

V. Kumar ¹, S. Murali ², J. Goldberg ³, B. Alonso ⁴, L. Moretó-Planas ⁴, A. Reid ⁵, A. Harshana ¹, S. Burza ^{1,6}, R. Mahajan ^{1,7}

¹Operational Centre Barcelona-Athens, Médecins Sans Frontières, New Delhi, India, ²Operational Centre Barcelona-Athens, Médecins Sans Frontières, Patna, India, ³Medical Department, Médecins Sans Frontières, London, UK, London, United Kingdom, ⁴Operational Centre Barcelona-Athens, Médecins Sans Frontières, Barcelona, Spain, ⁵Opérationnel Research Unit, Médecins Sans Frontières, Luxembourg, Luxembourg, ⁶London School of Hygiene and Tropical Medicine, London, United Kingdom, ⁷Care and Public Health Research Institute, Maastricht University, Maastricht, Netherlands.



Bacterial isolates demonstrate an alarmingly high rate of multidrug resistance among patients with advanced HIV disease in Patna, India.

Background

"Invasive and recurrent bacterial infections are prevalent among people living with HIV (PLHIV) and are key indicators of WHO clinical stages II, III, and IV. These infections serve as defining conditions for advanced HIV disease (AHD) in adults (stages III and IV) and in children over 5 years of age."

The rise of multidrug-resistant bacterial infections heightens the risk of morbidity and mortality in the general population, but especially in people living with HIV (PLHIV) with advanced HIV disease (AHD). In these patients, severe immunosuppression and common comorbidities, combined with multidrug resistance, significantly complicate clinical management.

Since 2019, MSF has been supporting a 40-bed ward in Patna, Bihar, delivering comprehensive medical and psychosocial care for patients with advanced HIV disease (AHD). The care package includes access to microbiological diagnosis and targeted antimicrobial therapy.

Methods

This retrospective analysis covers culture reports from patients admitted to the advanced HIV ward in Patna between May 2019 and March 2021.

All samples were processed at an external NABL-accredited laboratory, with culture and antibiotic susceptibility patterns reported according to CLSI guidelines.

As this data was part of routine clinical care, an exemption was granted by the MSF Ethics Review Board (MSF ERB decision 2252).

Results

Total A total of 1,586 samples from 577 patients were sent for culture, with a median of 2 (IQR 1–4) specimens per patient. The positivity rate was 3.3% for blood, 10% for pleural fluid, and 2.1% for CSF. Non-sterile sites showed higher positivity rates: urine 22.2%, stool 2.9%, and sputum 56%.

Among bacterial isolates, *Escherichia coli* (80; 13.9%) was the most common, followed by *Klebsiella pneumoniae* (54; 9.4%), *Pseudomonas aeruginosa* (22; 3.8%), *Klebsiella oxytoca* (10; 1.7%), *Proteus mirabilis* (9; 1.6%), and *Acinetobacter baumannii* (7; 1.2%).

Resistance patterns revealed that most bacterial isolates exhibited high resistance to commonly prescribed antibiotics, including third-generation cephalosporins, fluoroquinolones, and co-trimoxazole. Moderate resistance was observed against antibiotics from the WHO Watch group, such as meropenem and piperacillin/tazobactam.

Conclusion

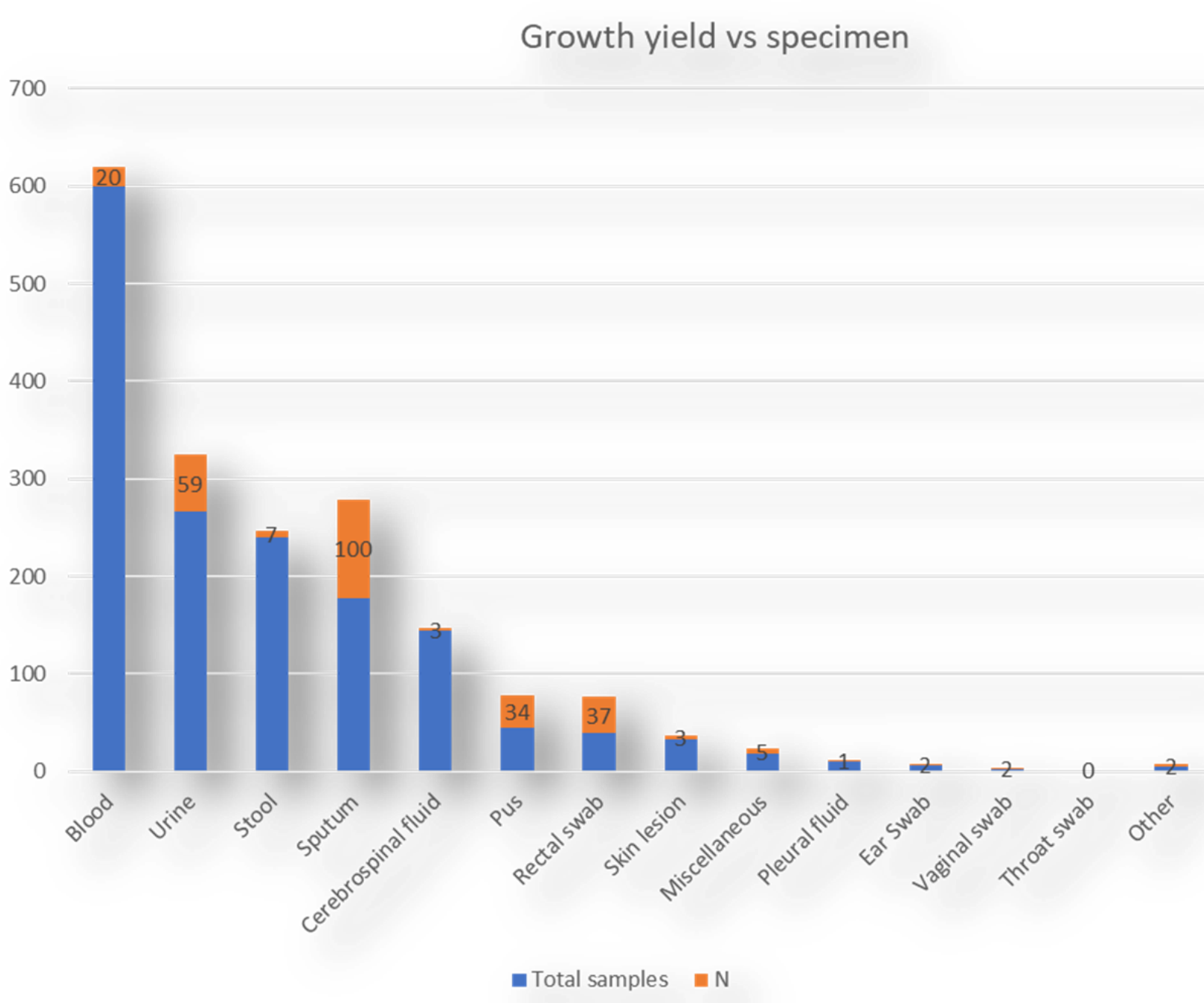
"Bacterial isolates from PLHIV admitted with advanced HIV disease (AHD) in Patna, Bihar, exhibit high rates of multidrug resistance, including ESBL and carbapenem-resistant (CR) strains."

"Hospital-based antibiograms are essential tools for clinicians to evaluate local susceptibility patterns, guide empiric antibiotic therapy, and track resistance trends over time."

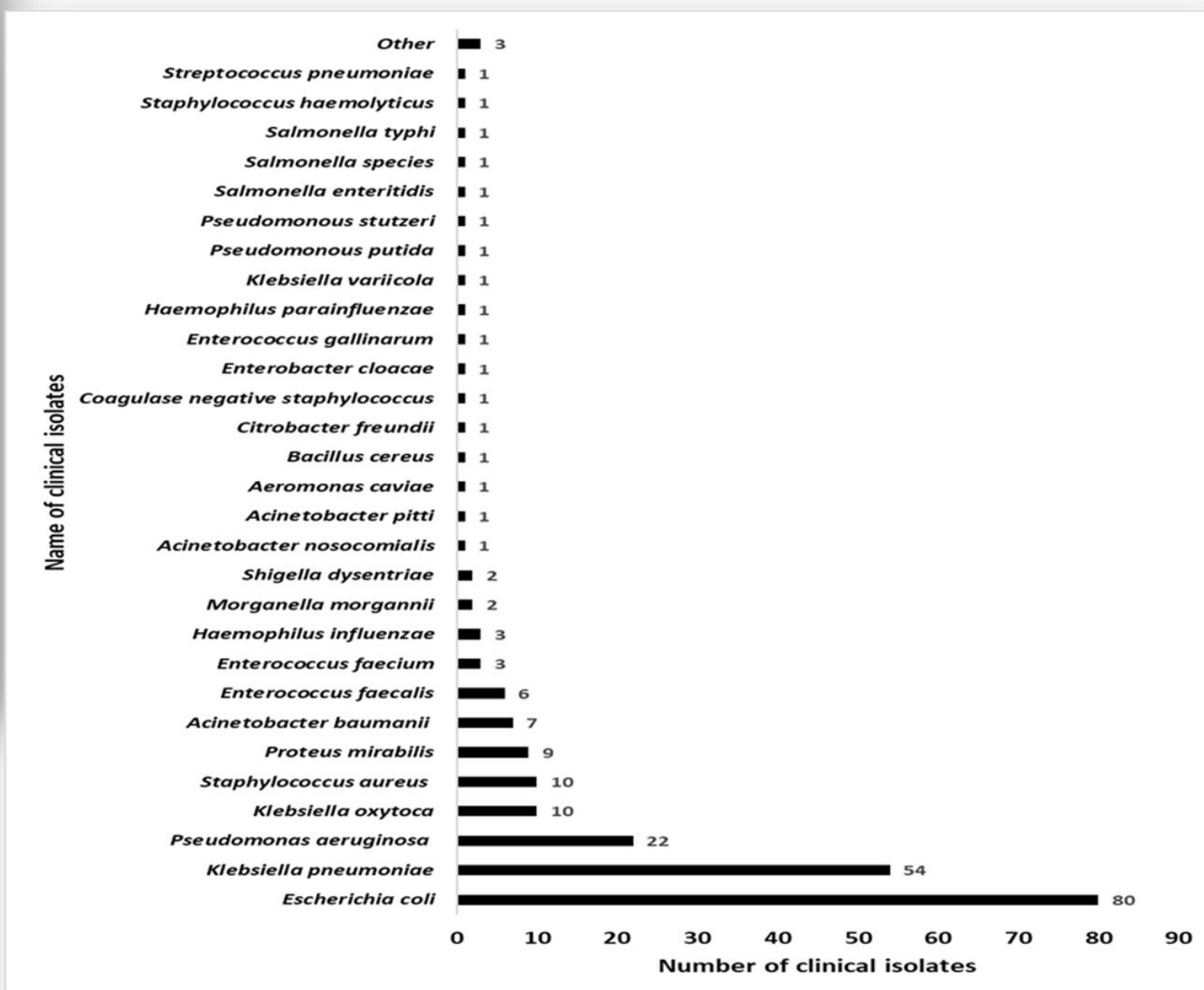
"There is a lack of data on the impact of bacterial drug resistance on morbidity and mortality in AHD patients in India, highlighting the need for further research."

Table 1. Demographic and clinical characteristics of patients admitted with AHD

Characteristics	n	%
Age group (years)		
<15	17	2.9
15 to <30	87	15.1
30 to <45	306	53.0
45 to <60	150	26.0
≥60	16	2.8
Missing data	1	0.2
Sex		
Female	144	25.0
Male	433	75.0
ART status		
ART naive	105	18.2
ART experienced	471	81.6
Missing data	1	0.2
WHO stage		
I	3	0.5
II	14	2.4
III	108	18.7
IV	430	74.5
Missing data	22	3.8
CD4 group (cells/mm ³)		
<100	310	53.7
100 to <200	133	23.1
≥200	87	15.1
Missing data	47	8.1
TB		
No	190	32.9
Yes	387	67.1
CRAg positive/cryptococcal meningitis		
No	508	88.0
Yes	69	12.0
Visceral leishmaniasis		
No	541	93.8
Yes	36	6.2
<i>Pneumocystis pneumonia</i>		
No	496	86.0
Yes	81	14.0
Bacterial pneumonia		
No	501	86.8
Yes	76	13.2



Bacterial growth Vs type of specimens
228 isolates found from 1586 clinical specimens



Number of clinical isolates



Demographics and clinical characteristics

Antibiotics	Bacterial Isolates	Gentamicin	Amikacin	Tobramycin	Netilmicin	Meropenem	Imipenem	Ertapenem	Ceftriaxone	Cefepime	Cefuroxime	Cefixime	Cefoperazone/Sulbactam	Cefotaxime	Ampicillin+Sulbactam	Ceftazidime	Amoxicillin clavulanic	Piperacillin tazobactam	Ampicillin	Ticarcillin - Clavulanate	Ciprofloxacin	Norfloxacin	Levofloxacin	Ofloxacin	co-trimoxazole	Colistin	Aztreonam	Nitrofurantoin	Doxicycline	Chloramphenicol	Tigecycline
		S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N	S	N
Escherichia coli	S	60	83	68	94	63	60	64	11	20	8.9	9.7	36	14	12	0	29	44	6.8	0	6.3	2.9	6.9	4.8	10	29	14	71	14	75	100
	N	80	80	25	16	80	80	59	80	80	79	31	31	44	26	1	80	80	59	1	80	34	29	21	77	59	29	21	4	4	
Klebsiella pneumoniae	S	52	63	37	44	51	54	56	5.7	28	3.8	5.3	21	6.5	5	0	20	41	R	R	15	12	5.3	6.7	19	21	16	20	19	50	33
	N	54	54	19	9	53	54	39	53	54	53	19	19	31	20	0	54	54	0	0	54	17	19	15	48	39	19	15	16	2	3
Klebsiella oxytoca	S	50	90	40	85.7	40	20	0	0	0	0	0	22.2	0	0	0	10	10	R	R	0	0	0	0	14.3	0	50	10	0	0	0
	N	10	10	10	7	10	10	10	10	10	10	10	9	1	10	0	10	10	0	0	10	10	10	10	7	10	10	10	10	0	0
Pseudomonas aeruginosa	S	86.4	81.8	66.7	77.3	77.3	R	R	77.3	0	0	0	100	R	77.3	R	68.2	R	50	54.5	0	54.5	0	R	36.4	66.7	R	R	R	R	
	N	22	22	3	22	22	22	22	22	22	22	22	1	22	22	22	22	22	2	22	22	22	22	22	22	9	9	9	9	9	
Proteus mirabilis	S	44.4	77.8	75	75	100	44.4	100	22.2	44.4	33.3	0	80	25	50	0	66.7	88.9	0	0	33.3	20	50	25	22.2	0	75	25	50	0	R
	N	9	9	4	4	9	9	5	9	9	9	5	5	4	4	0	9	9	5	0	9	5	4	4	9	3	4	4	4	4	4
Acinetobacter baumannii	S	14.3	42.9	0	0	0	R	0	16.7	0	0	0	0	0	0	0	R	0	R	0	14.3	0	14.3	14.3	42.9	R	0	0	0	R	100
	N	7	7	7	7	7	7	7	6	6	6	6	2	6	6	7	7	7	4	4	7	7	7	7	7	7	7	7	7	7	4

Antibiotic susceptibility patterns of gram negative bacteria from collected samples