994; vol. 26 (no. 2); p. 12-12

Publication Date: Feb 1994

Database: CINAHL

A novel midstream urine-collection device reduces contamination rates in urine cultures amongst women.

Author(s): Jackson, Simon R; Dryden, Mathew; Gillett, Paul; Kearney, Paddy; Weatherall, Rosemary

Source: BJU international; Aug 2005; vol. 96 (no. 3); p. 360-364

Publication Date: Aug 2005

Available in full text at BJU International - from John Wiley and Sons

Abstract:To evaluate a novel urine-collection device (UCD) that automatically collects a midstream urine (MSU) sample, and compare contamination rates to those of the conventional MSU sampling method, as the contamination of urine samples for microbiological analysis in women leads to diagnostic ambiguity and unnecessary costs, and may result in part from an incorrect collection procedure. In all, 2823 women from four centres, most from antenatal clinics, were randomized to two urine-collection methods: conventional MSU collection and collection with a novel MSU UCD (the Whiz, JBOL Ltd, Oxford, UK). Semi-quantitative growth and user acceptability were compared between the collection methods. MSU samples collected with the UCD had significantly fewer mixed growth samples (9% vs 14%, P = 0.001; 36% relative reduction), significantly fewer heavy mixed growth samples (1.2% vs 3.0%, P = 0.004; 60% relative reduction) and required significantly fewer retests (11% vs 16%, P = 0.002; 31% relative reduction). There were more samples with clinically insignificant growth than the conventional MSU group (86% vs 82%, P = 0.005). Those using the UCD preferred it to the conventional method (67.5%) and experienced significantly less spillage during sample collection (27% vs 46%, P = 0.001; relative reduction 41%). The UCD reduced contamination rates in urine samples and improved the predictive value of the urine culture in a manner acceptable to patients and staff.

Database: Medline

The laboratory diagnosis of urinary tract infection

Author(s): Graham J.C.; Galloway A.

Source: Journal of Clinical Pathology; 2001; vol. 54 (no. 12); p. 911-919

Publication Date: 2001

Available in full text at Journal of Clinical Pathology - from Free Access Content

Abstract: Urinary tract infection is common, and it is not surprising that urine specimens make up a large proportion of those samples submitted to the routine diagnostic laboratory. Many of these specimens will show no evidence of infection and several methods can be used to screen out negative samples. Those that grow bacteria need to be carefully assessed to quantify the degree of bacteriuria and hence clinical relevance. To influence treatment, a final report should be produced within 24 hours of specimen receipt, with turnaround times continuously monitored. Much work needs to be done to determine the cost effectiveness involved in processing urine specimens and the evidence base for the final report provided.

Database: EMBASE

Urine culture contamination: a College of American Pathologists Q-probes study of contaminated urine cultures in 906 institutions.

Author(s): Valenstein P; Meier F

Source: Archives of Pathology & Laboratory Medicine; Feb 1998; vol. 122 (no. 2); p. 123-129

Publication Date: Feb 1998

Available in full text at Archives of Pathology and Laboratory Medicine - from ProQuest

Database: CINAHL

Strategy 92309

#	Database	Search term	Results
1	Medline	(PCR).ti,ab	399584
2	Medline	("protein creatinine ratio").ti,ab	648
3	Medline	(PCR).ti,ab OR ("protein creatinine ratio").ti,ab	400175
4	Medline	("mixed growth").ti,ab	243
5	Medline	((PCR).ti,ab OR ("protein creatinine ratio").ti,ab) AND ("mixed growth").ti,ab	5
6	Medline	(contamin*).ti	38337
7	Medline	(midstream OR "mid stream").ti	133
8	Medline	("mixed growth").ti,ab AND (midstream OR "mid stream").ti	1
9	Medline	(msu).ti	75
10	Medline	("mixed growth").ti,ab AND (msu).ti	0
11	Medline	("mid urine stream").ti	0
12	Medline	(contam* ADJ4 "mixed growth").ti	0
13	EMBASE	("mixed growth").ti,ab	323
14	EMBASE	(midstream OR "mid stream").ti	151
15	EMBASE	(msu).ti	105
16	EMBASE	(midstream OR "mid stream").ti OR msu	1500
17	EMBASE	("mixed growth").ti,ab AND ((midstream OR "mid stream").t	3 i

OR (msu).ti)

EMBASE	exp "BACTERIUM CONTAMINATION"/	15158
EMBASE	((midstream OR "mid stream").ti OR (msu).ti) AND exp "BACTERIUM CONTAMINATION"/	i8
EMBASE	(retest* OR "re test*").ti,ab	35681
EMBASE	exp URINALYSIS/	91765
EMBASE	(exp "BACTERIUM CONTAMINATION"/ AND (retest* OR "re test*").ti,ab) AND exp URINALYSIS/	1
EMBASE	("mid urine stream").ti	0
EMBASE	exp "URINE CULTURE"/	10820
EMBASE	exp "BACTERIUM CONTAMINATION"/ AND exp "URINE CULTURE"/	89
CINAHL	("mixed growth").ti,ab	11
CINAHL	(midstream OR "mid stream").ti	22
CINAHL	(msu).ti	47
CINAHL	exp "BACTERIAL CONTAMINATION"/	1941
CINAHL	exp URINALYSIS/	3854
CINAHL	exp "BACTERIAL CONTAMINATION"/ AND exp URINALYSIS/	18
EMBASE	(urine culture contamination).ti	7
EMBASE	*"URINE CULTURE"/	876
	EMBASE EMBASE EMBASE EMBASE EMBASE EMBASE CINAHL	CONTAMINATION"/ EMBASE ((midstream OR "mid stream").ti OR (msu).ti) AND exp "BACTERIUM CONTAMINATION"/ EMBASE (retest* OR "re test*").ti,ab EMBASE (exp "BACTERIUM CONTAMINATION"/ AND (retest* OR "re test*").ti,ab) AND exp URINALYSIS/ EMBASE ("mid urine stream").ti EMBASE ("mid urine stream").ti EMBASE ("mid urine stream").ti EMBASE ("mid urine stream").ti CONTAMINATION"/ AND exp "URINE CULTURE"/ CINAHL ("mixed growth").ti,ab CINAHL (midstream OR "mid stream").ti CINAHL (msu).ti (msu).ti CINAHL (msu).ti CINAHL (msu).ti (msu).ti CINAHL (msu).ti (msu).ti CINAHL (msu).ti (msu).ti (msu).ti

34	EMBASE	exp "BACTERIUM CONTAMINATION"/ AND *"URINE CULTURE"/	27
35	EMBASE	("mixed culture" OR "mixed flora").ti	867
36	EMBASE	((midstream OR "mid stream").ti OR (msu).ti) AND ("mixed culture" OR "mixed flora").ti	i 1
37	EMBASE	exp URINALYSIS/ AND ("mixed culture" OR "mixed flora").ti	3
38	EMBASE	exp "URINE CULTURE"/ AND ("mixed culture" OR "mixed flora").ti	3
39	Medline	("mixed culture" OR "mixed flora").ti	657
40	Medline	(midstream OR "mid stream").ti AND ("mixed culture" OR "mixed flora").ti	0
41	Medline	exp "URINE SPECIMEN COLLECTION"/	194
42	Medline	("mixed culture" OR "mixed flora").ti AND exp "URINE SPECIMEN COLLECTION"/	0
43	Medline	exp URINALYSIS/	6096
44	Medline	("mixed culture" OR "mixed flora").ti AND exp URINALYSIS/	0
45	Medline	("multiple growth").ti,ab	710
46	Medline	exp URINALYSIS/ AND ("multiple growth").ti,ab	0
47	Medline	exp "URINE SPECIMEN COLLECTION"/ AND ("multiple growth").ti,ab	0
48	Medline	("polymicrobial growth").ti,ab	55

49	Medline	exp URINALYSIS/ AND ("polymicrobial growth").ti,ab	1
50	Medline	(urine culture contamination).ti	9
51	CINAHL	exp "URINE SPECIMEN COLLECTION"/	102
52	CINAHL	exp "BACTERIAL CONTAMINATION"/ OR exp "MICROBIAL CONTAMINATION"/	2981
53	CINAHL	exp "URINE SPECIMEN COLLECTION"/ AND (exp "BACTERIAL CONTAMINATION"/ OR exp "MICROBIAL CONTAMINATION"/)	8
54	CINAHL	("mixed culture" OR "mixed flora").ti	3
55	CINAHL	("multiple growth").ti,ab	25
56	CINAHL	("polymicrobial growth").ti,ab	6
57	CINAHL	("mixed culture" OR "mixed flora").ti OR ("multiple growth").ti,ab OR ("polymicrobial growth").ti,ab	34
58	CINAHL	exp "URINE SPECIMEN COLLECTION"/ AND (("mixed culture" OR "mixed flora").ti OR ("multiple growth").ti,ab OR ("polymicrobial growth").ti,ab)	0
59	CINAHL	exp URINALYSIS/	3859
60	CINAHL	(exp "BACTERIAL CONTAMINATION"/ OR exp "MICROBIAL CONTAMINATION"/) AND exp URINALYSIS/	25

61	CINAHL	(urine contaminat*).ti	10
62	Medline	(urine contaminat*).ti	145
63	EMBASE	*CONTAMINATION/	10346
64	EMBASE	*URINALYSIS/	11232
65	EMBASE	*CONTAMINATION/ AND *URINALYSIS/	36
66	EMBASE	*"BACTERIUM CONTAMINATION"/	5138
67	EMBASE	*URINALYSIS/ AND *"BACTERIUM CONTAMINATION"/	10
68	EMBASE	exp "CREATININE URINE LEVEL"/	8854
69	EMBASE	*"BACTERIUM CONTAMINATION"/ AND exp "CREATININE URINE LEVEL"/	0
70	EMBASE	*CONTAMINATION/ AND exp "CREATININE URINE LEVEL"/	
71	EMBASE	*"URINE CULTURE"/	876
72	EMBASE	*"BACTERIUM CONTAMINATION"/ AND *"URINE CULTURE"/	10
73	EMBASE	*CONTAMINATION/ AND *"URINE CULTURE"/	12
74	EMBASE	(urine contamin*).ti	16
75	EMBASE	*"MICROBIAL GROWTH"/	981
76	EMBASE	*"URINE CULTURE"/ AND *"MICROBIAL GROWTH"/	1
77	EMBASE	*URINALYSIS/ AND *"MICROBIAL GROWTH"/	0

78	EMBASE	(urin*).ti	175581
79	EMBASE	*URINALYSIS/ AND *"MICROBIAL GROWTH"/	0
80	EMBASE	*"MICROBIAL GROWTH"/ AND (urin*).ti	5
81	EMBASE	exp PROTEINURIA/	84853
82	EMBASE	*"MICROBIAL GROWTH"/ AND exp PROTEINURIA/	0
83	EMBASE	*"MICROBIAL GROWTH"/ AND (urin*).ti	5
84	EMBASE	exp "MICROBIAL GROWTH"/	111119
85	EMBASE	*"URINE CULTURE"/ AND exp "MICROBIAL GROWTH"/	56
86	EMBASE	exp "BACTERIAL COUNT"/	25902
87	EMBASE	*"URINE CULTURE"/ AND exp "BACTERIAL COUNT"/	66
88	Medline	(growth).ti,ab	1147646
89	Medline	exp "URINE SPECIMEN COLLECTION"/ AND (growth).ti,ab	4
90	Medline	exp URINALYSIS/ AND (growth).ti,ab	163
91	Medline	(urine contamin*).ti	156
92	EMBASE	exp "PROTEIN URINE LEVEL"/	15094
93	EMBASE	*"MICROBIAL GROWTH"/ AND exp "PROTEIN URINE LEVEL"/	-
94	EMBASE	exp "BACTERIAL COUNT"/ AND exp "PROTEIN URINE LEVEL"/	4

95 EMBASE	*"BACTERIUM CONTAMINATION"/ AND exp "PROTEIN URINE LEVEL"/	2
96 EMBASE	*CONTAMINATION/ AND exp "PROTEIN URINE LEVEL"/	5
97 EMBASE	(contamin* OR growth).ti	404806
98 EMBASE	exp "PROTEIN URINE LEVEL" AND (contamin* OR growth).ti	7/317
99 EMBASE	(urin*).ti	175581
100 EMBASE	(exp "PROTEIN URINE LEVEL"/ AND (contamin* OR growth).ti) AND (urin*).ti	122
101 EMBASE	exp "MICROBIAL GROWTH"/ AND (exp "PROTEIN URINE LEVEL"/ AND (contamin* OR growth).ti)	0
102 EMBASE	exp "MICROBIAL GROWTH"/ AND exp "PROTEIN URINE LEVEL"/	16
103 EMBASE	(overgrowth).ti,ab	12562
104 EMBASE	exp "URINE CULTURE"/ AND (overgrowth).ti,ab	8