

Modern Tools for Bacterial Identification and Antibiotic Susceptibility Testing
Prof. Vincent Cattoir, University Hospital of Rennes, France
Prof. A. Denver Russell Memorial Teleclass

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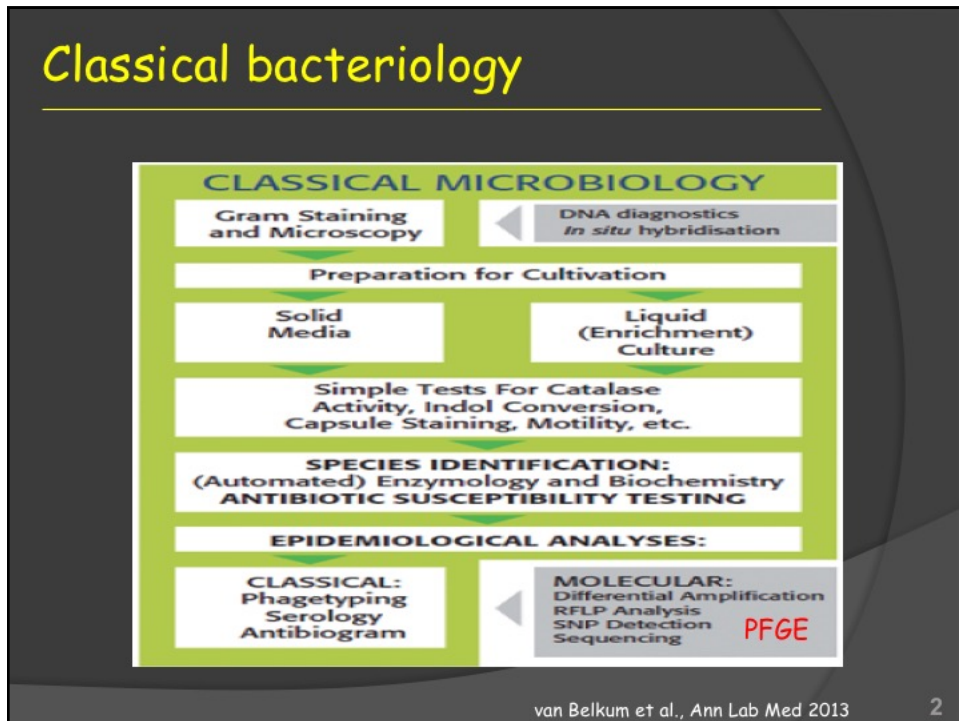
The A. Denver Russell
Memorial Teleclass

Modern tools for bacterial identification and antibiotic susceptibility testing

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Antibiogram Committee of the French Society for Microbiology (CA-SFM)

Hosted by Prof. Jean-Yves Maillard
Cardiff University, Wales

www.webbertraining.com April 9, 2019



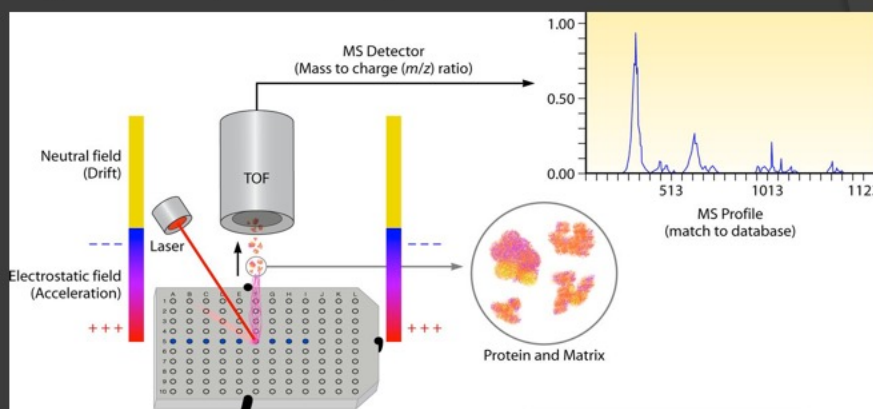
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Modern phenotypic approaches for
bacteriological diagnosis

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MALDI-TOF MS

Matrix-assisted laser desorption/ionization - Time-Of-Flight Mass Spectrometry



Clark et al., Clin Microbiol Rev 2013

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Commercial MALDI-TOF MS systems



Vitek MS
(bioMérieux)

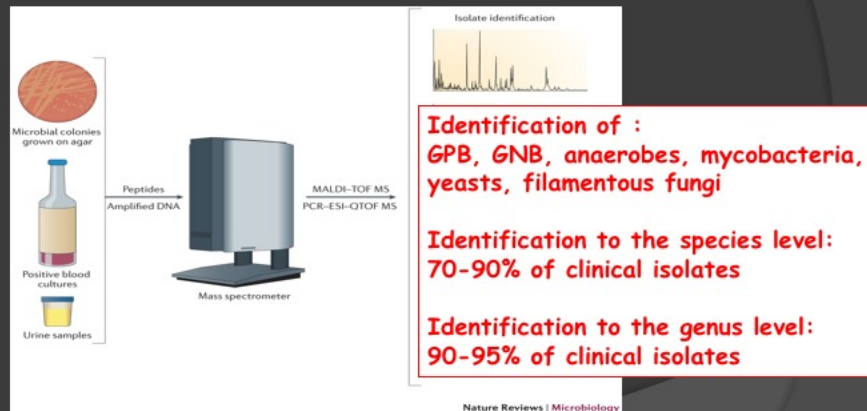


MALDI Biotyper CA system
(Bruker Daltonics)

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Application: Identification

Fast and reliable identification of bacteria and fungi from pure cultures as well as from positive BCs and urines ($>10^5$ CFU/mL)



Fournier et al., Nat Rev Microbiol 2013; Chen et al., J Clin Microbiol 2013; Feirrer et al., J Clin Microbiol 2013

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Advantages and limits

Detection method	Advantages	Disadvantages
Conventional; culture on microbiological media and identification by biochemical tests	<ul style="list-style-type: none"> • Sensitive • Inexpensive 	<ul style="list-style-type: none"> • Lengthy and time consuming process • Might require 24–48 h
MALDI-TOF MS	<ul style="list-style-type: none"> • Fast (3–5') • Accurate • Less expensive than molecular and immunological-based detection methods (1–2 €) • Trained laboratory personnel not required 	<ul style="list-style-type: none"> • High initial cost of the MALDI-TOF equipment (150 k€)

Some difficulties to identify some bacterial isolates:

- *E. coli* and *Shigella* spp.
- *S. pneumoniae* and *S. mitis/oralis*
- *Corynebacteria*
- *E. cloacae* complex
- Mucoïd strains

Singhal et al., Front Microbiol 2015

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Clinical impact

Prospective monocentric study (USA) comparing ID using MALDI-TOF MS vs. conventional method in patients with BCs positive for GNB (role of the antimicrobial stewardship+++)

Outcome	Pre-intervention cohort (n = 157)	Intervention cohort (n = 112)	P value
30-Day all-cause mortality	33 (21)	10 (8.9)	0.01
60-Day all-cause mortality	48 (30.6)	14 (12.5)	0.001
Inpatient mortality	29 (18.5)	9 (8)	0.02

Table 4 Univariate and multivariate logistic regression— independent predictors of 30-day mortality.

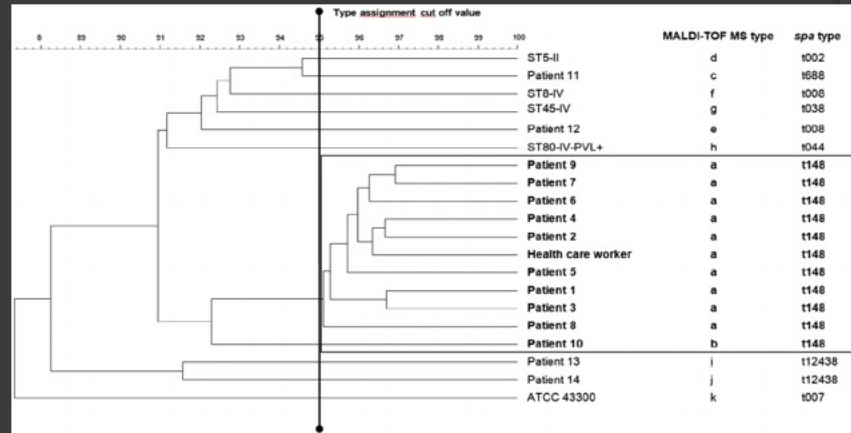
Variable	Univariate analysis			Multivariate analysis ^a		
	OR	95% CI	P value	OR	95% CI	P value
Nosocomial acquisition	2.35	1.21–4.55	0.01	1.03	0.38–2.84	0.95
Pre-infection LOS	1.02	1.0–1.05	0.04	1.01	0.98–1.04	0.49
APACHE II	1.15	1.08–1.22	<0.001	1.18	1.10–1.27	<0.001
Respiratory source	2.13	1.08–4.23	0.03	0.82	0.35–1.96	0.66
Genitourinary source	0.31	0.1–0.7	0.003	0.37	0.17–1.12	0.07
MALDI-TOF MS + antimicrobial stewardship	0.37	0.17–0.78	0.009	0.28	0.12–0.71	0.008
Time to active therapy	1.00	1.00–1.01	0.02	1.00	1.00–1.01	0.007

Perez et al., J Infect 2014

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Application: Typing

Comparison of MRSA clinical isolates during an outbreak in a neonatal ICU

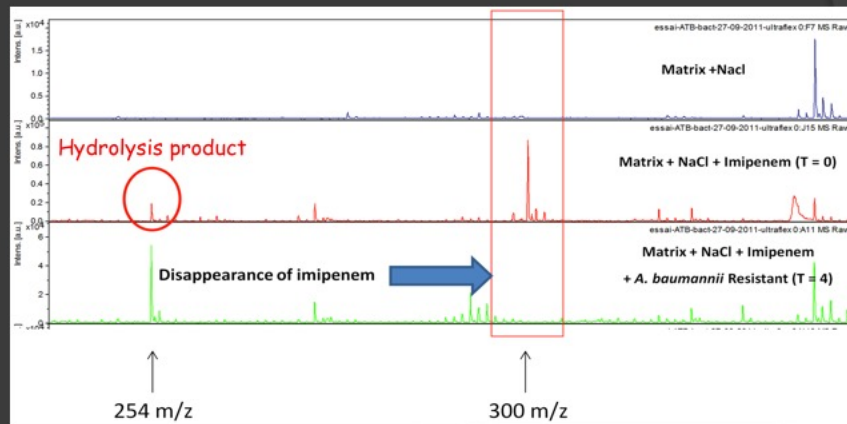


Steensels et al., Acta Clin Belg 2016

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Application: Detection of resistance

Detection of an enzymatic activity → resistance to carbapenems by production of carbapenemases in GNB (incubation: 0.5-4 hours)



Kempf et al., PLoS One 2016

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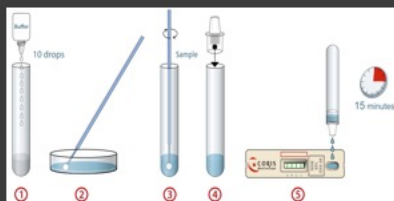
Chromogenic tests (ESBL-PE, CPE)

Principle/name of the test	Targeted enzymes	Required additional supplies	Delay for first/definitive results	Performances on cultured bacteria	Performances on clinical specimen
Colorimetric-chromogenic substrate					
β-Lacta test®	ESBL ^b	None	15 min	Sensitivity: 88% Specificity: 71%	Urine: sensitivity: 94%, specificity: 100% (positive blood culture: sensitivity: 95.7%, specificity: 100%)
β-CARBA test®	Carbapenemase	None	30 min	No direct comparison: sensibility 87%, specificity 100%	
Colorimetric-non-chromogenic substrate					
Rapid ESBL NP test®	ESBL ^b	None	20 min	Sensitivity: 95% Specificity: 100%	Urine: sensitivity 98%, specificity 99.8%, positive blood culture: sensitivity 100%, specificity 100%
Rapid ESBL Screen kit®	ESBL ^b	None	30 min/2 h	Sensitivity: 92% Specificity: 83%	
Rapidec® Carba NP test	Carbapenemase	None	30 min/2 h	Sensitivity: 99% Specificity: 100%	Positive blood culture: preliminary experimental data
Rapid CARB Screen®	Carbapenemase	None	5 min/2 h	Sensitivity: 89.5% Specificity: 70.9%	
Rapid Carb Blue kit®	Carbapenemase	None	15 min/1 h	No direct comparison: sensitivity 100%, specificity 100%	

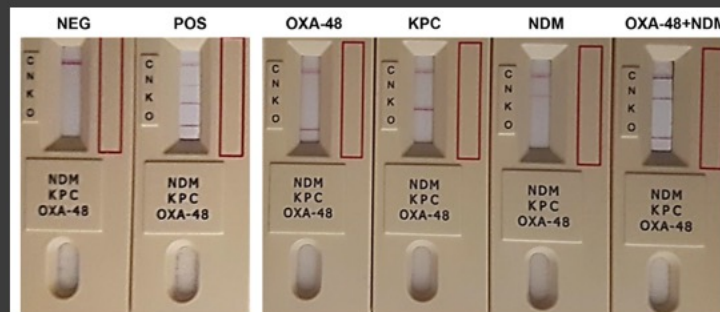
Fast (<2 hours), reliable, cheap
Usable on colonies, positive BCs and urines
Clinical impact poorly investigated

Decousser et al., Expert Rev Mol Diagn 2017 11

Immunochromatographic tests (CPE)



112 CPE clinical isolates
 100% sensitivity and specificity
 <15 €



O.K.N. kit (Coris)

Wareham et al., J Clin Microbiol 2017

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Modern genotypic approaches for bacteriological diagnosis

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Rapid molecular tests

- ✓ **Specific detection of bacterial pathogens:**
 - Screening for carriage: MRSA, VRE, CPE, GBS
 - Diagnosis of infection:
 - . *S. aureus*
 - . *C. difficile*
 - . *M. tuberculosis*

- ✓ **Detection of a panel of pathogens :**
 - Meningitis/Encephalitis
 - Bacteremia (positive BCs)
 - Gastroenteritis
 - Respiratory infections

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Commercial tests for MRSA

Organism detected	Assay	Company	Analysis platform	Probes	DNA target sequence	Specimen type	Time to result (h)
MRSA	BD GeneOhm MRSA ACP	Becton Dickinson	SmartCycler System	Molecular beacons	SCC _{mec} at <i>orfX</i> junction.	Nasal swab	2.5
	BD MAX MRSA	Becton Dickinson	BD MAX System	Taqman [®] probes	SCC _{mec} at <i>orfX</i> junction.	Nasal swab	2
	Xpert MRSA	Cepheid	GeneXpert Dx System	Taqman [®] probes	Insertion site (<i>attBc</i>) of SCC _{mec}	Nasal swab	1
	MRSA Advanced Test	Roche	LightCycler	FRET probes	Insertion site SCC _{mec} at <i>orfX</i> junction	Nasal swab	2
	NucliSENS EasyQ MRSA	bioMérieux	EasyQ System (NASBA)	Molecular beacons	SCC _{mec} at <i>orfX</i> junction and <i>mecA</i> gene for oxacillin resistance	Nasal swab	3

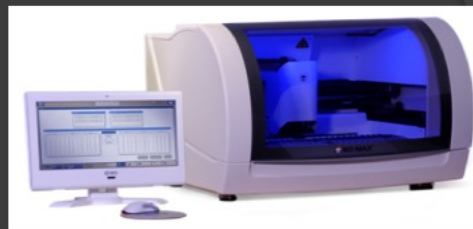
Sensitivity et specificity >90 %
 NPV > 95%

Palavecino, Meth Mol Biol 2014

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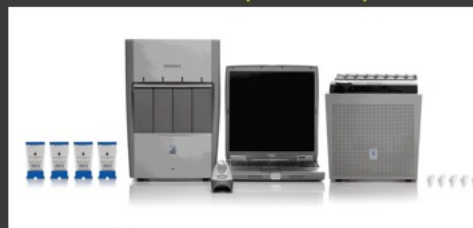
Automated systems

BD MAX system
 (Becton Dickinson)



~2 min HOT per sample

GeneXpert
 (Cepheid)



Widen et al., J Clin Microbiol 2014

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Clinical impact

Cluster randomized crossover trial (2008-2010) in Belgium comparing the Xpert MRSA kit (Cepheid) to the enriched chromogenic culture

Outcome	Intervention	Control	P value
Median reporting time for MRSA admission screening (h)	11	88	<0.001
Median time from admission to isolation of newly detected MRSA carriers (h)	25	96	<0.001
Proportion of isolation days/total MRSA positive patient days (%)			
For newly detected MRSA carriers	82 (943/1147)	73 (528/724)	
For all MRSA carriers	79(1955/2461)	82(1949/2385)	
MRSA acquisition during hospital stay			
No cases/No patients at risk (%)	3.2	3.2	0.986
No cases/1 000 patient-days	2.6	2.8	0.692

Roisin et al., PLoS One 2014

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Commercial tests for VRE

2 commercial kits for direct detection of VRE from stools/rectal swabs:

	Sens.	Spe.	PPV	NPV
Xpert <i>vanA/vanB</i>				
<i>vanA</i>	74-100	93-99	67-89	81-100
<i>vanB</i>	87-100	15-86	3-33	71-100
BD GeneOhm VanR				
<i>vanA</i>	43-88	96-100	82-100	67-97
<i>vanB</i>	75-100	21-85	7-37	100

Many false-positive results, especially for *vanB* → *van* genes identified in Gram-positive anaerobes:

- *vanB* : *Clostridium* spp., *Eggerthella lenta*, *Ruminococcus* spp.
- *vanD*, *vanG* : *Ruminococcus* spp.

Bourdon et al., Diagn Microbiol Infect Dis 2010 ; Usacheva et al., Am J Clin Pathol 2010 ; Gazin et al., Eur J Clin Microbiol Infect Dis 2012

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Clinical impact

Prospective study (2012) in France comparing Xpert *vanA/vanB* vs. enriched chromogenic culture

	Investigation of the first case in the diabetology unit (n=31 patients)	Investigation of a secondary case in the nephrology unit (n=22 patients)
From sampling, to sample reception	2.6 (1.7-2.6)	2.8 (1.1 - 3.8)
From sampling, to results	70.5 (69.4 - 70.5)	4.6 (4.0 - 18.9)
Total cost of microbiological testing	333.50	870.40
Overall loss of income (€)	13,968.70 to 85,175.00	0
Overall cost of the strategy (€)	14,302.20 to 86,175.50 [¶]	870.40 to 2,611.20 [¶]

→ Rapid decision about the best infection control strategy without loss of income due to discontinuation of patient transfers and admissions

Birgand et al., Antimicrob Resist Infect Control 2013

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Commercial tests for CPE

Numerous kits for detection directly from stools/rectal swabs

Test/Method	Turnaround time	Target species (n*)	Target carbapenemases	Sensitivity (%)	Specificity (%)	PPV† (%)	NPV‡ (%)
Check-Direct CPE	<180 min	Gram -negative bacilli (83-450)	KPC, VIM, NDM, OXA-48	97-1-100-0	94-0-100-0	100-0	0-0-70-0
LAMP/Leazyplex [®] superBug complete A	25-60 min	Gram -negative bacilli (14-450)	KPC, VIM, NDM, OXA-48	100-0	100-0 (83-0 for OXA-48 like genes)	ND	ND
TaqMan PCR	<120 min	Enterobacteriaceae (59, 1308)	Classes A, B & D	100-0	100-0	ND	ND
NucliSENSeasyQKPC	<120 min	Enterobacteriaceae (300)	KPC only	100-0	100-0	ND	ND
Xpert [®] Carba-R kit	52 min	Gram-negative bacilli (450)	KPC, VIM, NDM, OXA-48	100-00	100-0 (83-0 for OXA-48 like genes)	ND	ND
Microarray (Alere technologies)	2-8 h	Gram-negative bacilli (117)	Classes A, B, D	98-2	97-4	ND	ND
Microarray (Verigene BC-GN)	2 h	Gram-negative bacilli (104)	Classes A, B, D	96-8	100-0	ND	ND
Microarray (Check-MDR CT101-103)	≤6 h	Gram-negative bacilli (57-187)	Classes A, B, D	90.5-100.0 (KPC-85.0)**	95.7-100.0	97.6-100.0	99.0-100.0
Xpert MDR0 assay	<1 h	Gram-negative bacilli (328)	KPC, NDM, VIM	100-0	99-0-99-4	81-8-93-0	100-0

>90%

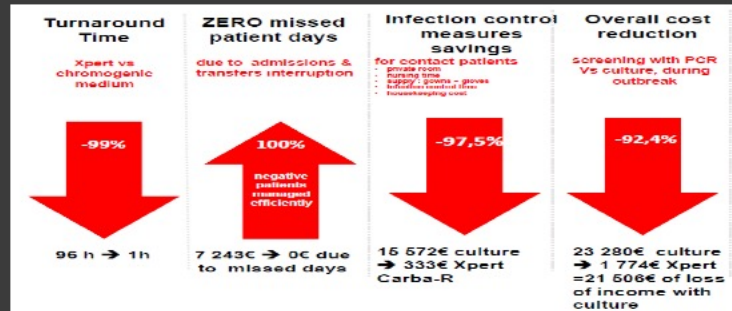
Sekyere et al., J Appl Microbiol 2015

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Clinical impact

Monocentric study (France, 2014) comparing the impact of the implementation of the Xpert Carba-R on infection control management and cost effectiveness respect to standard culture (1 OXA-48 case and 14 contact patients)



- No interruption of admissions and transfers
- No secondary case

Dubouix-Bourandy et al., ECCMID 2015

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Commercial tests for GBS

PCR Studies	n, sample size	Sensitivity, % (95% CI)	Specificity, % (95% CI)	Time to run test (mins)	Test – Site
Bergeron et al 2000 ²⁷	112	97.0 (82.5-99.8)	100 (86.9-100)	30-100	Conventional PCR vs. new fluorogenic PCR – Single center
Davies et al* 2004 ²⁸	803	94.0 (90.1-97.8)	95.9 (94.3-97.4)	40	IDI Strep – Multicenter
Gavino et al* 2007 ²⁹	55	95.8 (76.9-99.8)	64.5 (45.4-80.2)	<75	Xpert GBS Assay – Single center
Edwards et al 2008 ³⁰	784	91.1 (86.1-94.7) 79.3 (72.8-84.8)	96.0 (94.0-97.4) 95.4 (93.4-96.9)	75	Xpert GBS Assay vs. IDI Strep – Multicenter
Money et al* 2008 ³¹	190	90.7 (79.7-96.9)	97.6 (93.1-99.5)	99	IDI Strep – Canadian single center
El Helali et al 2009 ³²	968	98.5 (94.8-99.6)	99.6 (98.8-99.9)	<75	Xpert GBS Assay – French single center
Young et al* 2011 ³³	559	90.8 (84.6-95.2)	97.6 (95.6-98.8)	41	Xpert GBS Assay – Single center

† Vaginal/rectal samples and intrapartum standard culture as gold standard.
 *These studies also had comparisons with antepartum culture results.

<http://contemporaryobgyn.modernmedicine.com/> 22

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Commercial tests for *S. aureus*/MRSA

Organism detected	Assay	Company	Analysis platform	Probes	DNA target sequence	Specimen type	Time to result (h)
<i>S. aureus</i> and MRSA	Xpert MRSA/SA SSTI	Cepheid	GeneXpert System	Taqman [®] probes	<i>spa</i> for <i>S. aureus</i> , <i>SSCMec</i> and <i>mechA</i> gene for methicillin resistance	Wound swab	<1
	Xpert SA Nasal Complete	Cepheid	GeneXpert System	Taqman [®] probes	<i>spa</i> for <i>S. aureus</i> , <i>SSCMec</i> and <i>mechA</i> gene for methicillin resistance	Nasal swab	<1
	Xpert MRSA/SA Blood Culture [†]	Cepheid	GeneXpert System	Taqman [®] probes	<i>spa</i> for <i>S. aureus</i> , <i>SSCMec</i> and <i>mechA</i> gene for methicillin resistance	Blood Culture	<1
	StaphSR	BD GeneOhm	Smart Cycler	Molecular beacons	<i>nuc</i> gene for <i>S. aureus</i> , Insertion site (<i>attBcc</i>) of <i>SSCMec</i> for methicillin resistance	Blood Culture	1-1.5
	BC-GP [®]	Nanosphere	Verigene	Gold nanoparticles	<i>gyrB</i> for <i>S. aureus</i> and <i>mechA</i> gene for methicillin resistance	Blood culture	2.5

Sensitivity et specificity >90 %
 NPV > 95%

Palavecino, Meth Mol Biol 2014

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Performances in BSI (positive BCs)

Detection of *S. aureus*

Kit	No. HC	Sensitivity (%)	Specificity (%)
Xpert MRSA/SA BC	792	99.6	99.5
GeneOhm StaphSR	782	99.2	96.5

Detection of MRSA

Kit	No. HC	Sensitivity (%)	Specificity (%)
Xpert MRSA/SA BC	792	98.1	99.6
GeneOhm StaphSR	782	94.3	97.8

Possibility to use the Xpert MRSA/SA SSTI kit in PJIs and VAPs

Buchan et al., J Clin Microbiol 2015

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Clinical impact

Monocentric study (USA) comparing the Xpert MRSA/SA BC kit (group 1) vs. conventional method (group 2) in patients whose BCs revealed Gram-positive cocci in clusters (GPCC)

TABLE 2. Data on Drug Therapy for Patients with Bacteremia due to Methicillin-Susceptible *Staphylococcus aureus* at the Michael E. DeBakey Veterans Affairs Medical Center in Houston, Texas (2008–2009)

Variable	Group 1 ^a (n = 12)	Group 2 ^b (n = 48)	P ^c
Mean time to initiate MSS drug therapy, hours	5.2	49.8	.007
Median time to initiate MSS drug therapy, hours	0	48.5	.004
Mean duration of MRS drug therapy, hours	19.7	80.7	.003
No. (%) of patients not initially treated with MRS drug	3 (25.0)	5 (10.4)	
No. (%) of patients treated with MRS drug for unrelated condition	3 (25.0)	4 (8.3)	
No. (%) of patients treated with MRS drug for staphylococcal bacteremia	6 (50.0)	39 (81.3)	.025

But no difference in time to initiation of therapy for MRSA between groups ($P = 0.33$)

Parta et al., Infect Control Hosp Infect 2010 25

Commercial tests for *C. difficile*

Assay	Method	Target	DNA extraction	HOT (min) [†]	TAT (min) [†]	Cost per test	Sens. (%)	Spe. (%)
BD GeneOhm Cdiff	RT-PCR	tcdB	Manual	45	120	\$47 [†]	82-98	91-100
Ilumigene <i>C. difficile</i>	LAMP	tcdA	Manual	10	60	\$33 [†]	73-98	91-100
Xpert <i>C. difficile</i>	Multiplex RT-PCR	tcdB, cdt, tcdC1/117	Automated	10	60	\$52 [†]	93-100	91-99
BD MAX Cdiff	RT-PCR	tcdB	Automated	10	100	\$43 [†]	90-98	98-100
Portrait <i>C. difficile</i>	HDA	tcdB	Automated	10	100	\$25	98	93
ProGastro Cd	RT-PCR	tcdB	Automated (easyMAG)	45	180	\$25	77-100	93-99
Seeplex Diarrhea ACE	Multiplex PCR	tcdB	Manual	N/A	240	\$41 [†]	90	97

[†]HOT and TAT for a batch of 5 samples.

Limits :

Risk of false-negative results (mutations, deletions)

Do not detect free toxins in stools

Clinical benefit++

Le Guern et al., Expert Rev Mol Diagn 2013 26

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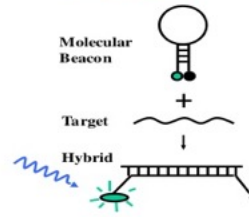
Detection of MTB

The Xpert MTB/RIF Molecular Beacon Assay

rpoB GENE 81 bp RIF RESISTANCE DETERMINING REGION

```
5' - GCACCAGCCAGCTGAGCCAAATTCATGGACCAGAAACAACCGCTGTGGGGTTGACCCACAAGCGGGACTGTGGGGCTG - 3'
3' - CGTGTCCGTGCAGCTCGTTAAGTACCTGGTCTTGTGGGACACAGCCCAACTGGGTTCGCGGCTGACAGCCGGAC - 5'
```

5-Probes bind to wild type (do not bind to mutant sequence)
1-Probe for SPC (*B. globigii*)
6-fluorescent dyes detected simultaneously
Delta Ct Max 5



<2 hours

Resp. and non-resp. samples:
Sensitivity of 100 % and 86 %
specificity of 100 % and 97 %

Malbruny et al., Int J Tuberc Lung Dis 2011

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Broad molecular panels

→ Syndromic approach

POTENTIAL ADVANTAGES

- Increase diagnostic yield as multiple targets are tested in one sample
- Conserve and optimize analysis of samples difficult to obtain (spinal fluid, vitreous fluids, synovial fluids)
- Simplify ordering algorithm as only one test needs to be requested
- Streamline workflow in the laboratory and reduce hands-on time
- Potential saving in reagents by testing multiple organisms at once compared to testing each pathogen separately
- Standardize testing

POTENTIAL DISADVANTAGES

- False positive results due to cross reactivity or unspecific amplification caused by multiple primers/targets present in the reaction
- False-negative results due to use of preferential amplification of one target over another
- Negative internal control due to exhaustion of reagents in samples with a high amount of one particular target
- Added cost of testing targets that may not be necessary in some patient populations
- High cost of commercial kits and instruments

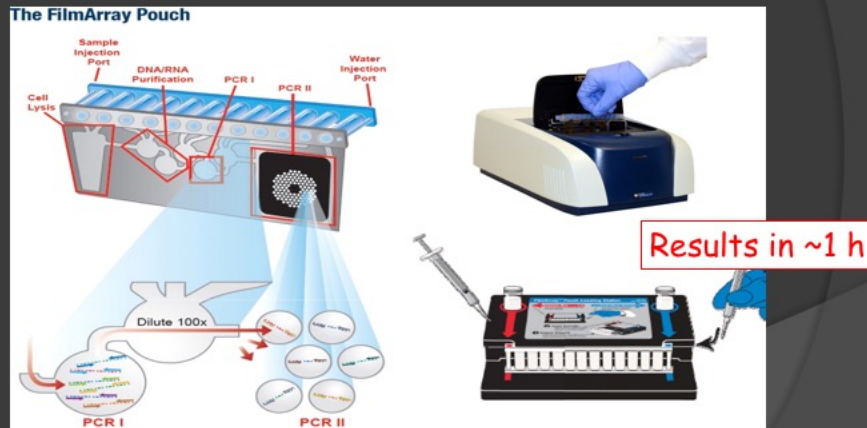
4 FDA-cleared systems (mostly automated)

<https://www.aacc.org/publications/cln/articles/2015/april/one-sample-multiple-results>

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FilmArray (Biofire, bioMérieux)

Principle: Two-stage nested PCR, the second stage involving parallel singleplex reactions followed by melt analysis

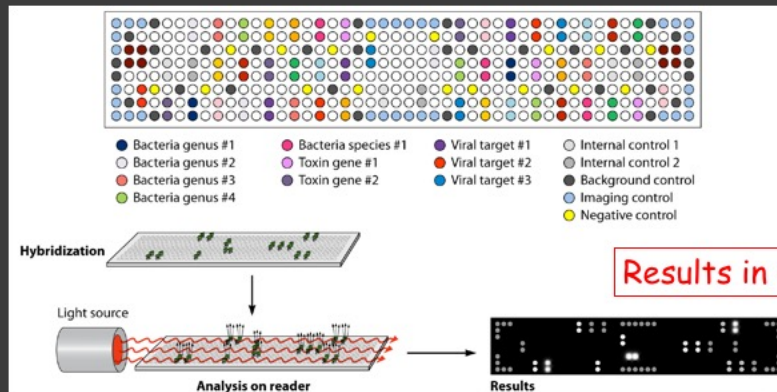


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Verigene (Nanosphere)



Principle: Multiplex PCR followed by solid-microarray detection using nanoparticle-conjugated probes



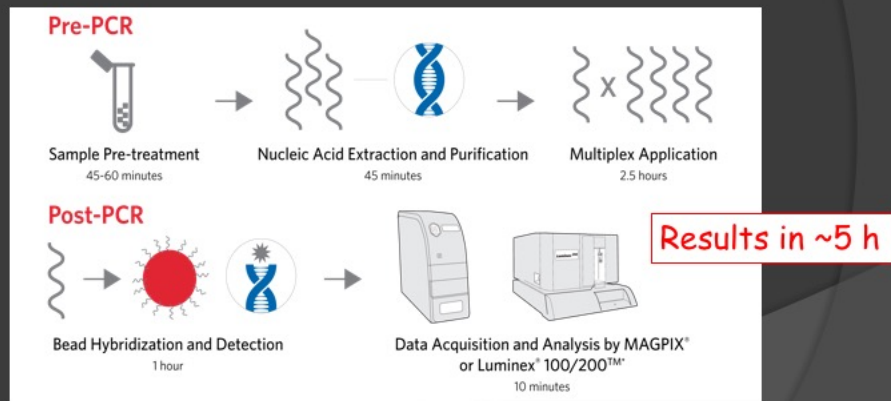
Buchan & Ledebauer, Clin Microbiol Rev 2015

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xTAG (Luminex)

Principle: Initial multiplex PCR by liquid-microarray detection using microbead-conjugated probes

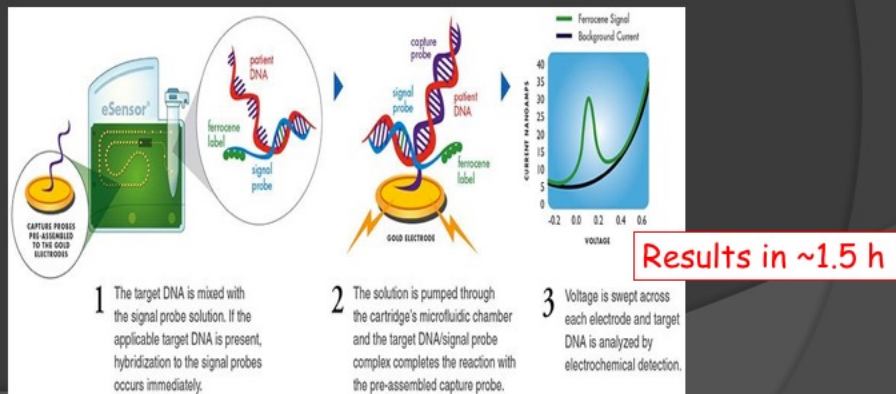


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ePlex (GenMark Dx)



Principle: Competitive DNA hybridization and electrochemical detection (eSensor)



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Meningitis/Encephalitis

		Sensitivity/PPA ^b			Specificity/NPA ^b		
		TP/(TP + FN) ^c	%	95% CI	TN/(TN + FP) ^c	%	95% CI
n = 1,643 CSF							
6	Bacteria						
	<i>E. coli</i> K1	2/2	100	34.2–100	1,557/1,558	99.9	99.6–100
	<i>H. influenzae</i>	1/1	100		1,558/1,559	99.9	99.6–100
	<i>L. monocytogenes</i>	0/0			1,560/1,560	100	99.8–100
	<i>N. meningitidis</i>	0/0			1,560/1,560	100	99.8–100
	<i>S. agalactiae</i>	0/1	0.0		1,558/1,559	99.9	99.6–100
	<i>S. pneumoniae</i>	4/4	100	51.0–100	1,544/1,556	99.2	98.7–99.6
7	Viruses						
	CMV	3/3	100	43.9–100	1,554/1,557	99.8	99.4–99.9
	EV	44/46	95.7	85.5–98.8	1,507/1,514	99.5	99.0–99.8
	HSV-1	2/2	100	34.2–100	1,556/1,558	99.9	99.5–100
	HSV-2	10/10	100	72.2–100	1,548/1,550	99.9	99.5–100
	HHV-6	18/21	85.7	65.4–95.0	1,532/1,536	99.7	99.3–99.9
	HPeV	9/9	100	70.1–100	1,548/1,551	99.8	99.4–99.9
VZV	4/4	100	51.0–100	1,553/1,556	99.8	99.4–99.9	
1	Yeast						
	<i>C. neoformans/C. gattii</i>	1/1	100		1,555/1,559	99.7	99.3–99.9

Leber et al., J Clin Microbiol 2015 33

Bacteremia (positive BCs)

2 automated systems

Gram-positive bacteria	Gram-negative bacteria	Candida species	Verigene (Nanosphere, Inc.)	
FilmArray Blood Culture Identification Panel (BioFire Diagnostics, LLC)			Gram-Positive Blood Culture Test	Gram-Negative Blood Culture Test
<i>Staphylococcus</i> species	<i>Klebsiella oxytoca</i>	<i>Candida albicans</i>	<i>Staphylococcus aureus</i>	<i>Escherichia coli</i>
<i>Staphylococcus aureus</i>	<i>Klebsiella pneumoniae</i>	<i>Candida glabrata</i>	<i>Staphylococcus epidermidis</i>	<i>Klebsiella pneumoniae</i>
<i>Streptococcus</i> species	<i>Serratia</i> species	<i>Candida krusei</i>	<i>Staphylococcus lugdunensis</i>	<i>Klebsiella oxytoca</i>
<i>Streptococcus agalactiae</i>	<i>Proteus</i> species	<i>Candida parapsilosis</i>	<i>Streptococcus anginosus</i> group	<i>Pseudomonas aeruginosa</i>
<i>Streptococcus pyogenes</i>	<i>Acinetobacter baumannii</i>	<i>Candida tropicalis</i>	<i>Streptococcus agalactiae</i>	<i>Acinetobacter</i> species
<i>Streptococcus pneumoniae</i>	<i>Haemophilus influenzae</i>		<i>Streptococcus pneumoniae</i>	<i>Citrobacter</i> species
<i>Enterococcus</i> species	<i>Neisseria meningitidis</i>		<i>Streptococcus pyogenes</i>	<i>Enterobacter</i> species
<i>Listeria monocytogenes</i>	<i>Pseudomonas aeruginosa</i>	19+5	<i>Enterococcus faecalis</i>	<i>Proteus</i> species
	Enterobacteriaceae		<i>Staphylococcus</i> species	
	<i>Escherichia coli</i>		<i>Streptococcus</i> species	11
	<i>Enterobacter cloacae</i> complex		<i>Listeria</i> species	8
Resistance genes	Resistance genes	3	Resistance genes	Resistance genes
<i>mecA</i>	<i>bla_{IPC}</i>		<i>mecA</i>	<i>bla_{NDM}</i>
<i>vanA/vanB</i>			<i>vanA</i>	<i>bla_{IPC}</i>
			<i>vanB</i>	<i>bla_{OXA2}</i>
				<i>bla_{VIM}</i>
				<i>bla_{CTX-M}</i>

Patel, Mayo Clin Proc 2016 34

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Prof. A. Denver Russell Memorial Teleclass

Clinical impact

Retrospective monocentric (USA) evaluating the clinical impact of rapid PCR (Verigene BC-GN) on positive BCs (n = 195 patients)

Clinical outcome	Pre-BC-GN	Post-BC-GN	P value
Mean time from initial Gram stain to BC-GN identification, h	NA ^a	3.5	NA
Mean time from initial Gram stain to organism identification, h	37.9	10.9	<0.001 ^b
Mean time from initial Gram stain to effective therapy, h			
All cases	10.2	6.5	0.12 ^b
Cases on suboptimal empirical therapy	30.3	19.1	0.12 ^b
No. of cases in which therapy was de-escalated	33	37	0.66 ^c
Mean time from initial Gram stain to de-escalation, h	40.9	34.1	0.14 ^b
Recurrence of bacteremia, no. (%)	8 (8.2)	3 (3.1)	0.21 ^c
Mean total length of stay in hospital, days	15.2	18.0	0.52 ^b
Mean length of hospital stay after positive culture, days	9.7	9.4	0.87 ^b
Mean length of stay in ICU, days	16.2	12.0	0.03 ^b
30-day mortality, no. (%)	19 (19.2)	8 (8.1)	0.04 ^c
ESBL cases, no.	15	11	0.53 ^c
Length of stay in hospital, days	12.0	13.5	0.59 ^b
Mean time to effective therapy, h (no.) ^d	41.4 (9)	7.3 (9)	0.04 ^b
30-day mortality, no. (%)	4 (26.7)	0 (0)	0.11 ^c

Walker et al., J Clin Microbiol 2016

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Gastroenteritis

Target	Targets on the panel		
	FilmArray Gastrointestinal Panel (BioFire Diagnostics, LLC)	xTAG Gastrointestinal Pathogen Panel (Luminex Corporation)	Verigene Enteric Pathogens Test (Nanosphere, Inc.)
Bacteria			
<i>Campylobacter</i> species	✓	✓	✓
<i>Clostridium difficile</i>	✓	✓	✓
<i>Plesiomonas shigelloides</i>	✓	✓	✓
<i>Salmonella</i> species	✓	✓	✓
<i>Yersinia enterocolitica</i>	✓	✓	✓
<i>Vibrio cholerae</i>	✓	✓	✓
<i>Vibrio</i> species	✓	✓	✓
Enteroaggregative <i>Escherichia coli</i>	✓	✓	✓
Enteropathogenic <i>Escherichia coli</i>	✓	✓	✓
Enterotoxigenic <i>Escherichia coli</i>	✓	✓	✓
Shiga toxin-producing <i>Escherichia coli</i>	✓	✓	✓
<i>Escherichia coli</i> O157	✓	✓	✓
<i>Shigella</i> species (enteroinvasive <i>Escherichia coli</i>)	✓	✓	✓
Parasites			
<i>Cryptosporidium</i> species	✓	✓	✓
<i>Cyclospora cayentanensis</i>	✓	✓	✓
<i>Entamoeba histolytica</i>	✓	✓	✓
<i>Giardia lamblia</i>	✓	✓	✓
Viruses			
Adenovirus serotypes 40/41	✓	✓	✓
Astrovirus	✓	✓	✓
Norovirus	✓	✓	✓
Rotavirus	✓	✓	✓
Sapovirus	✓	✓	✓

Patel, Mayo Clin Proc 2016

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Respiratory infections

From nasopharyngeal swab specimens

Assay*	Manufacturer	Methodology	Preextraction required	Viruses reported ^b
FilmArray RP ^c	BioFire Diagnostics	Endpoint melt curve analysis	No	AdV; CoV HKU1, NL63; influenza virus A (H1/2009, H1, H3); influenza virus B; MPV; PIV1, -2, -3, -4; RSV; RhV/EV
eSensor RVP	GenMark Dx	Voltammetry	Yes	AdV (C, B/E); influenza virus A (H1/2009, H1, H3); influenza virus B; MPV; PIV1, -2, -3; RSV (A/B); RhV
xTAG RVP1	Luminex Molecular Diagnostics	Fluorescence-labeled bead array	Yes	AdV; influenza virus A (H1, H3); influenza virus B; MPV; PIV1, -2, -3; RSV (A/B); RhV/EV
xTAG RVP fast	Luminex Molecular Diagnostics	Fluorescence-labeled bead array	Yes	AdV; influenza virus A (H1, H3); influenza virus B; MPV; RSV; RhV/EV
ePlex RPP	GenMark Dx	Voltammetry	No	AdV; CoV (229E, HKU1, NL63, OC43); influenza virus A (H1/2009, H1, H3); influenza virus B; MPV; PIV1, -2, -3, -4; RSV (A/B); RhV/EV

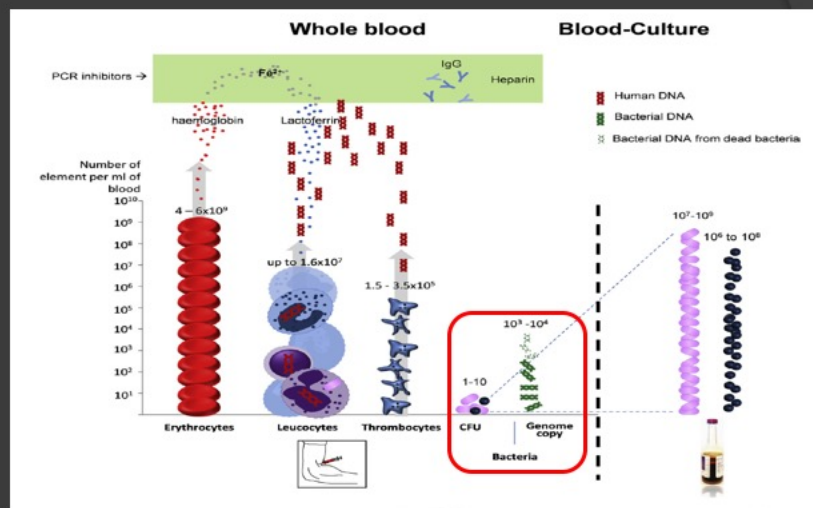
*Bacteria detected: *B. pertussis*, *M. pneumoniae*, *C. pneumoniae*

**Bacteria detected: *M. pneumoniae*, *C. pneumoniae*

Popowitch et al., J Clin Microbiol 2013

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Bloodstream infections (BSI)



Opota et al., Clin Microbiol Infect 2015

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Iridica platform (Abbott)

Technology PCR-ESI-MS
 (new version of the Plex-ID)

Expensive equipment



ASSAY	COVERAGE	SAMPLE TYPE
BAC BSI	750+ Bacteria, Candida and 4 Antibiotic Resistance Markers: <i>mecA</i> , <i>vanA</i> , <i>vanB</i> and <i>kpc</i>	Serif EDTA whole blood
BAC SFT		Sterile fluids and tissues
BAC LRT	Identical coverage as BAC BSI and BAC SFT with additional semi-quantitative threshold	BAL and ETA
Fungal	200+ fungi	BAL and Isolates
Viral IC	130+ viruses in 13 reporting groups	Plasma

Direct detection from blood ~6-8 h
 Detection of R genes (*mecA*, *vanA*, *vanB*, *bla_{KPC}*)

Ecker et al., Nat Rev Microbiol 2008 ; Lavigne et al., Clin Chem Lab Med 2012 ; Wolk et al., J Mol Diagn 2012

41

NGS in bacteriology

✓ Genomics (Whole Genome Sequencing - WGS)

- List of virulence genes
- In silico antibiogram
- Molecular typing

✓ Metagenomics

- Microbiota diversity
- Personalized medicine

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Current NGS platforms

Platform	Instrument	Form factor	Sequencing technology ^a	Instrument cost	Read length (bp)	Run time (modes)	Single read output (modes) ^c	Sequence output (modes)	Approx cost per isolate (bacterial)
Illumina	MiniSeq	Benchtop	SBS	\$50,000	2 x 150	24 h/17 h	25 M/8 M	7.5 Gb/2.4 Gb	TBD
	MiSeq(Dx)	Benchtop	SBS	\$99,000	2 x 300	56 h	25 M	15 Gb	\$60-70
	NextSeq(Dx)	Benchtop	SBS	\$250,000	2 x 150	29 h/26 h	400 M/130 M	120 Gb/39 Gb	\$50-60
	HiSeq (various models)	Capital	SBS	\$750,000	2 x 125	6 days/40 h		1 Tb/180 Gb	\$50-60
ThermoFisher IonTorrent	PGM	Benchtop	Semiconductor	\$50,000	400	7 h	5.5 M	2 Gb	\$60-70
	Proton	Benchtop	Semiconductor	\$150,000	200	4 h	83 M	10 Gb	\$60-70
	SS	Benchtop	Semiconductor	\$65,000	400	2.5 h/4 h	5 M/80 M	15 Gb	\$50-60
	SSXL	Benchtop	Semiconductor	\$150,000	400	2.5 h/4 h	5 M/80 M	15 Gb	\$50-60

MacCannell, Clin Microbiol News 2016

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In silico antibiogram of *S. aureus*

Creation of a panel of resistance mechanisms (501 reference strains) tested against 401 clinical isolates:

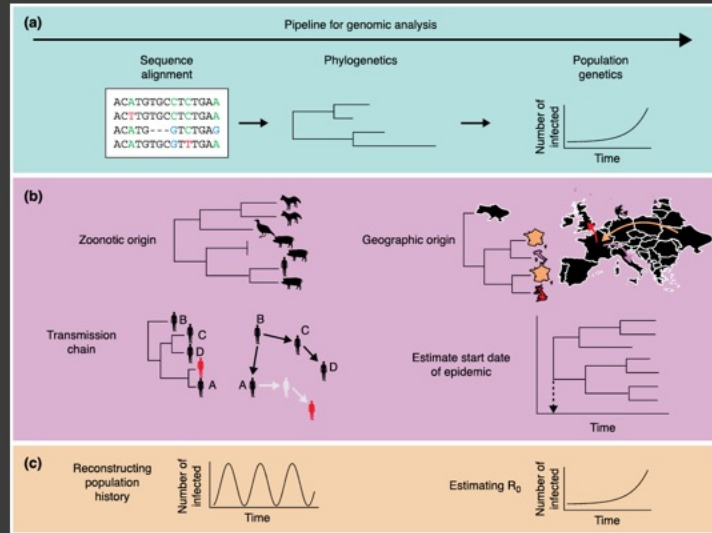
Antimicrobial agent	No. of isolates resistant by phenotype		No. of isolates susceptible by phenotype		Total no. of isolates	Very major error rate (%) (95% CI)	Major error rate (%) (95% CI)	Sensitivity (95% CI)	Specificity (95% CI)
	Susceptible by genotype ^a	Resistant by genotype	Susceptible by genotype	Resistant by genotype ^b					
Penicillin	3 (2)	379	84	25 (9)	491	0.6 (0.1-1.8)	5.1 (3.3-7.4)	0.99 (0.98-1.00)	0.77 (0.68-0.84)
Methicillin	2 (1)	55	432	2 (1)	491	0.4 (0.05-1.5)	0.4 (0.05-1.5)	0.96 (0.87-0.99)	1.00 (0.98-1.00)
Ciprofloxacin	6 (4)	64	420	1 (0)	491	1.2 (0.4-2.6)	0.2 (0.05-1.1)	0.91 (0.82-0.96)	1.00 (0.98-1.00)
Erythromycin	4 (2)	79	405	3 (3)	491	0.8 (0.2-2)	0.6 (0.1-1.8)	0.95 (0.87-0.98)	0.99 (0.98-1.00)
Clindamycin	2 (2)	77	2	0	81	2.5 (0.3-8.6)	0.0 (0-4.4)	0.97 (0.90-1.00)	1 (0.20-1.00)
Tetracycline	0	18	471	2 (2)	491	0.0 (0-0.7)	0.4 (0.05-1.5)	1.00 (0.78-1.00)	1.00 (0.98-1.00)
Vancomycin	0	0	491	0	491	0.0 (0-0.7)	0.0 (0-0.7)	N/A ^c	1.00 (0.99-1.00)
Fusidic acid	4 (4)	39	448	0	491	0.8 (0.2-2)	0.0 (0-0.7)	0.91 (0.77-0.97)	1.00 (0.99-1.00)
Trimethoprim	2 (2)	1	197	2 (1)	202	1.0 (0.1-3.5)	1.0 (0.1-3.5)	0.33 (0.02-0.87)	0.99 (0.96-1.00)
Gentamicin	2 (2)	2	487	0	491	0.4 (0.05-1.5)	0.0 (0-0.7)	0.50 (0.09-0.91)	1.00 (0.99-1.00)
Mupirocin	0	2	489	0	491	0.0 (0-0.7)	0.0 (0-0.7)	1.00 (0.20-1.00)	1.00 (0.99-1.00)
Rifampin	0	5	486	0	491	0.0 (0-0.7)	0.0 (0-0.7)	1.00 (0.46-1.00)	1.00 (0.99-1.00)
Overall	25 (19)	644	4,410	35 (16)	5,112	0.5 (0.3-0.7)	0.7 (0.5-0.9)	0.97 (0.95-0.98)	0.99 (0.99-1.00)

FDA cutoffs : <1,5 % <3 %

Gordon et al., J Clin Microbiol 2014

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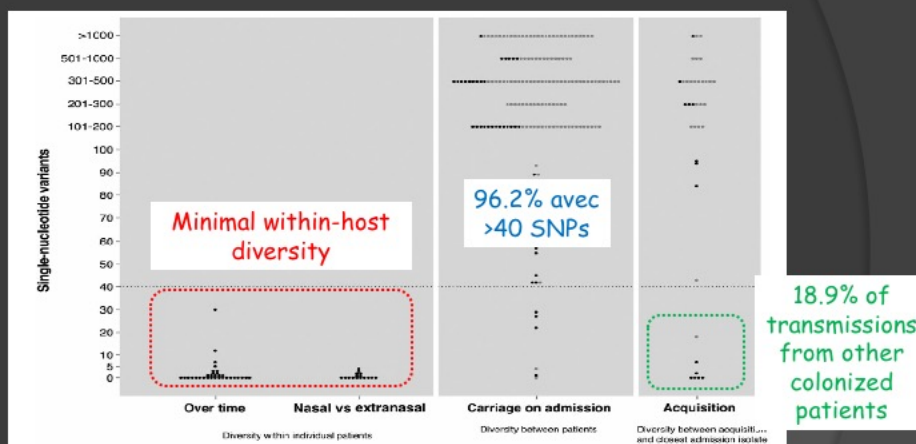
Molecular epidemiology by WGS



Li et al., Genome Biol 2014

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Transmission mapping



Conventional methods falsely identified 3 patient-to-patient transmissions (all MRSA) and failed to detect 2 acquisitions and 4 transmissions (2 MRSA)

Price et al., CID 2014

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Current limits of WGS

Current limitations

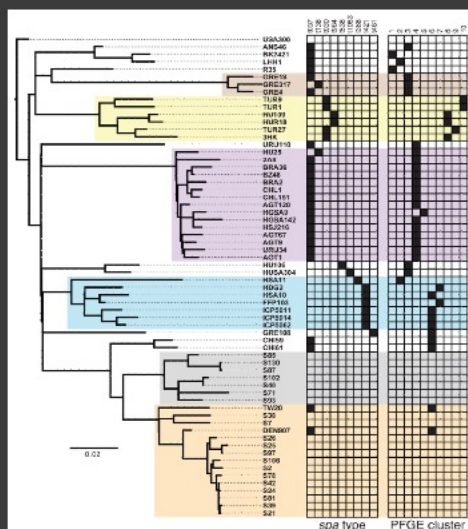
- Cost of personal genome sequencing platforms
- Speed of data analysis
- Limited user-friendly bioinformatics platforms available for sequence assembly and data analysis
- Education because of poor knowledge of genomics and bioinformatics among diagnostic microbiologists
- Limited reference sequence data for many species
- Difficulties with DNA extraction directly from clinical samples

+ Interpretative criteria for typing?

Sherry et al., J Clin Microbiol 2013 ; Croucher & Didelot, Curr Opin Microbiol 2015 ; Gilchrist et al., Clin Microbiol Rev 2015

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'Molecular clock'



Evolution and diversification within a bacterial population by accumulation of mutations over time

May depend of different settings, hosts or lineages

In *S. aureus*:

- Mutation rate from 2.0 to 3.4 × 10⁻⁶ mutations per site/year
- ie 5.6 to 9.5 mutations / year
- ie 1 SNV / 5-10 weeks

Definition of a clone ?
 Species specific?

Harris et al., Science 2010 ; Price et al., J Hosp Infect 2013 ; Price et al., Clin Infect Dis 2014 48

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Third-generation NGS

- Long-read sequencing (3-20 kb)
- No amplification of DNA fragments
- High error rates but recent improvements

Platform	Instrument	Form factor	Sequencing technology ^a	Instrument cost	Read length (bp)	Run time (modes)	Single read output (modes) ^c	Sequence output (modes)	Approx cost per isolate (bacterial)
Pacific BioSciences	RSII	Capital	SMRT	\$700,000	10,000-15,000	4 h	50,000	1 Gb	\$500-600
	Sequel	Capital	SMRT	\$350,000	10,000-20,000	6 h	350,000	7 Gb	TBD
Oxford Nanopore	MinION Mki	Portable	Nanopore	\$1,000	>10,000	1 min to 48 h	2.2 M/4.4 M	Up to 42 Gb	TBD
	PromethION	Benchtop	Nanopore	TBD ^b	>10,000	1 min to 48 h	625 M/1.25 B	6 Tb/12 Tb	TBD

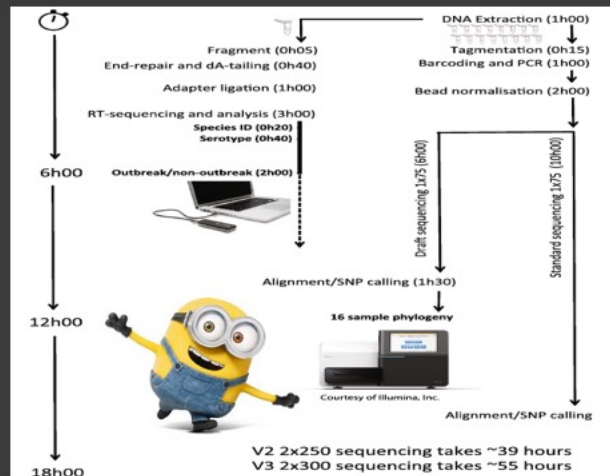
^aSBS, sequencing by synthesis; SMRT, single-molecule real-time sequencing.
^bTBD, to be determined.

MacCannell, Clin Microbiol News 2016

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Applications - MinION

Hospital outbreak of *Salmonella* Enteritidis (>30 cases)

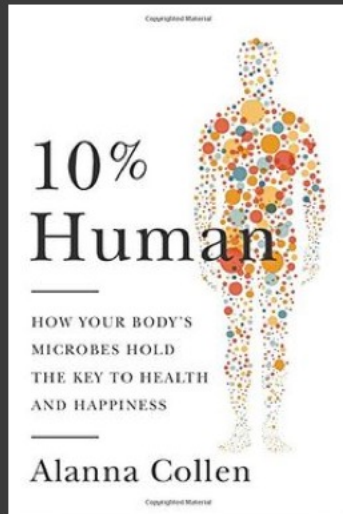


Quick et al., Genom Biol 2015

50

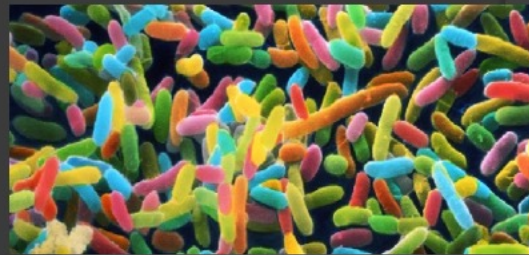
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Human microbiota and microbiome



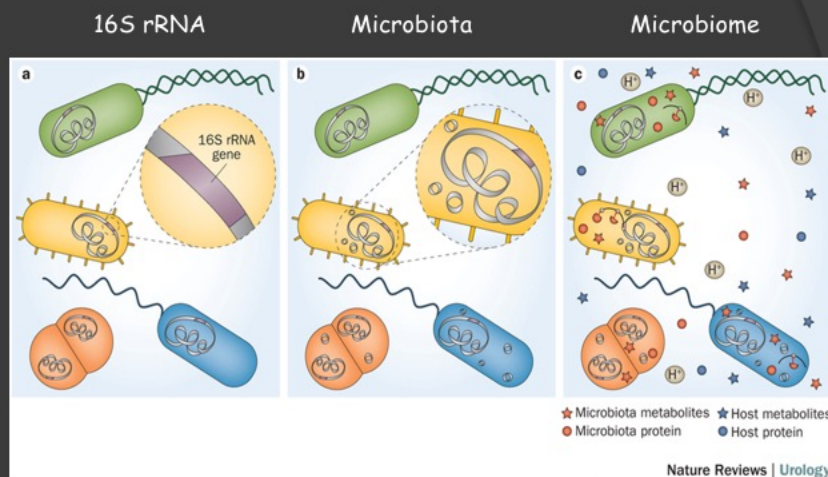
10¹⁴ bacteria, ie :

- 10 x more than human cells
- 1-3 % du poids (1-2 kg)
- >1000 different species
- 150 x more of bacterial genes
- No identical human microbiota



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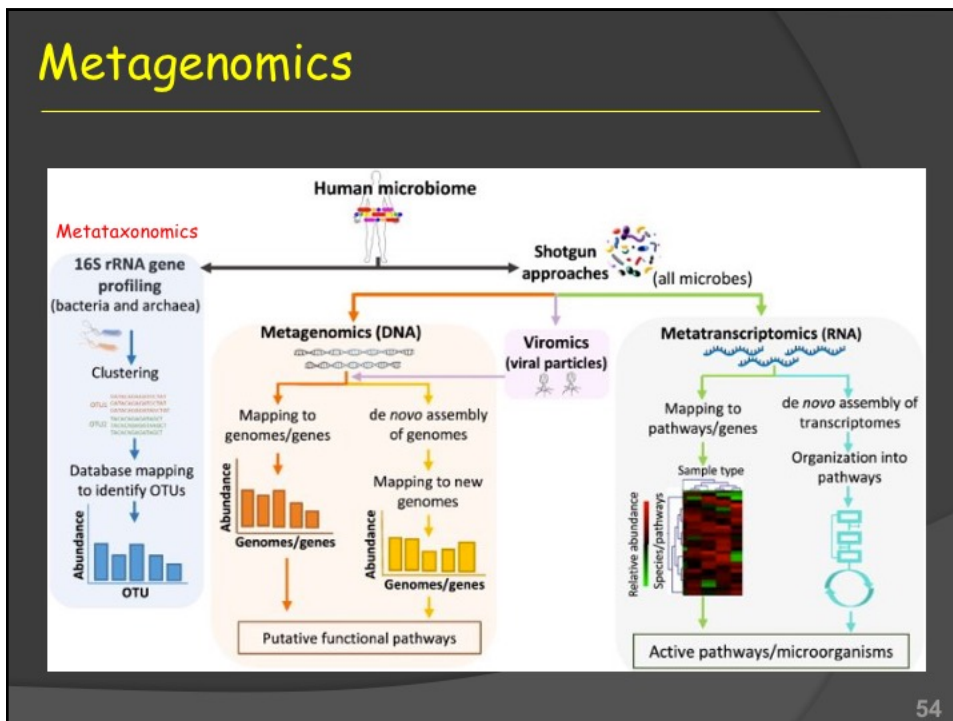
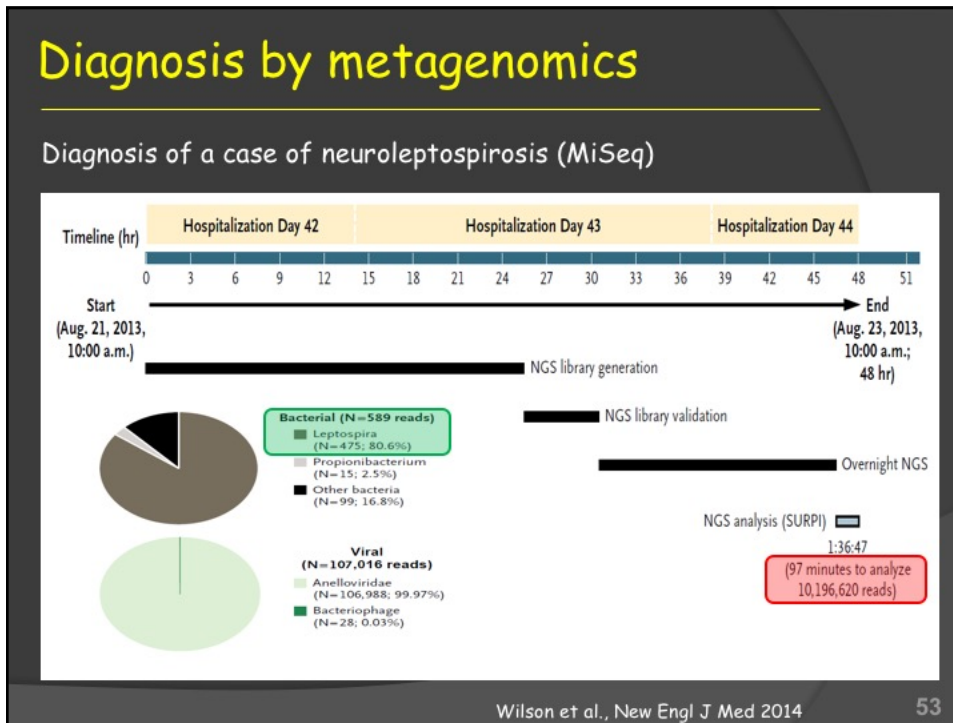
Microbiota & Microbiome



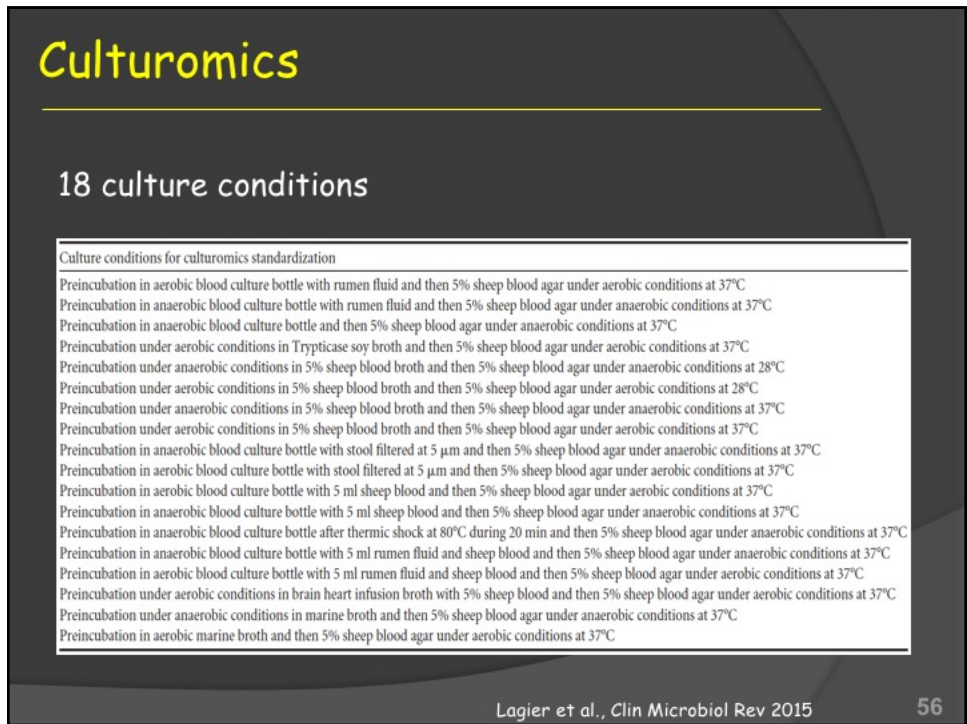
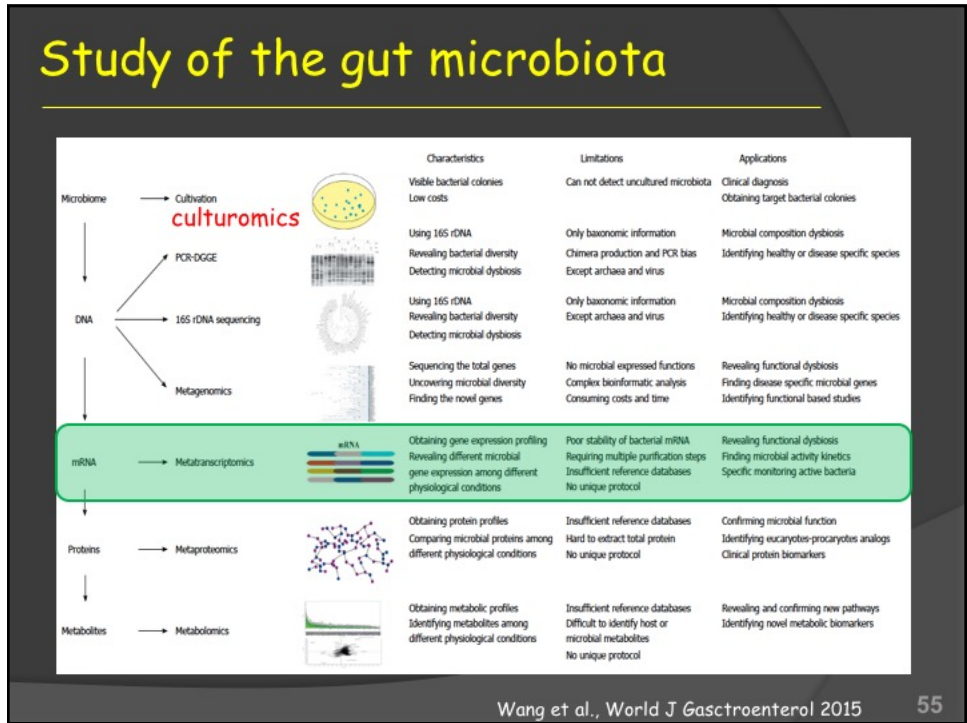
Whiteside et al., Nat Rev Urol 2015

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Challenges in bioinformatics

Processing and long-term archiving of huge amounts of data (x 10,000 compared to 1995)

Simplification of bioinformatic tools (user-friendly softwares)



Need of academic training for clinical microbiologists

Improvement of DB quality
Integration and standardization of meta-data

Caboche et al., Pathogens 2014

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Softwares



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Databases

Center for Genomic Epidemiology

Home Organization Project Services Contact

Services

- Identification of acquired antibiotic resistance genes: *ShigaToxin*
- Identification of functional integron antibiotic resistance determinants: *ShigaToxin*
- Identification of acquired antibiotic resistance genes using *ShigaToxin*
- Prediction of a bacterium's conjugative events: *ShigaToxin*
- Identification of acquired antibiotic genes: *ShigaToxin*
- Determination of antibiotic resistance: *ShigaToxin*
- SNP/indel identification: *ShigaToxin*
- SNP/indel identification: *ShigaToxin*
- SNP/indel identification: *ShigaToxin*

The Comprehensive Antibiotic Resistance Database

A bioinformatic database of resistance genes, their products and associated phenotypes.
 3670 Ontology Terms, 2353 Reference Sequences, 944 SNPs, 2283 Publications, 2356 AMR Detection Models

ARD - Antibiotic Resistance Genes Database

Welcome to ARDB Home Page

Our motivations in creating ARDB are to:

- provide a centralized compendium of information on antibiotic resistance
- facilitate the consistent annotation of resistance information in newly sequenced organisms
- facilitate the identification and characterization of new genes

Database Statistics

Version: 1.1
Last Update: July 5, 2009
Genes: 2337
Types: 380
Antibiotics: 249
Genomes: 532
Species: 1737
Genes: 257
Vectors: Plasmids: 2881

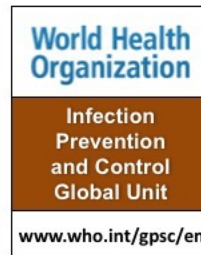
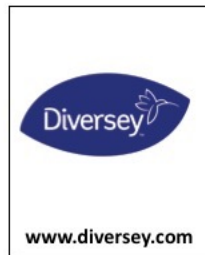
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www.webbertraining.com/schedule1.php	
April 18, 2019	<p>INFECTON CONTROL ISSUES IN HEALTHCARE CONSTRUCTION, PART 1 - RENOVATION</p> <p>Speaker: Andrew Streifel, University of Minnesota</p> <p><i>(FREE ... WHO Teleclass - Europe ... Special Lecture for 5 May)</i></p> <p>CLEAN CARE FOR ALL - IT'S IN YOUR HANDS</p> <p>Speaker: Prof. Didier Pittet and Prof. Benedetta Allegranzi, World Health Organization, Geneva</p> <p>Sponsored by the World Health Organization Infection Control Global Unit</p>
May 3, 2019	<p>IMMIGRANT AND REFUGEE POPULATIONS: A PUBLIC HEALTH AND POLICY PERSPECTIVE ON A CONTINUING GLOBAL CRISIS</p> <p>Speaker: Prof. Sotirios Tsiodras, National and Kapodistrian University of Athens, Greece</p>
May 16, 2019	<p><i>(FREE Teleclass – Broadcast live from the IPAC Canada conference)</i></p> <p>To be announced</p> <p>Speaker: To be confirmed</p>
May 27, 2019	<p><i>(FREE Teleclass – Broadcast live from the IPAC Canada conference)</i></p> <p>ONE HEALTH: THE RISKS AND REWARDS OF LOVING ANIMALS</p> <p>Speaker: Prof. Jason Stull, Ohio State University</p>
May 29, 2019	

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