MDROs & Diagnostic Stewardship

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NAMS AIIMS BHOPAL: 10 Oct 2019

Bad Bugs, No Drugs

As Antibiotic Discovery Stagnates ...
A Public Health Crisis Brews

IDSA
Infectious Diseases Society of America

July 2004

Adapted from Infectious Diseases Society of American (IDSA). Available at http://www.idsociety.org/pa/IDSA_Paper4_final_web.pdf. Accessed July 2005;


Potent
antibiotics

13tlid1071

The Lancet Infectious Diseases Commission

D-13-01071

NH

Version 1

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Antibiotic resistance—the need for global solutions

Ramanan Laxminarayan, Adriano Duse, Chand Wattal, Anita K M Zaidi, Heiman F L Wertheim, Nithima Sumpradit, Erika Vlieghe, Gabriel Levy Hara, Ian M Gould, Herman Goossens, Christina Greko, Anthony D So, Maryam Bigdeli, Göran Tomson, Will Woodhouse, Eva Ombaka, Arturo Quizhpe Peralta, Farah Naz Qamar, Fatima Mir, Sam Kariuki, Zulfiqar A Bhutta, Anthony Coates, Richard Bergstrom, Gerard D Wright, Eric D Brown, Otto Cars

The causes of antibiotic resistance are complex and include human behaviour at many levels of society; the consequences affect everybody in the world. Similarities with climate change are evident. Many efforts have been made to describe the many different facets of antibiotic resistance and the interventions needed to meet the challenge. However, coordinated action is largely absent, especially at the political level, both nationally and internationally. Antibiotics paved the way for unprecedented medical and societal developments, and are today indispensible in all health systems. Achievements in modern medicine, such as major surgery, organ transplantation, treatment of preterm babies, and cancer chemotherapy, which we today take for granted, would not be possible without access to effective treatment for bacterial infections. Within just a few years, we might be faced with dire setbacks, medically, socially, and economically, unless real and unprecedented global coordinated actions are immediately taken. Here, we describe the global situation of antibiotic resistance, its major causes and consequences, and identify key areas in which action is urgently needed.

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http://dx.doi.org/10.1016/S1473-3099(13)70316-5, and
http://dx.doi.org/10.1016/S1473-3099(13)70299-8

Part 1: Global epidemiology of antibiotic resistance and use

The rise of resistance

The decreasing effectiveness of antibiotics in treating common infections has quickened in recent years, and

Resistance has spread worldwide. Antibiotic-resistant gonorrhoea emerged in Vietnam in 1967,[5] then spread to the Philippines, and finally the USA.[6] NDM enzymes, first reported in 2008, are now found worldwide.[7] The distribution of resistance genes, such as Enterobacteriaceae-

The NEW ENGLAND JOURNAL of MEDICINE

Antibiotic-Resistant Bugs in the 21st Century — A Clinical Super-Challenge

- It is more difficult than ever to eradicate infections caused by antibiotic- resistant “superbugs,”
- And the problem is exacerbated by a dry pipeline for new antimicrobials with bactericidal activity against gram-negative bacteria

Cesar A. Arias. NEJM 2009, 360:439-443

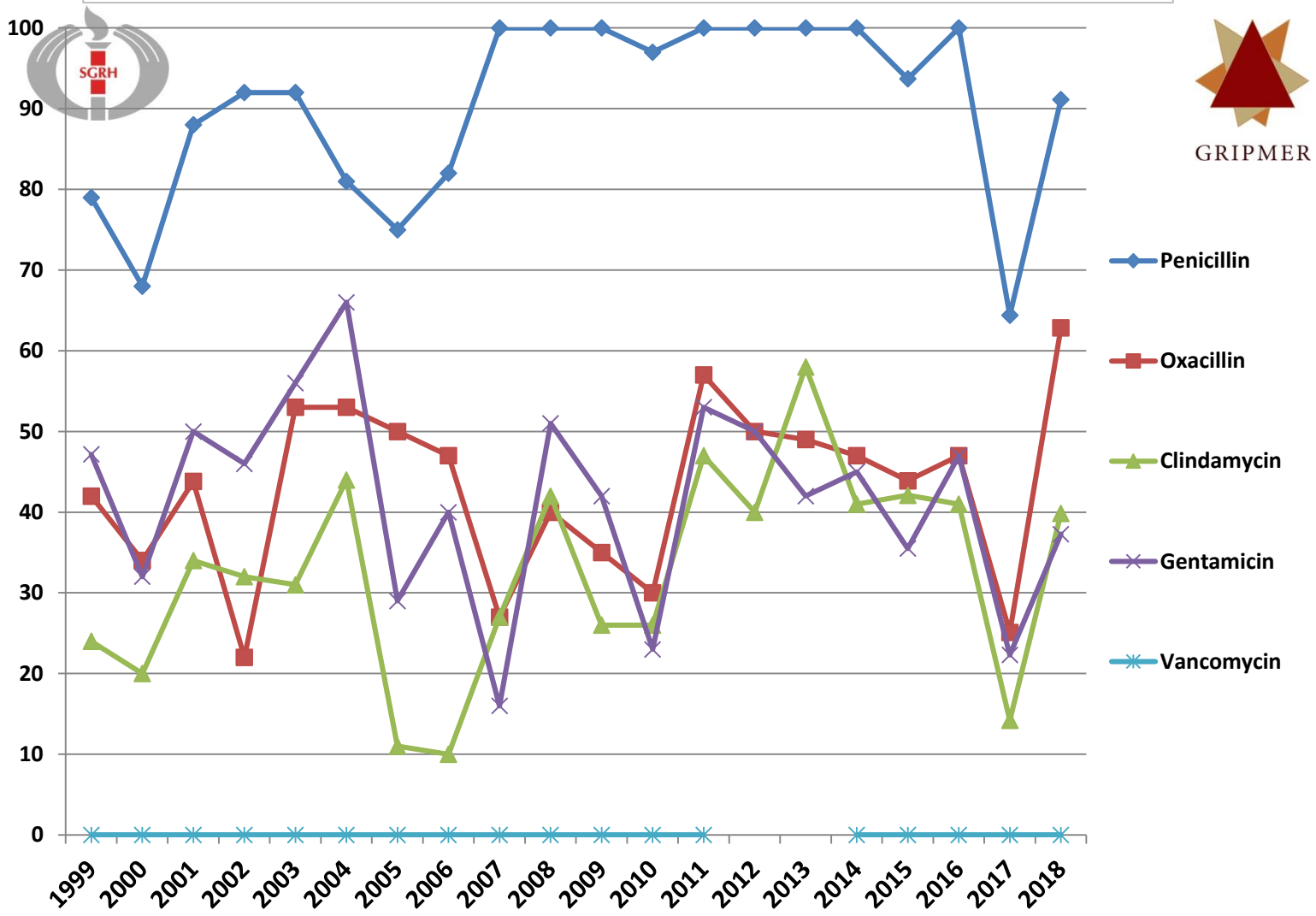
MDROs

NEED TO IDENTIFY ANTIBIOTIC RESISTANCE?

1. PRP Meningitis
2. MRSA: Squeezing the balloon
3. VRE / LRE
4. Colistin resistant *: Klebsiella pneumoniae; Acinetobacter baumannii, Pseudomonas aeruginosa and E.coli*

Time Series Analysis of AMR at a Tertiary Care Hospital Delhi. India.

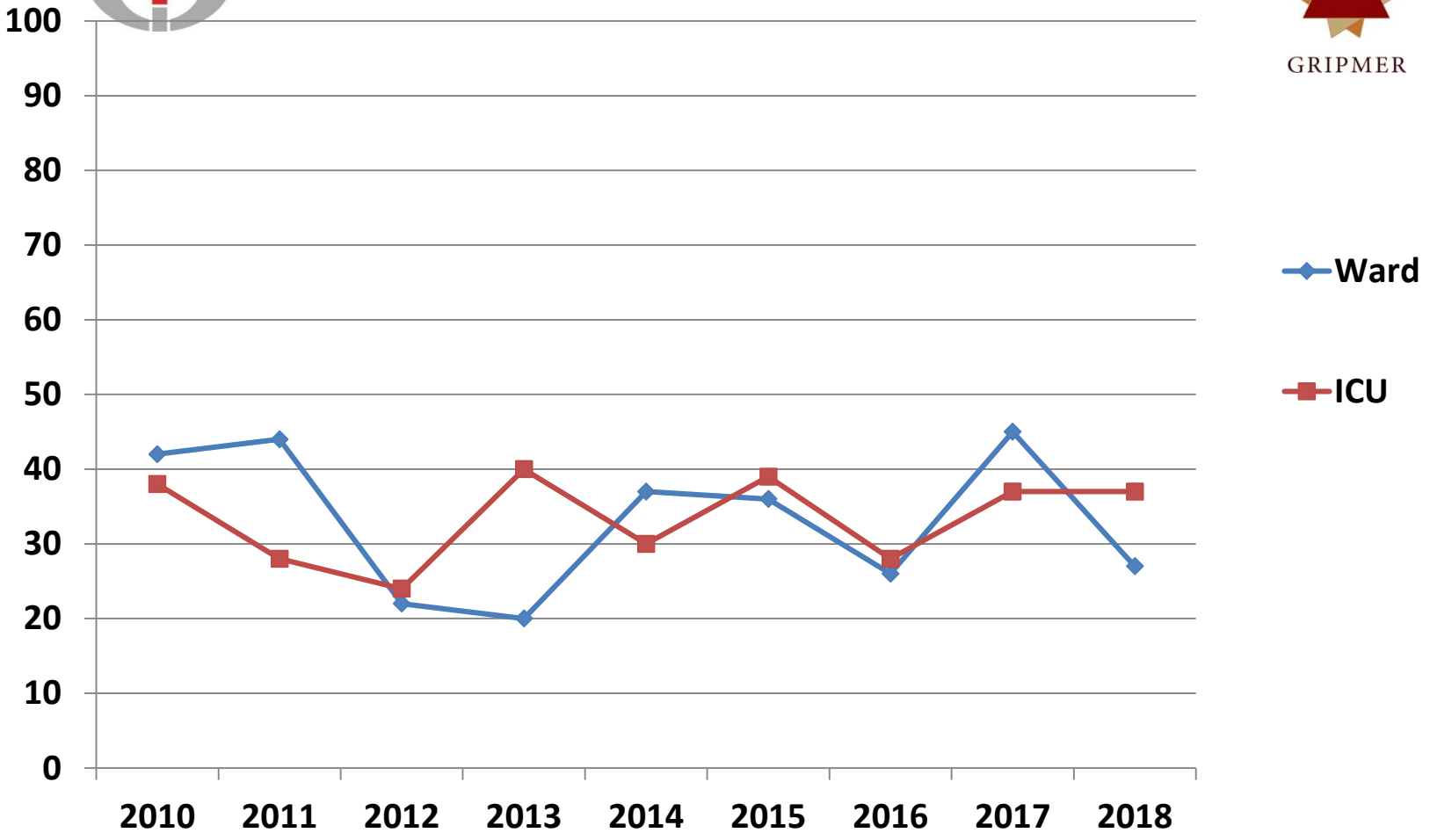
% Resistance - *S. aureus* - Blood Isolates - IPD



GRIPMER

www.sgrh.com/publications/Microbiology Newsletter;Jan 1999-July 2018

% Vancomycin Resistance *Enterococci* spp. - Blood Isolates



Indian J Med Res 135, June 2012, pp 907-912

A ten year analysis of multi-drug resistant blood stream infections caused by *Escherichia coli* & *Klebsiella pneumoniae* in a tertiary care hospital

Sanghamitra Datta, Chand Wattal, Neeraj Goel, Jaswinder K. Oberoi, Reena Raveendran & K.J. Prasad

Department of Clinical Microbiology, Sir Ganga Ram Hospital, New Delhi, India

Received October 11, 2010

***Background & objectives*: Extensive use of antibiotics has added to the escalation of antibiotic resistance. This study was undertaken to evaluate the association, if any between antibiotic use and resistance in a hospital setting, and also detect the predominant mechanism of antibiotic resistance in *Escherichia coli* and *Klebsiella pneumoniae* over a period of 10 years.**

Trends of resistance: *K . pneumoniae*

K.pneumoniae (% resistance)	Years										p value
	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	
Cefotaxime	75	80	94	89	81	89	98	95	95	97	0.008
Amikacin	70	70	76	90	77	77	89	76	59	45	0.17
Ciprofloxacin	64	80	64	83	82	66	81	86	64	84	0.411
Piperacillin+ Tazobactum			55	71	51	64	67	60	88	84	0.055
Carbapenems			2.4	1.7	0	0	7	3	47	52	0.039
ESBL			48	55	68	74	66	58	44	40	0.332
Amp C	–	–	–	–	–	–	–	–	–	8%	–
Carbapenemase producer	–	–	–	–	–	–	–	–	–	51%	–

Klebsiella pneumoniae has moved to the next level of resistance: NDM,OKA48,Porin Loss

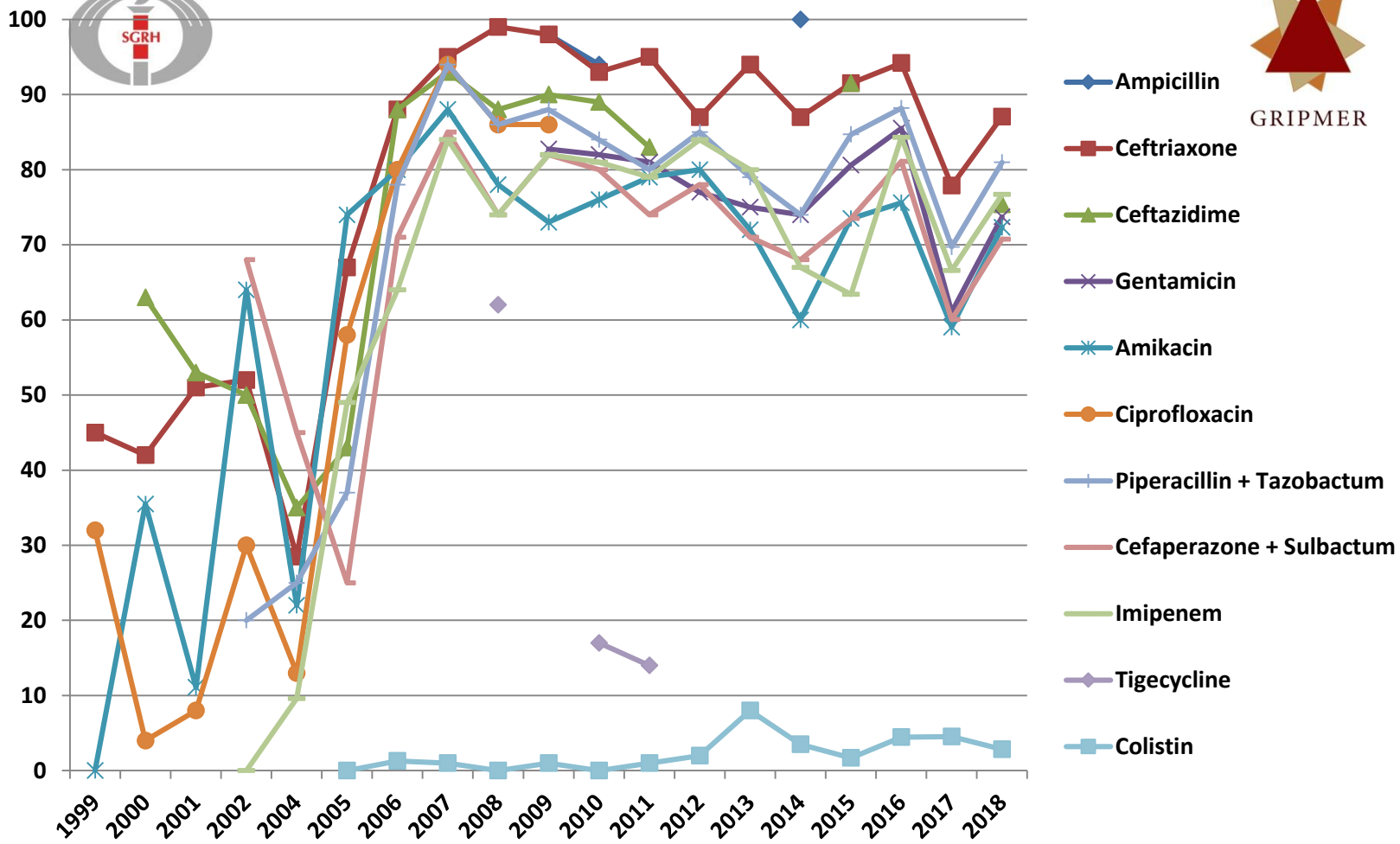
Indian J Med Res 135, June 2012, pp 907-912

Trends of Antimicrobial Resistance *E.coli*

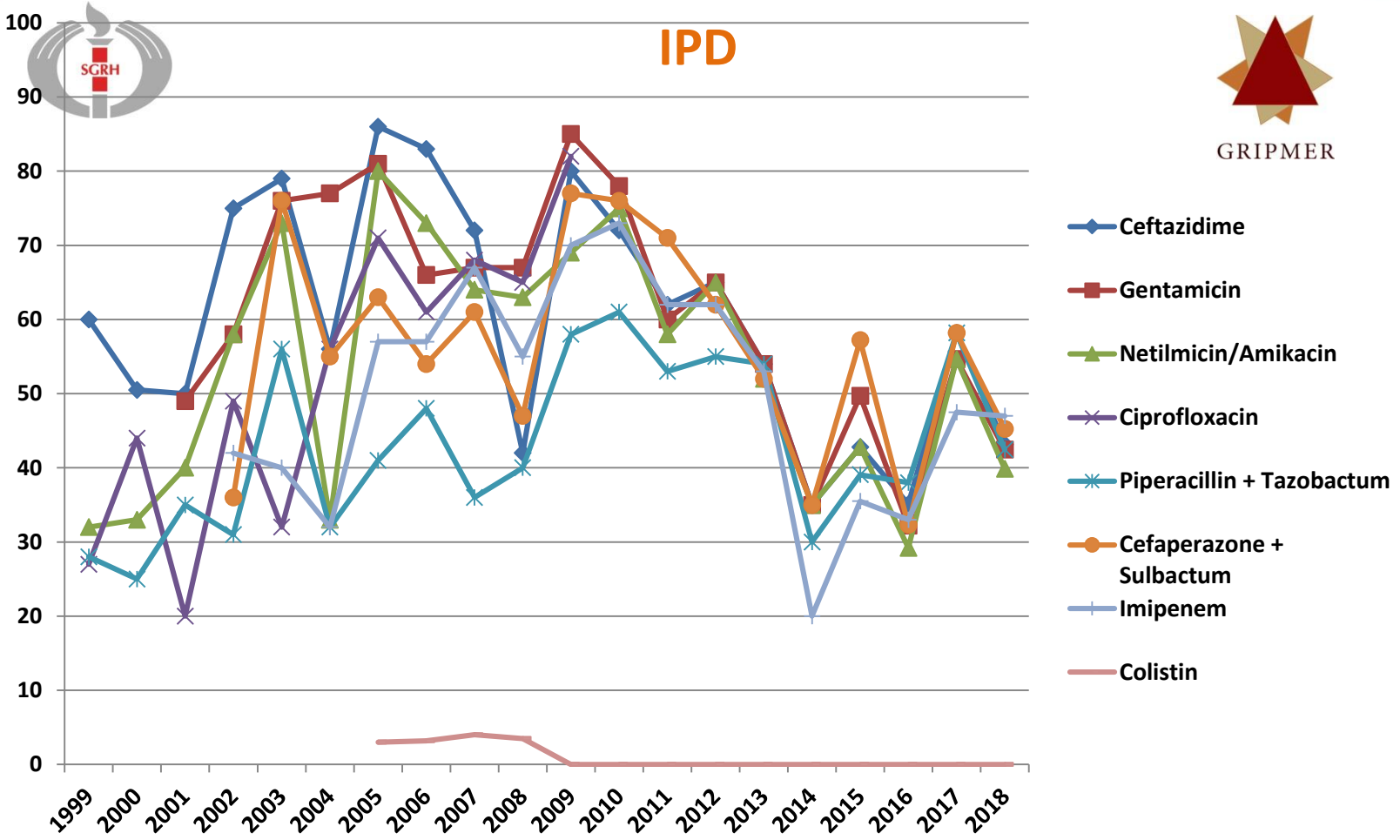
(% resistance)	2000	2001	2002	2003	Years 2004	2005	2006	2007	2008	2009	p value
Cefotaxime	64	67	73	71	71	79	77	88	83	75	0.005
Amikacin	57	63	68	87	75	69	58	67	57	14	0.115
Ciprofloxacin	53	62	84	90	49	86	89	95	98	91	0.037
Piperacillin+ Tazobactum			53	67	47	37	30	27	10	42	0.08
Carbapenem			3	2	0	0	2	6	10	6	0.105
ESBL			40	45	58	60	75	78	61	61	0.05
Amp C	_	_	_	_	_	_	_	_	_	8%	–
Carbapenemase producer	_	_	_	_	_	_	_	_	_	15%	–

Indian J Med Res 135, June 2012, pp 907-912

% Resistance - Acinetobacter - Blood Isolates



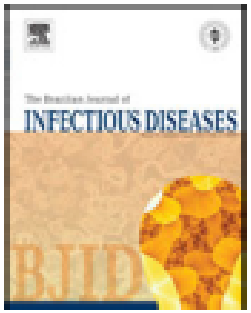
% Resistance - Pseudomonas - Blood Isolates - IPD



BRAZ J INFECT DIS. 2014;18(3):245–251

The Brazilian Journal of
INFECTIOUS DISEASES

www.elsevier.com/locate/bjid



Original article

Ecology of blood stream infection and antibiotic resistance in intensive care unit at a tertiary care hospital in North India

Chand Wattal[a,*], *Reena Raveendran*[a], *Neeraj Goel*[a], *Jaswinder Kaur Oberoi*[a], *Brijendra Kumar Rao*[b]

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Colistin Sensitivity at SGRH: Blood Isolates - ICU (2018)

S. No.	Organism	Isolate No.	% Sensitive*
1	*Klebsiella pneumoniae*	130	83
2	*E.coli*	39	100
3	*Acinetobacter baumannii*	69	100
4	*Pseudomonas aeruginosa*	26	100

* BMD confirmed isolates only

Colistin Sensitivity at SGRH: Respiratory Isolates - ICU (2018)

S. No.	Organism	Isolates No.	% Sensitive*
1	*Klebsiella pneumoniae*	373	80
2	*E.coli*	76	100
3	*Acinetobacter baumannii*	326	100
4	*Pseudomonas aeruginosa*	206	96

* BMD confirmed isolates

%Sensitivity of Yeast Fungi (Blood Isolates 2017)

Species (no. of Isolates Tested)	Amphotericin B**	Flucytosine	Fluconazole	Voriconazole	Caspofungin
C. tropicalis (40)	100	97.5	100	100	100
C. albicans (33)	100	100	100	100	100
C. pelliculosa (33)	96.9	51.7	84.8	96.9	100
C. parapsilosis (32)	100	100	72	90.62	100
C. haemulonii (23)	0	100	0	91.3	100
C. glabrata (17)	100	100	52.9	94.1	100
C. krusei (8)	100	25	0	100	100
C. lusitaniae (4)	100	100	100	100	100
C. utilis (3)	100	100	100	100	100
C. rugosa (3)	100	100	66.6	100	100
C. guillermondi (2)	100	50	0	0	100
Kodamea ohmeri (2)	100	100	100	100	100
Cryptococcus neoformans (2)	100	100	100	100	0
Trichosporon spp. (4)	75	-	50	75	0

Antifungal Susceptibility Results Interpreted as per CLSI M27S4 Document (Dec 2012)

Species (no. of Isolates Tested)	Amphotericin B**	Flucytosine	Fluconazole	Voriconazole	Caspofungin
C. tropicalis (40)	100	97.5	97.5	100	100
C. albicans (33)	100	100	93.9	100	100
C. parapsilosis (32)	100	100	62.5	68.75	100

Figures in parenthesis indicate the number of isolates tested

Figures in parenthesis indicate then number of isolates tested. (- = Not done).

Antifungal susceptibility results have been interpreted as per CLSI M27A3 document

*YST-AST Cards Vitek 2 (bioMerieux, France), E Test (Rpt. isolates excluded), CLSI M-39A Vol. 22, No. 8; 2002 (global consensus guidelines).

**Isolates with MIC of <1 µg/ml

83.6% yeasts isolated from blood samples were non-*C. albicans* Candida spp. in line with the trend noticed previous year (84%). Overall, *C. tropicalis* was the most common species (41 cases; 20.2%), followed by *C. albica* *C. pelliculosa* (33 cases each; 15.8%), *C. parapsilosis* (32 cases; 15.3%), *C. haemulonii* (23cases; 11.05%) and *C. glabrata* (18 cases; 8.6%). *C. pelliculosa* was the most common cause of candidaemia in neonatal consistent with the previous year. Nearly all the isolates were completely sensitive to amphotericin B, the notable exception being *C. haemulonii*.

Indian J Med Res 136, December 2012, pp 997-1003

Non-*albicans Candida* species in blood stream infections in a tertiary care hospital at New Delhi, India

Jaswinder Kaur Oberoi, Chand Wattal, Neeraj Goel, Reena Raveendran, S. Datta & Kamaljeet Prasad

Department of Clinical Microbiology & Immunology, Sir Ganga Ram Hospital, New Delhi, India

Received October 18, 2010

***Background & objectives*: During recent decades, there has been a change in the epidemiology of *Candida* infections, characterized by a progressive shift from a predominance of *Candida albicans* to non-*albicans Candida* species. This study was undertaken to analyze the change in the epidemiology of candidaemia and antifungal use at tertiary care hospital in New Delhi, India, over a period of 10 years.**

***Methods*: A retrospective review of candidaemia between 1999 and 2008 and antifungal use from 2000 to 2008 was performed at Sir Ganga Ram Hosptial, New Delhi. Initially (1999-2005), isolates were differentiated as *C. albicans* and non- *albicans Candida* species. Between 2006-2008, these were identified to the species level and antifungal susceptibility was performed.**

***Results*: The occurrence of candidaemia and total antifungal use increased significantly. Candidaemia due to non-*albicans* species increased and this was correlated with an increasing use of fluconazole. There**

What is “diagnostic stewardship”?

“Coordinated guidance and interventions to improve appropriate use of microbiological diagnostics to guide therapeutic decisions. It should promote appropriate, timely diagnostic testing, including specimen collection, and pathogen identification and accurate, timely reporting of results to guide patient treatment.”

GLASS Manual ; WHO/DGO/AMR/2016.3 ; http://www.who.int/

Era of MDROs

Diagnostic Stewardship can help Management of difficult to treat infection related cases

The main objective of microbiological diagnostic stewardship is to deliver

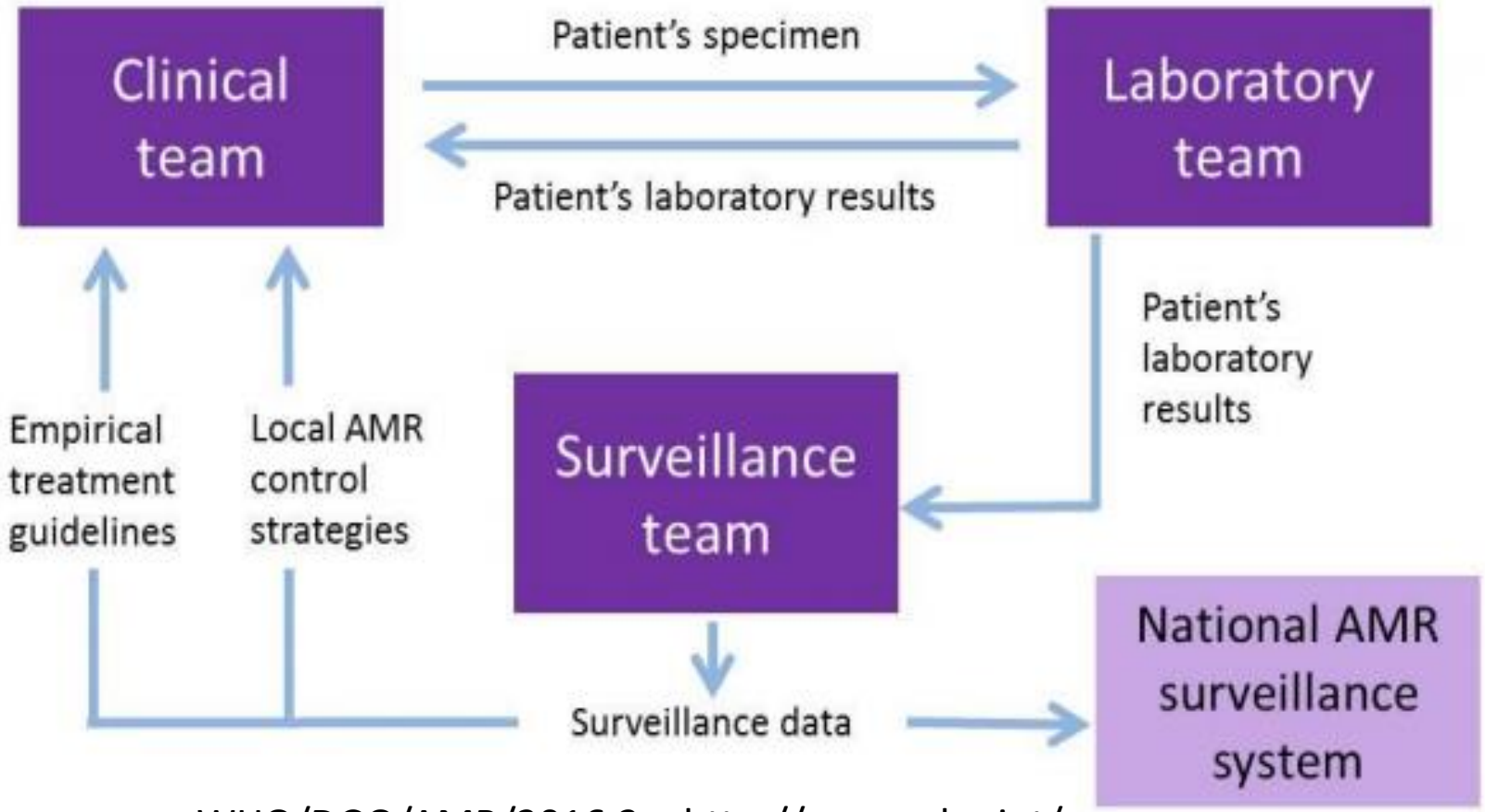
1. Patient management guided by timely microbiological data to deliver safer and more effective and efficient patient care; and
2. Accurate and representative AMR surveillance data to inform treatment guidelines, and AMR control strategies

Diagnostic stewardship

1. Is an integral part of antibiotic stewardship programmes and is also essential for infection prevention and control activities
2. Timely and accurate results help clinicians to select the most appropriate antibiotics or antibiotic combinations for their patients,
3. Also helps implement the necessary precautions to reduce the risk of transmission and prevent outbreaks due to bacterial pathogens in health-care facilities.

Dik JW, Poelman R, et al. An integrated stewardship model: antimicrobial, infection prevention and diagnostic (AID). Future Microbiology 2015

Relationship between individual care and surveillance data



WHO/DGO/AMR/2016.3 ; http://www.who.int/

Diagnostic Stewardship

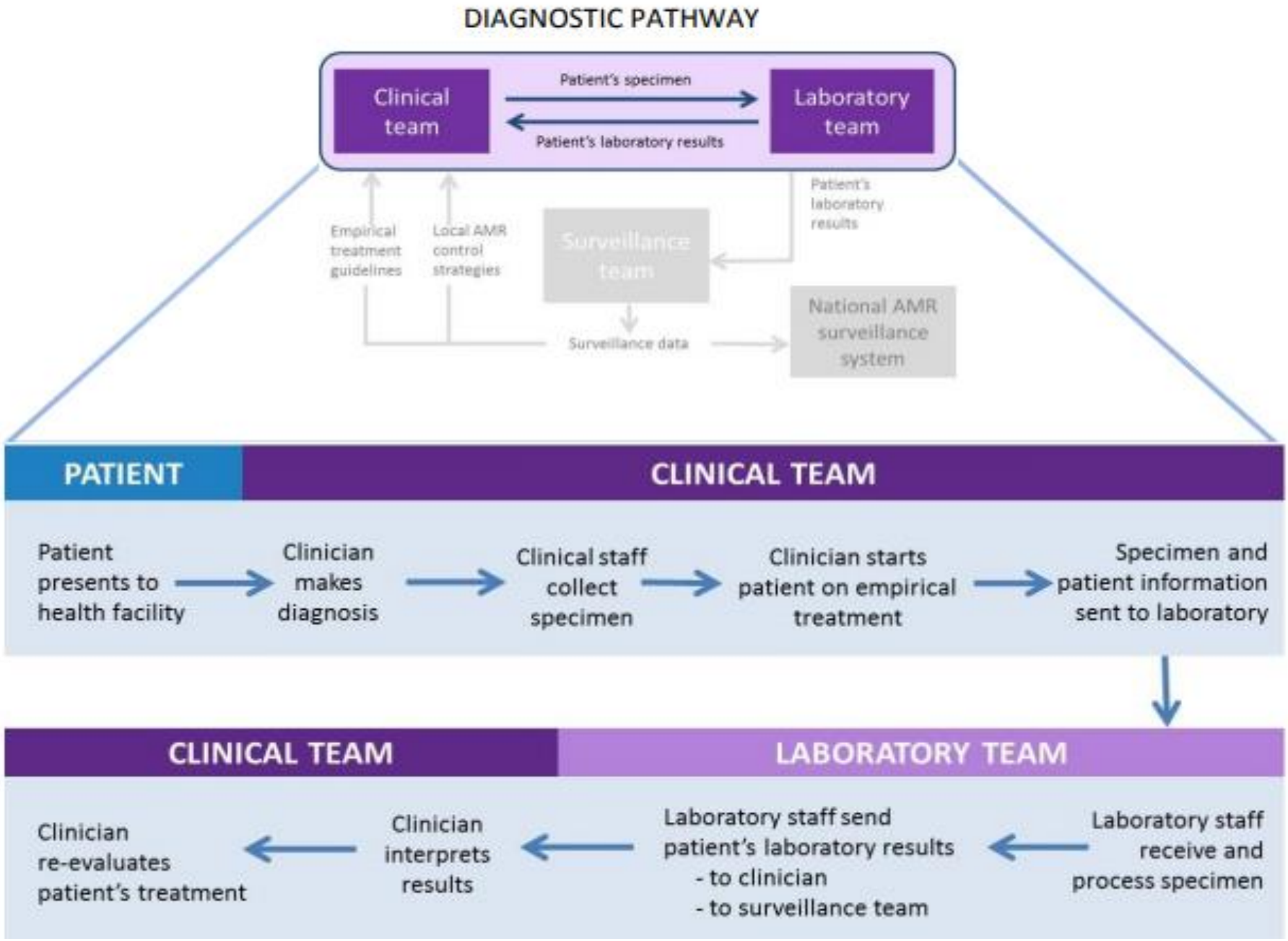
Two distinct components:

1. Diagnostic Pathway
2. Organisational Pathway

WHO/DGO/AMR/2016.3 ; http://www.who.int/

The diagnostic pathway.....

1. Specimen selection and collection
2. Turn-around time
3. Storage and transport
4. pre-analytical specimen management at point-of-care
5. Laboratory processing and procedures.
6. Feedback and reporting of results



WHO/DGO/AMR/2016.3 ; http://www.who.int/

Organizational Pathway

Pre-requisites are:

- Assessment of conditions for implementation at the surveillance site
- Resources and budget
- Roles and responsibilities: Team work
    - **Clinical staff**
    - **Microbiology laboratory staff**
    - **Surveillance/epidemiological staff**
- Communication
- Training: clinical, laboratory and surveillance staff
- Monitoring and evaluation of the diagnostic stewardship programme

WHO/DGO/AMR/2016.3 ; http://www.who.int/

Role of Diagnostic Stewardship

In Steering AMSP

The diagnostic stewardship need to aim at the following:

1. To assess the probability of bacterial etiology
2. Collection of the most representative sample
3. Guide the decision to order the most relevant & useful investigations
4. Optimal utilization of bio markers
5. Molecular applications matching the gold standard to **decrease turn around time**
6. Identification of the organism to the species level
7. Performance of susceptibility testing as per the internationally recommended guidelines
8. Syndromic approach towards diagnosis using **multiplex assays**

What are the barriers: implementation of diagnostic stewardship,

1. Within the health-care system as a whole
2. At the level of the health-care facility even with sufficient laboratory capacity
   - ❑ Economic and logistic constraints
   - ❑ Lack of understanding and training.

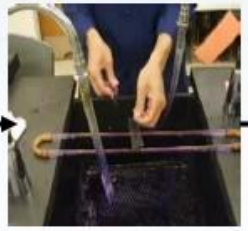
What is needed to achieve DS

1. Good laboratory practices
2. Affordable access to laboratories with good quality management,
3. Capacity and capability to perform timely and reliable microbiological diagnostics are essential.

Revolution in Work Flow and Time to Results

Today's Microbiology



24-48 hr

24-48 hr

5-24 hr

1 hr

1,5 to 2 days

Vitek MS: SGRH Experience (May 2013- April 2014) Total isolates tested:12003

ORGANISMS (12003)	DEFINITIVE DETECTION 11122 (92.66%)	LOW QUALITY RESULTS (881)		
		Detected on repeat testing 521(4.34%)	Not detected on repeat testing (353) (2.94%)	Misidentification (8)
GNB (8105)	7575 (93.44%)	342 (4.22%)	188 (2.33%)	8*
GPC (2576)	2404 (93.32%)	117 (4.54%)	55 (2.13%)	
GPB (20)	19 (95%)	-	1 (5%)	
YEAST (1248)	1097 (87.9%)	62 (4.96%)	89 (7.13%)	
FUNGUS (20)	16 (80%)	-	4 (20%)	

* Shigella identified as *E. coli*

Wattal , Oberoi .Eur J Clin Microbiol Infect Dis 2016 .DOI 10.1007/s10096-016-2864-9

Gram Negative Bacilli: 8105

Organism	Identified	Not Identified
A baumanii (1346)	1331	15
Aeromonas hydrophila (6)	5	1
Citrobacter freundii (19)	17	2
Commamonas testosteroni (3)	2	1
E.cloacae (35)	33	2
E.coli (2373)	2334	39
E.meningosepticum (7)	6	1
K.pneumoniae (2390)	2312	78
Morganella morganii (48)	47	1
Myroides spp. (10)	9	1
P.aeruginosa (1155)	1129	26
P. flouresens (1)	0	1
P.mirabilis (211)	208	3
P.putida (38)	37	1
Pantoea (2)	0	2
Salmonella typhi (51)	44	7
Serratia marcescens (66)	64	2
Steno maltophila (79)	78	1
Burkholderia psuedomallei (3)	0	3
Brucella melitensis (2)	0	2
Others (260)	**260**	0
	7916	**189**

97.6% Identified

Wattal , Oberoi .Eur J Clin Microbiol Infect Dis 2016 .DOI 10.1007/s10096-016-2864-9

Gram Positive Cocci: 2576

ORGANISM	IDENTIFIED	NOT IDENTIFIED
E.avium (7)	6	1
E.faecalis (335)	330	5
E.faecium (746)	736	10
S.aureus (471)	463	8
S.epidermidis (409)	402	7
S.saprophyticus (6)	5	1
S.warneri (3)	2	1
S.haemolyticus (231)	229	2
S.hominis (150)	148	2
Strept. agalactiae (25)	22	3
Strept. anginosus (23)	21	2
Strept. mitis/ oralis (44)	40	4
Strept. ovis (1)	0	1
Strept. parasanguinus (24)	23	1
Strept. pyogenes(27)	20	7
Others (74)	74	0
	2521	55

97.8% Identified

Wattal , Oberoi .Eur J Clin Microbiol Infect Dis 2016 .DOI 10.1007/s10096-016-2864-9

Yeasts: n=1248

ORGANISM	IDENTIFIED	NOT IDENTIFIED
C.albicans (381)	367	14
C. famata (13)	9	4
C.glabrata (215)	213	2
C.haemulonii (35)	1	34
C.kefyr (8)	7	1
C.krusei (26)	24	2
C.lipolytica (2)	1	1
C.parapsilosis (72)	60	12
C.pelliculosa (17)	14	3
C.tropicalis (370)	358	12
Trichosporon asahii (60)	56	4
Others (49)	49	0
	1159	89

92.8% Identified

Wattal , Oberoi .Eur J Clin Microbiol Infect Dis 2016 .DOI 10.1007/s10096-016-2864-9

Eur J Clin Microbiol Infect Dis
DOI 10.1007/s10096-016-2864-9

ORIGINAL ARTICLE

Matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS) for rapid identification of micro-organisms in the routine clinical microbiology laboratory

C. Wattal[1] · J. K. Oberoi[1] · N. Goel[1] · R. Raveendran[1] · S. Khanna[1]

What makes us slog

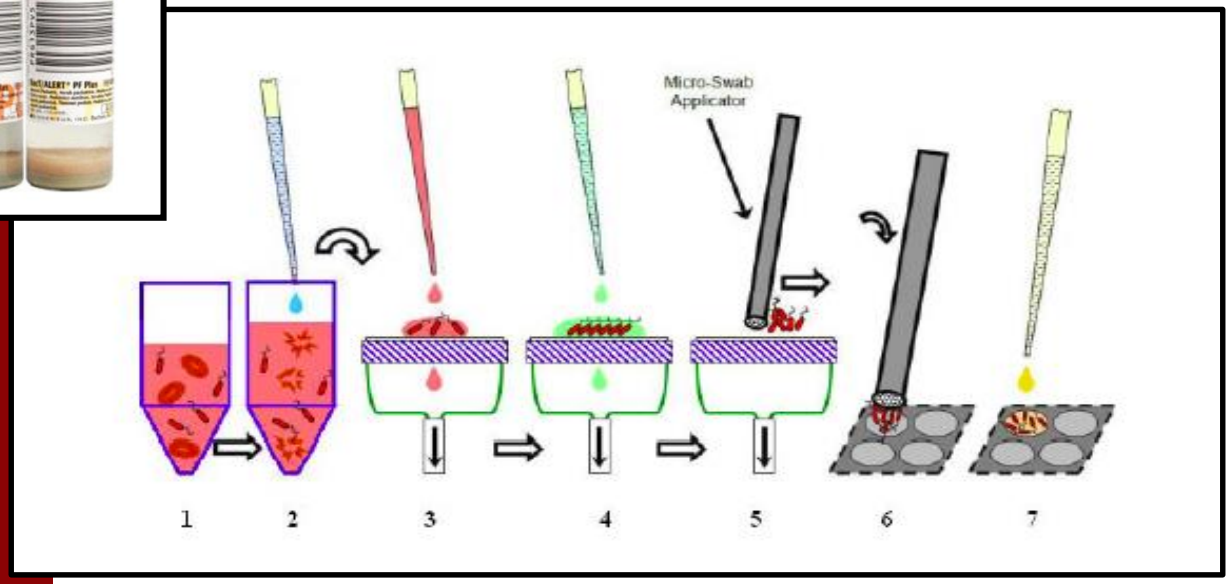
1. Isolation
2. Identification:
3. **Sensitivity**

While ensuring quality control as per CLSI/EUCAST guidelines

Need cutting edge technologies

Material and Method

Lysis Filtration Method



Eur J Clin Microbiol Infect Dis (2016) 35:75-82; DOI 10.1007/s10096-015-2510-y

Time Benefit

Table 5 Comparison of time to antimicrobial susceptibility testing (AST) for direct identification (ID) between lysis-filtration method (LFM) and standard approach (hours)

Microorganism	LFM			Standard approach			P value
	Time to ID (h)	Time to AST (h)	Time to ID & AST (h)	Time to ID (h)	Time to AST (h)	Time to ID & AST (h)	
GNB	1	10.45	11.45	18	9.78	27.8	
GPC	1	12.41	13.41	18	11.1	29.1	
Total	1	11.02	12.02	18	10.17	28.2	<0.001

Susceptibility Errors

Table 4 Susceptibility errors in the direct approach in comparison with other studies using lysis-filtration method (LFM)

Organism	Present study (1 %)		Machen et al. [6]; 2014 (3 %)	
	Major error (false R)	Very major error (false S)	Major error (false R)	Very major error (false S)
E. coli	0	1	1	0
K. pneumoniae	1	1	0	0
Acinetobacterbaumanii	1	1	0	0
Salmonella spp	0	0	–	–
Morganellamorganii	0	1	0	0
Proteus mirabilis	2	0	0	4
S. epidermidis	0	0	12	5
E. faecalis	1	0	0	0

Eur J Clin Microbiol Infect Dis (2016) 35:75-82; DOI 10.1007/s10096-015-2510-y

Microbial identification and automated antibiotic susceptibility testing directly from positive blood cultures using MALDI-TOF MS and VITEK 2

C. Wattal & J. K. Oberoi

Eur J Clin Microbiol Infect Dis (2016) 35:75-82; DOI 10.1007/s10096-015-2510-y

Hard Truth

- More than 70% of clinical decisions in healthcare are based on laboratory results.
- Less than 25% of microbiology reports are used for guiding therapy.

  Reason
- Delay in reports

Cunney et al. International Journal of Antimicrobial Agents 2000;14:13–19
Fell L. et al Chair's Message, ASCP Associate Council. Lab Med. 2005;36:13

Gaps In Diagnostics:TAT

- Need to culture the organism
  - ID & AST: 2-4 days
- Molecular tests
  - Single or multiplex
  - Batching of the samples
- Non specific presentation
  - Meningitis/Encephalitis
  - Respiratory
  - Gastrointestinal
  - sepsis
    - Varied etiology: Bacterial/tubercular/Virus/Fungal/Parasitic

SYNDROMIC DIAGNOSIS COULD BE THE ANSWER

Need for syndromic diagnosis

FilmArray /Biofire System

Sample Prep

+

Amplification

+

Detection

Meningitis/Encephalitis

Biofire: Bridging the Gap

Encephalitis / Meningitis panel, Film Array

GRIPMER

14 pathogens

Bacteria:

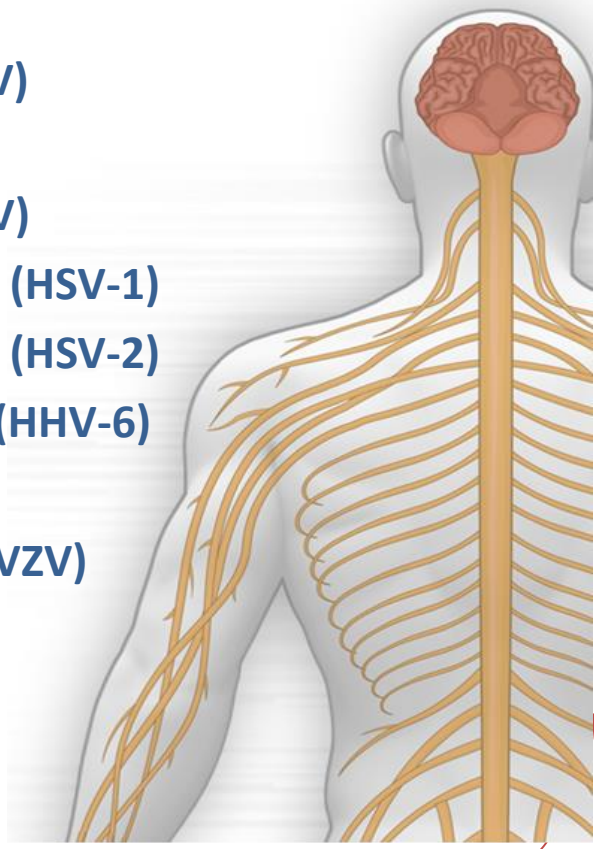
- *E. coli*
- *H. influenzae*
- *L. monocytogenes*
- *N. meningitidis*
- *S. agalactiae*
- *S. pneumoniae*

Fungi:

- *Cryptococcus neoformans / gattii*

Viruses:

- Cytomegalovirus (CMV)
- Enterovirus
- Epstein-Barr virus (EBV)
- Herpes simplex type 1 (HSV-1)
- Herpes simplex type 2 (HSV-2)
- Human herpesvirus 6 (HHV-6)
- Parechovirus
- Varicella zoster virus (VZV)



Sample : Cerebral Spinal Fluid

(200µl CSF)

Bacteria -6, Viruses- 7, Fungal -1

SGRH ME Biofire Panel Data: Jun 2017 – May 2019

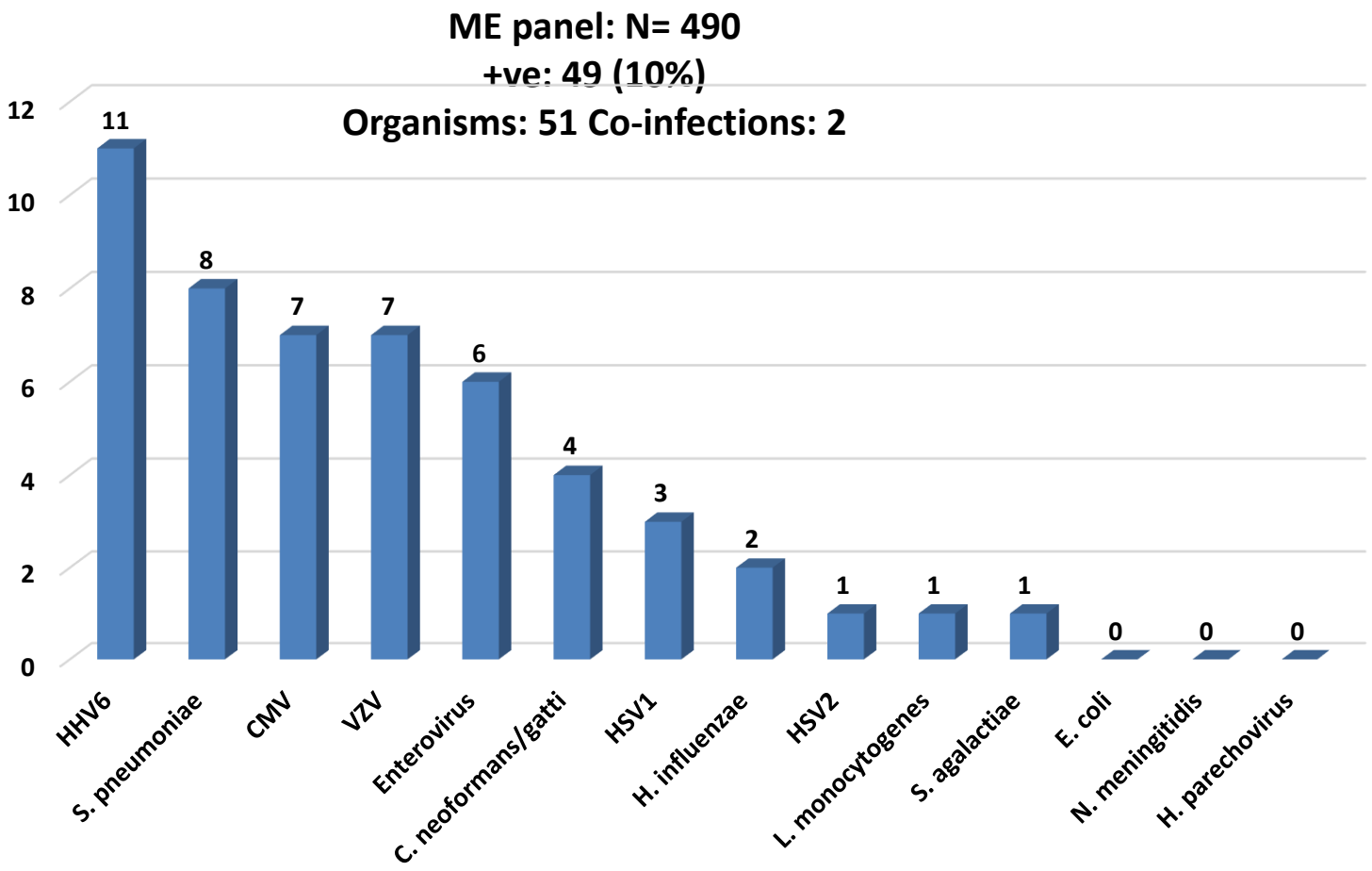


Table 17. Limit of Detection (LoD) for FilmArray ME Panel Analytes

ME Panel Test Result	Species/Isolate Tested	LoD Concentration	Detection at LoD Concentration[a]
BACTERIA			
***E. coli* K1**	*E. coli* K1, strain C5 [Bort]; type O18ac:K1:H7 ATCC 700973	1×10^3 CFU/mL	20/20 100%
H. influenzae	*H. influenzae*, strain AMC 36-A-1 [572] type b, biotype I ATCC 10211	1×10^3 CFU/mL	20/20 100%
L. monocytogenes	*L. monocytogenes*, strain 1071/53, type 4b ATCC 13932	1×10^3 CFU/mL	20/20 100%
N. meningitidis	*N. meningitidis*, strain M-1574 [199/W135] ATCC 43744	100 CFU/mL ($\sim1.80\times10^3$ copies/mL)	19/20 95%
S. agalactiae	*S. agalactiae*, type strain, G19, group B ATCC 13813	1×10^3 CFU/mL	20/20 100%
S. pneumoniae	*S. pneumoniae*, strain SV 1, serotype 1 ATCC 33400	100 cells/mL ($\sim1.50\times10^3$ copies/mL)	19/20 95%
VIRUSES			
CMV[b]	CMV, strain AD-169 Zeptometrix 0810003CF	100 $TCID_{50}$/mL (4.30×10^3 copies/mL)	20/20 100%
EV (Species A-D)	Coxsackievirus A6, species A, strain Gdula ATCC VR-1801	50 $TCID_{50}$/mL	20/20 100%
	Coxsackievirus A9, species B Zeptometrix 0810017CF	5 $TCID_{50}$/mL	20/20 100%
	Coxsackievirus A17, species C, strain G-12 ATCC VR-1023	5 $TCID_{50}$/mL	20/20 100%
	EV 70, species D, strain J670/71 ATCC VR-836	50 $TCID_{50}$/mL	20/20 100%
HSV-1	HSV-1, strain MacIntyre Zeptometrix 0810005CF	250 $TCID_{50}$/mL (1.51×10^3 copies/mL)	20/20 100%
HSV-2	HSV-2, strain MS Zeptometrix 0810006CF	50 $TCID_{50}$/mL (1.29×10^3 copies/mL)	20/20 100%
HHV-6	HHV-6A, strain U1102 NCPV 0003121v	1×10^4 copies/mL	19/20 95%
	HHV-6B, strain HST NCPV 0006111v	1×10^4 copies/mL	19/20 95%
HPeV	HPeV, type 3 Zeptometrix 0810147CF	500 $TCID_{50}$/mL	19/20 95%
VZV	VZV, strain Ellen Zeptometrix 0810171CF	0.10 $TCID_{50}$/mL (1.66×10^3 copies/mL)	20/20 100%
YEAST			
C. neoformans/gattii	*C. neoformans* var. *grubii*, type strain, H99 [H99JP, NYSD 1649] ATCC 208821	100 CFU/mL	20/20 100%
	C. gattii, strain A6MR38, AFLP6C, VGIIc ATCC MYA-4877	100 CFU/mL	20/20 100%

[a] Detection data are from LoD confirmation testing performed on the FilmArray system.
[b] A dilution series of the World Health Organization (WHO) CMV International Standard (NIBSC 09/162) was also tested on FilmArray

GRIPMER

Analytical SE: 10^2- 10^3 CFU/ml

Rapid Biofire GI Panel

GRIPMER

22 pathogens

Bacteria:

Campylobacter
Clostridium difficile (Toxin A/B)
Plesiomonas shigelloides
Salmonella
Vibrio
Vibrio cholerae
Yersinia enterocolitica

Diarrheagenic *E. coli* / *Shigella*

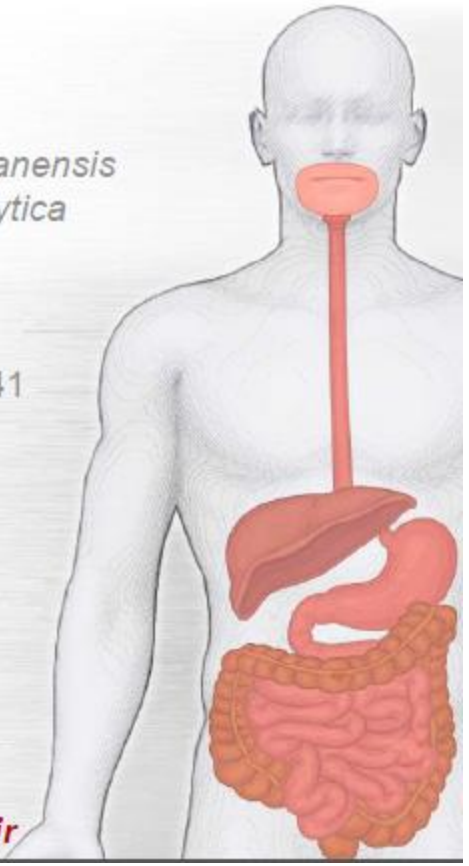
E. coli O157
Enteroaggregative *E. coli* (EAEC)
Enteropathogenic *E. coli* (EPEC)
Enterotoxigenic *E. coli* (ETEC)
Shiga-like toxin-producing *E. coli* (STEC)
Shigella/Enteroinvasive *E. coli* (EIEC)

Protozoa:

Cryptosporidium
Cyclospora cayetanensis
Entamoeba histolytica
Giardia lamblia

Viruses:

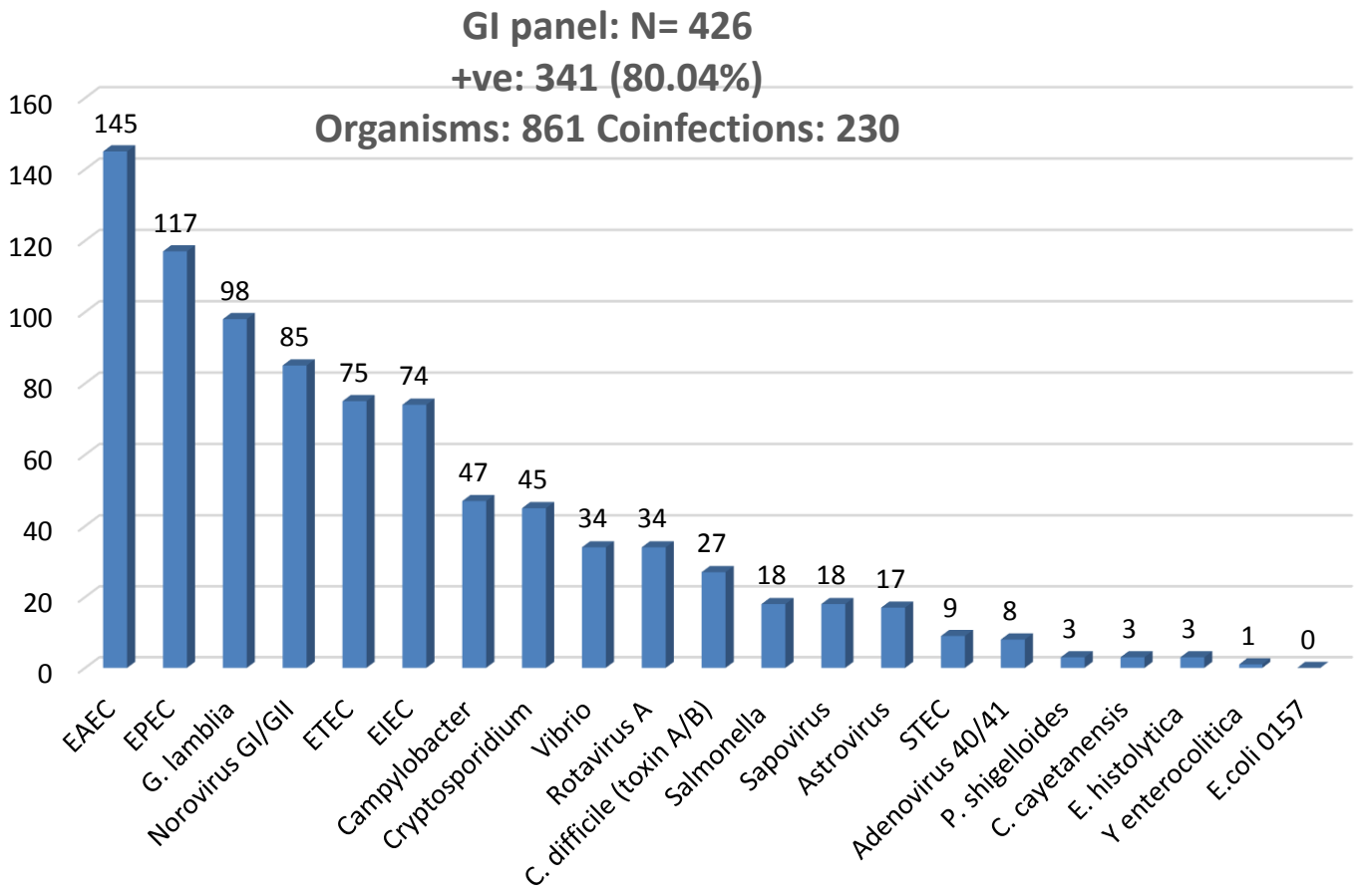
Adenovirus F 40/41
Astrovirus
Norovirus GI/GII
Rotavirus A
Sapovirus



Sample : Stool resuspended in Cary Blair

Bacteria: 13 Protozoa: 4 Viruses: 5

SGRH GI Biofire Panel Data: Jun 2017 – May 2019



Rapid Biofire: Respiratory Panel

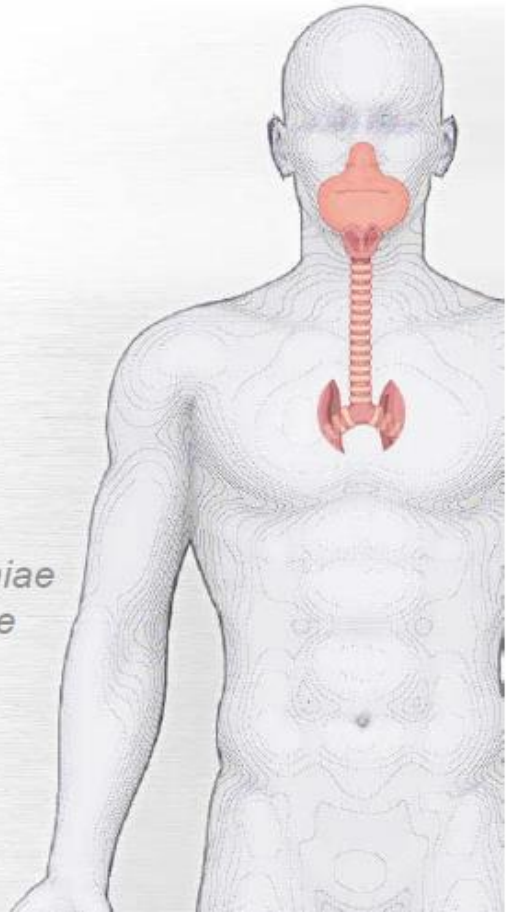
20 pathogens

Viral

- Adenovirus
- Coronavirus 229E
- Coronavirus HKU1
- Coronavirus OC43
- Coronavirus NL63
- Human Metapneumovirus
- Human Rhinovirus/ Enterovirus
- Influenza A
- Influenza A/H1
- Influenza A/H1-2009
- Influenza A/H3
- Influenza B
- Parainfluenza 1
- Parainfluenza 2
- Parainfluenza 3
- Parainfluenza 4
- RSV

Bacterial

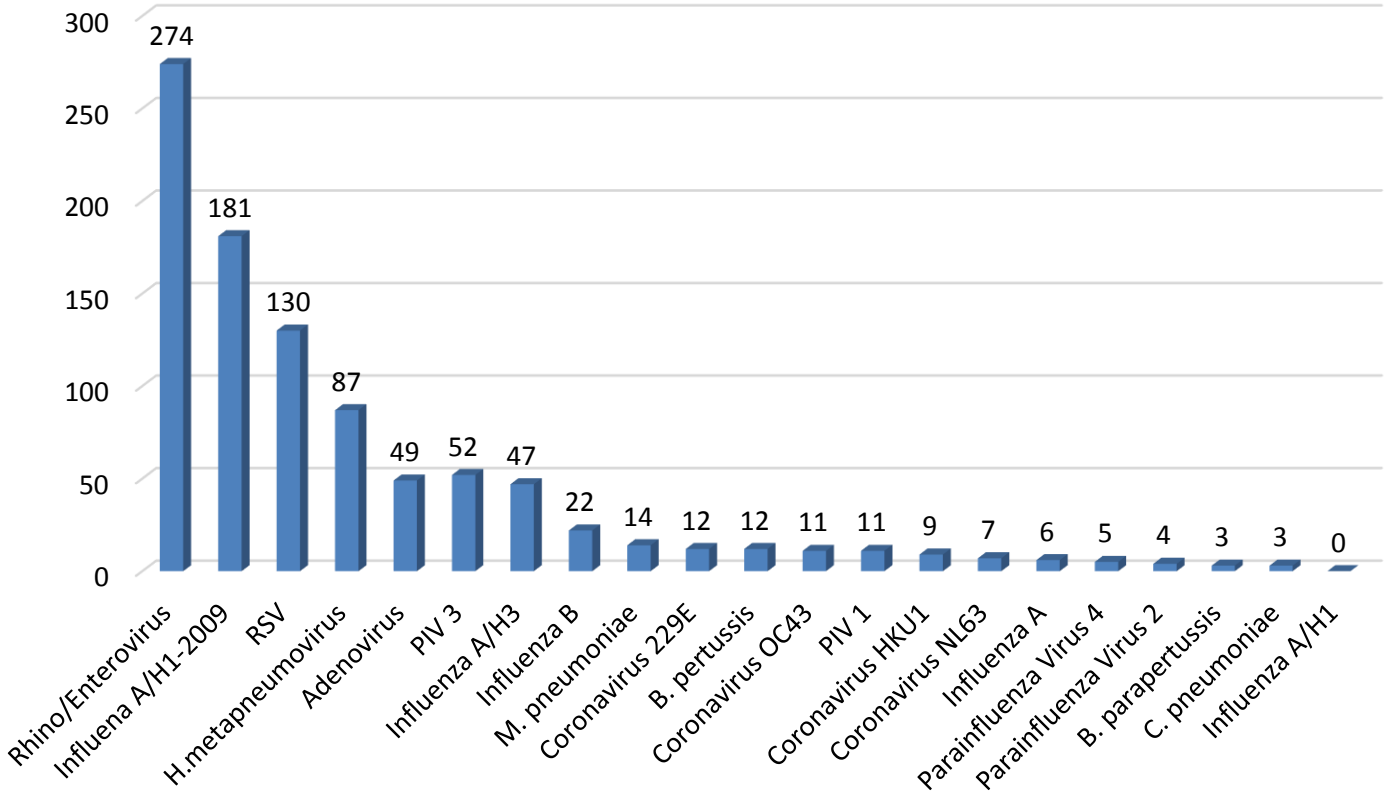
- *Bordetella pertussis*
- *Chlamydophila pneumoniae*
- *Mycoplasma pneumoniae*



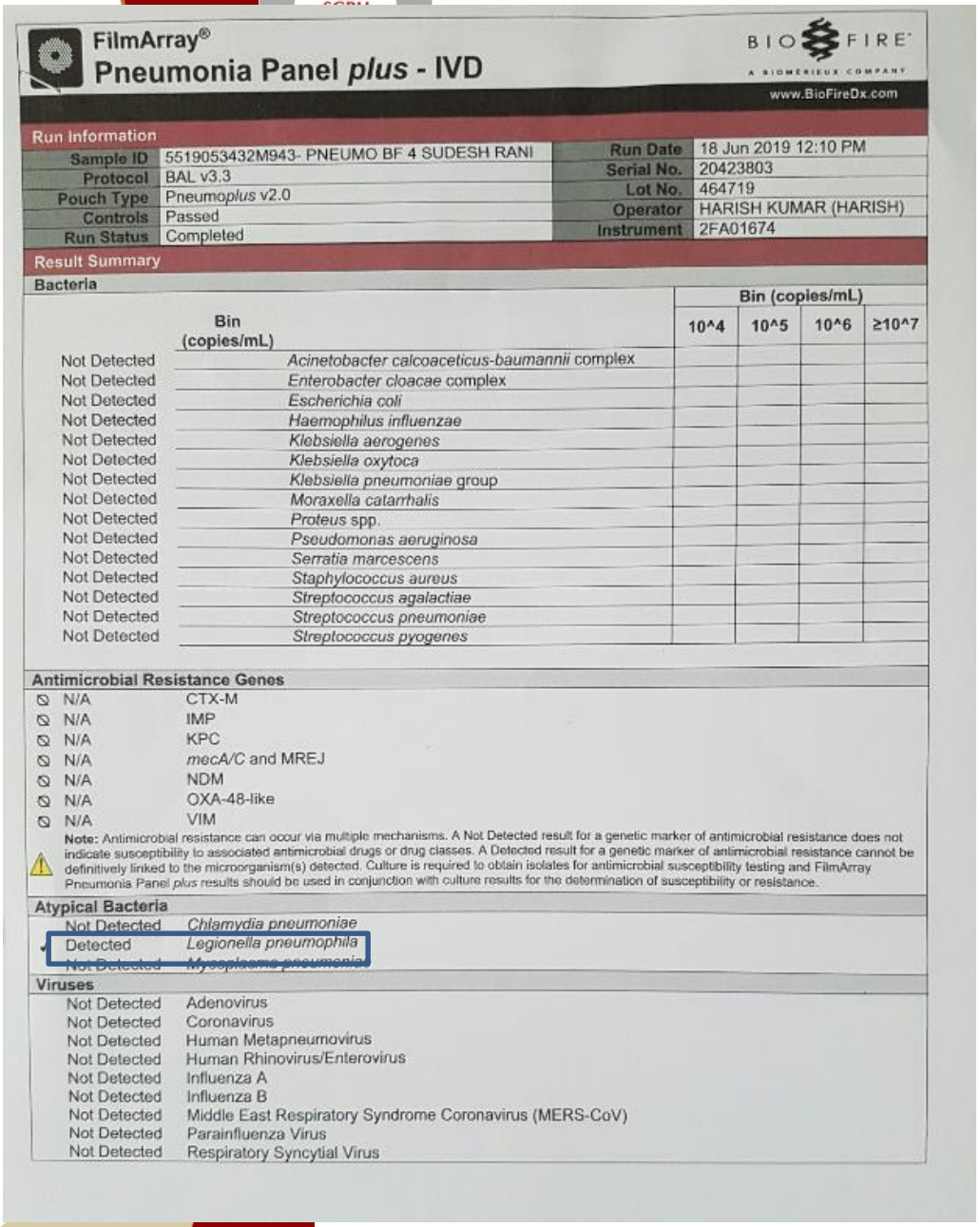
Sample : Nasopharyngeal Swabs

SGRH Respiratory Biofire Panel Data: Jun 2017 – May 2019

Respiratory panel: N= 1373
+ve: 819 (59.7%)
Organisms: 939 Coinfections: 112



Biofire Pneumonia Panel Ordered: Syndromic Approach



FilmArray®
Pneumonia Panel *plus* - IVD

BIOFIRE
A BIOMÉRIEUX COMPANY
www.BioFireDx.com

Run Information

Sample ID	5519053432M943- PNEUMO BF 4 SUDESH RANI	Run Date	18 Jun 2019 12:10 PM
Protocol	BAL v3.3	Serial No.	20423803
Pouch Type	Pneumo*plus* v2.0	Lot No.	464719
Controls	Passed	Operator	HARISH KUMAR (HARISH)
Run Status	Completed	Instrument	2FA01674

Result Summary

Bacteria

Bin (copies/mL)		Bin (copies/mL) 10^4	10^5	10^6	≥10^7
Not Detected	*Acinetobacter calcoaceticus-baumannii* complex				
Not Detected	*Enterobacter cloacae* complex				
Not Detected	*Escherichia coli*				
Not Detected	*Haemophilus influenzae*				
Not Detected	*Klebsiella aerogenes*				
Not Detected	*Klebsiella oxytoca*				
Not Detected	*Klebsiella pneumoniae* group				
Not Detected	*Moraxella catarrhalis*				
Not Detected	*Proteus* spp.				
Not Detected	*Pseudomonas aeruginosa*				
Not Detected	*Serratia marcescens*				
Not Detected	*Staphylococcus aureus*				
Not Detected	*Streptococcus agalactiae*				
Not Detected	*Streptococcus pneumoniae*				
Not Detected	*Streptococcus pyogenes*				

Antimicrobial Resistance Genes

N/A	CTX-M
N/A	IMP
N/A	KPC
N/A	*mecA*/C and MREJ
N/A	NDM
N/A	OXA-48-like
N/A	VIM

Note: Antimicrobial resistance can occur via multiple mechanisms. A Not Detected result for a genetic marker of antimicrobial resistance does not indicate susceptibility to associated antimicrobial drugs or drug classes. A Detected result for a genetic marker of antimicrobial resistance cannot be definitively linked to the microorganism(s) detected. Culture is required to obtain isolates for antimicrobial susceptibility testing and FilmArray Pneumonia Panel *plus* results should be used in conjunction with culture results for the determination of susceptibility or resistance.

Atypical Bacteria

Not Detected	*Chlamydia pneumoniae*
Detected	*Legionella pneumophila*
Not Detected	*Mycoplasma pneumoniae*

Viruses

Not Detected	Adenovirus
Not Detected	Coronavirus
Not Detected	Human Metapneumovirus
Not Detected	Human Rhinovirus/Enterovirus
Not Detected	Influenza A
Not Detected	Influenza B
Not Detected	Middle East Respiratory Syndrome Coronavirus (MERS-CoV)
Not Detected	Parainfluenza Virus
Not Detected	Respiratory Syncytial Virus

27 pathogens
15 bacteria: semi quantitative results
3 bacteria: Atypical pneumonia
9 viruses
Resistance genes: MRSA, ESBL, CRE

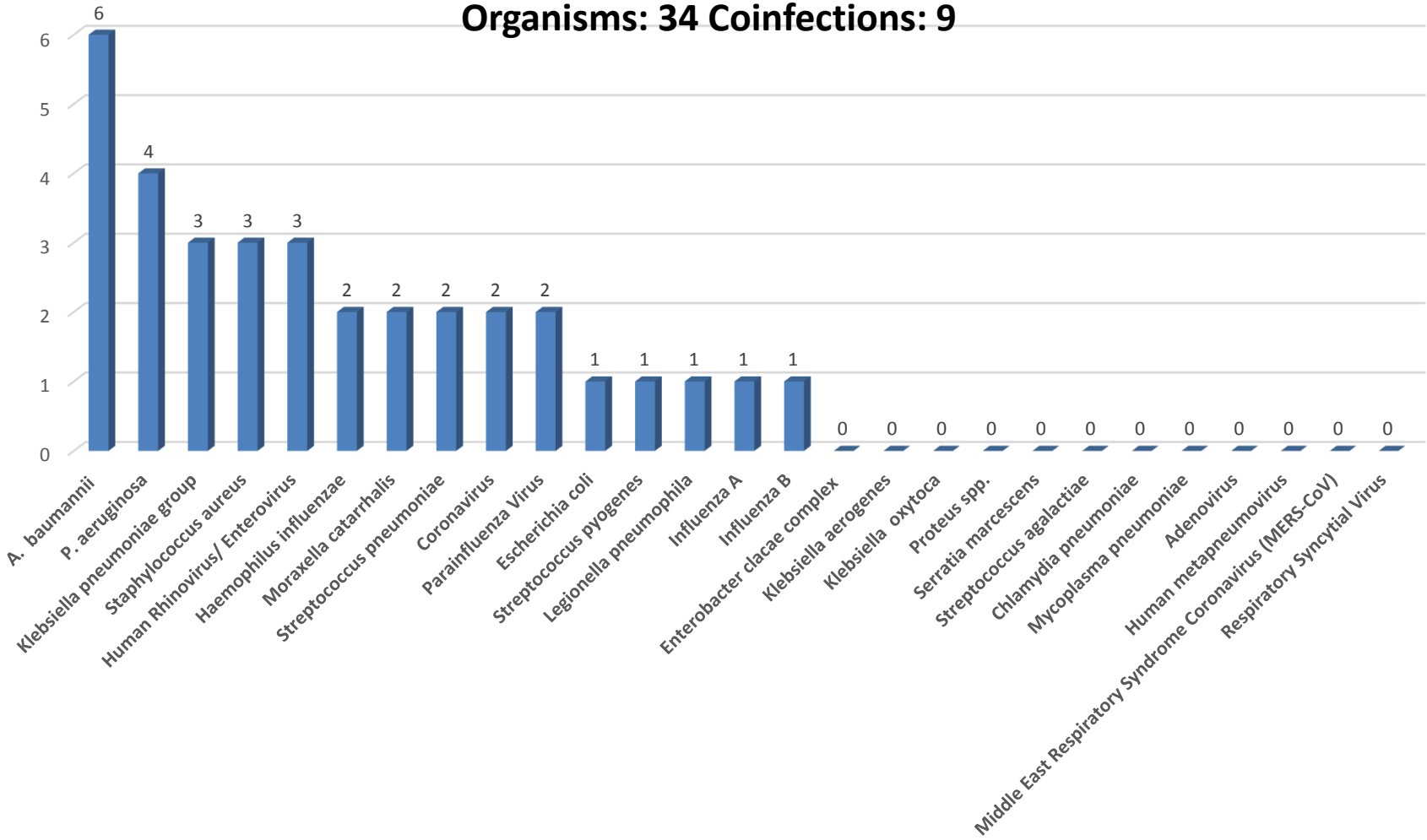
Ordering of Test

2 hour

TEST COMPLETE

SGRH Biofire Pneumonia Panel Data: June–Oct 2019

N= 55
+ve: 33 (59.7%)
Organisms: 34 Coinfections: 9




Actv
Thanks