

# Epidemiology and resistance map to aid antibiotic guideline development

## Single center retrospective study from an ED

Ria Benkő<sup>1,2,3</sup>, Márió Gajdács<sup>4</sup>, Mária Matuz<sup>1,2</sup>, Gabriella Bodó<sup>2</sup>, Andrea Lázár<sup>5</sup>, Edit Hajdú<sup>6</sup>, Erika Papfalvi<sup>6</sup>, Péter Hannauer<sup>3</sup>, Péter Erdélyi<sup>3</sup> and Zoltán Pető<sup>3</sup>



<sup>1</sup>Department of Clinical Pharmacy, University of Szeged; Szeged; [benkoria@gmail.com](mailto:benkoria@gmail.com)

<sup>2</sup>Central Pharmacy Department, Albert Szent-Györgyi Health Center, Szeged

<sup>3</sup>Department of Emergency Medicine, Albert Szent-Györgyi Health Center; Szeged

<sup>4</sup> Department of Pharmacodynamics and Biopharmacy, University of Szeged, Szeged

<sup>5</sup>Institute of Clinical Microbiology, Albert Szent-Györgyi Health Center; Szeged

<sup>6</sup>Infectious Disease Ward, 1<sup>st</sup> Department of Internal Medicine, Albert Szent-Györgyi Health Center, Szeged

**Background and importance:** Antimicrobial resistance (AMR) is one of the most important global threats and antibiotic use is one of the main drivers behind. Previously we identified suboptimal antibiotic use at our Emergency Department. International antibiotic guidelines for specific conditions cannot be adopted without the knowledge of local epidemiology and resistance, these are the essential first steps to develop an empiric antibiotic protocol.

**Aim and objectives:** To identify predominant isolates, clinical specimens and reveal resistance patterns of bacterial isolates.

**Materials and methods:** The study (2014-2019) was performed at the Emergency Department of the University of Szeged. All positive microbiological isolates were retrieved for a five year period.. Non-bacterial isolates, contaminants and duplicate isolates were screened and excluded. Bacterial identification was performed using MALDI-TOF MS. Antibiotic susceptibility-testing and interpretation of drug resistance were based on ESCMID/EUCAST standards.

### Most frequent bacterial isolates

Gram negative  
(N=4502;100%)

	frequency	%
Escherichia spp	2194	48.7
Klebsiella spp	664	14.7
Proteus spp	526	11.7

Σ ~ 75%

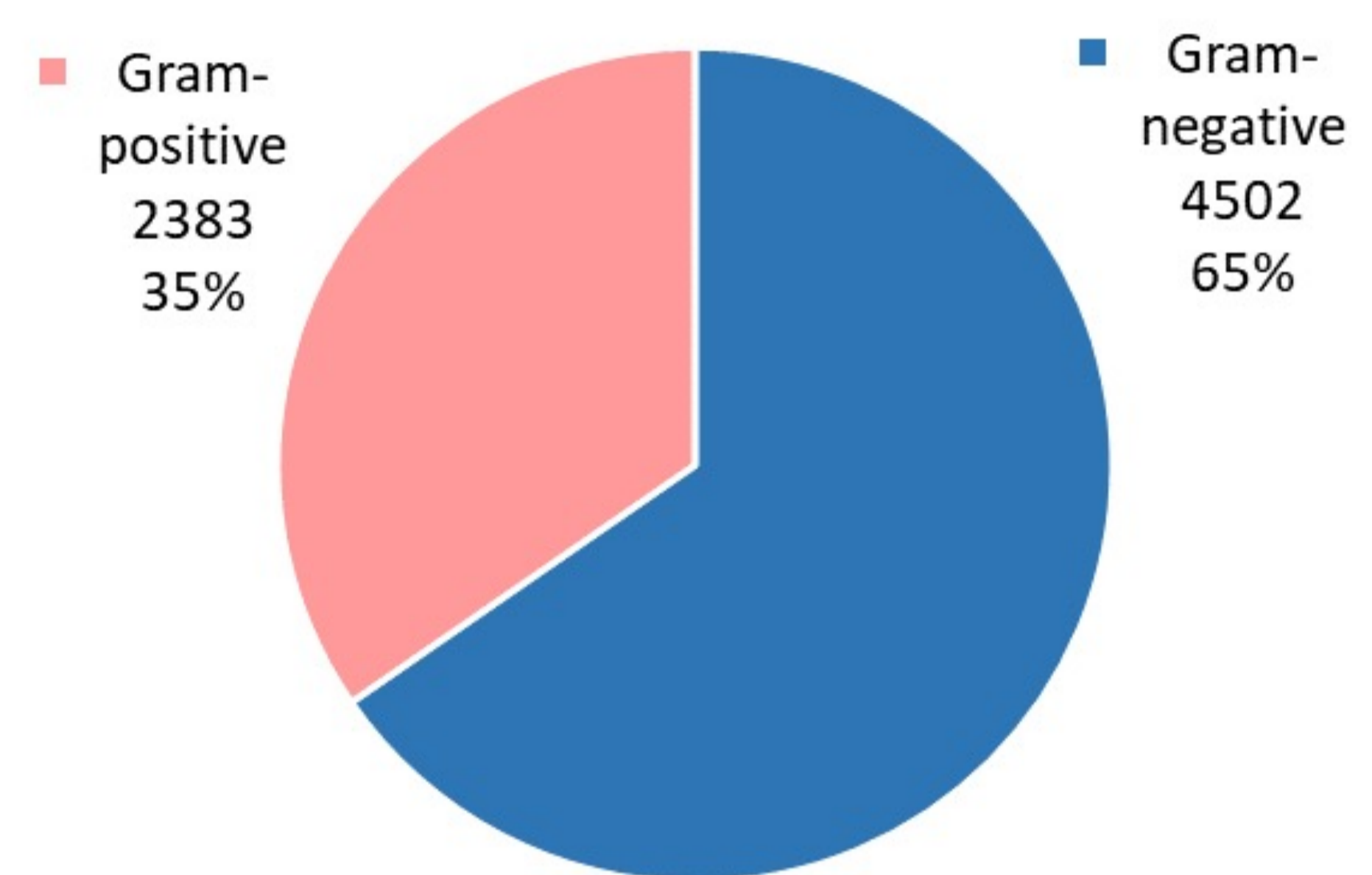
Gram positive  
(N=2383; 100%)

	frequency	%
Staphylococcus spp	906	38.0
Enterococcus spp	471	19.8
Streptococcus spp	431	18.1

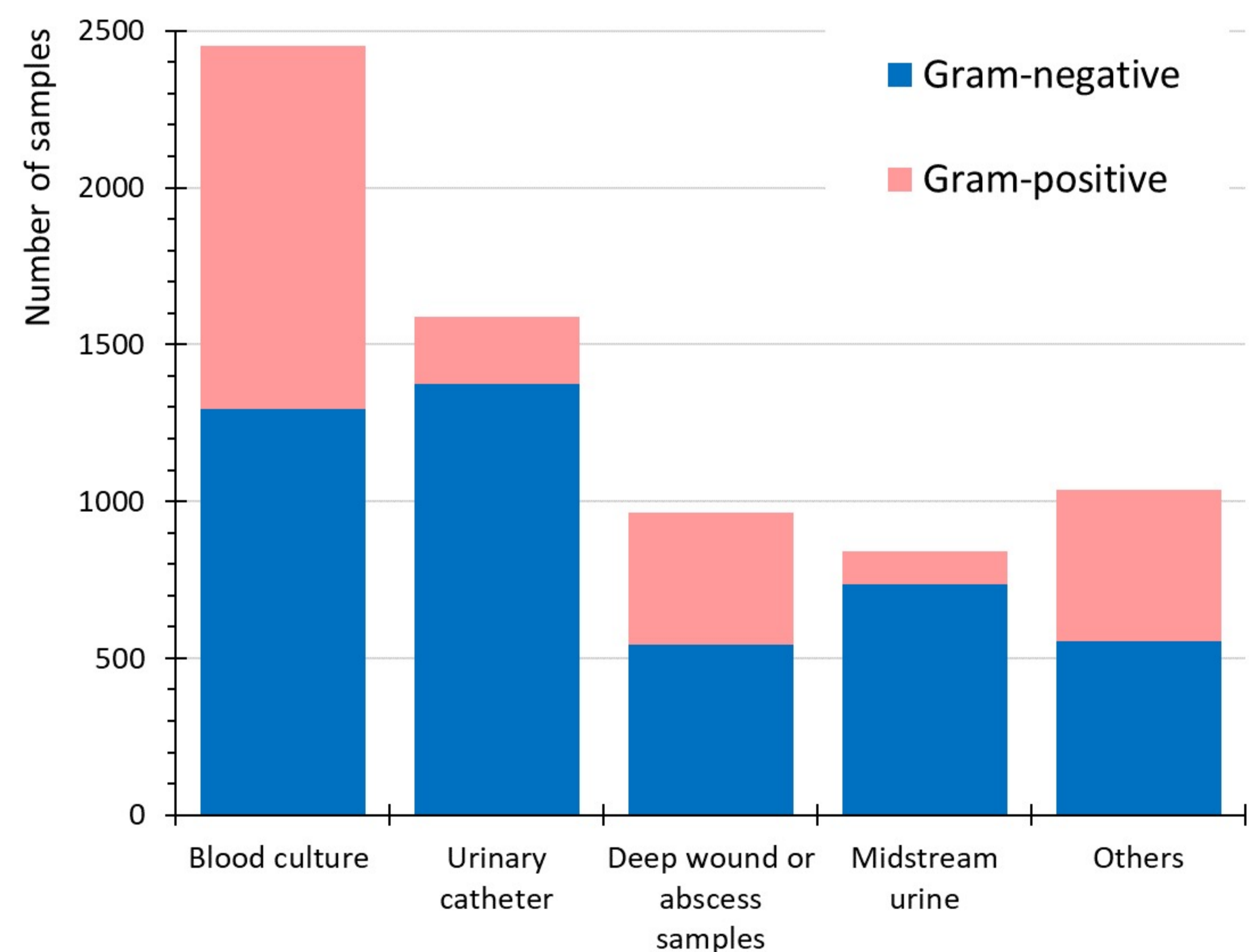
Σ ~ 75%

**Conclusion and relevance:** The most frequent bacteria and current resistance patterns were identified. Some of the revealed resistance patterns (e.g. high fluoroquinolone resistance among Gram-negative bacteria) may pose therapeutic challenges. The results of this survey will guide the development of our local antibiotic guideline.

### Results of the Gram stain



### Most frequent clinical specimens



### Resistance pattern of the most frequently isolated bacteria (resistance %)

Gram-negative

	ampicillin	amoxicillin	amoxicillin and clavulanic acid	cefuroxime	cefotaxime	ceftriaxone	ceftazidime	cefepime	piperacillin and tazobactam	meropenem	ciprofloxacin	amikacin	gentamycin	sulphamethoxazole-trimethoprim
<i>Klebsiella pneumoniae</i>	100	NT	32	33	27	31	31	23	24	0	37	21	21	34
<i>Escherichia coli</i>	52	NT	18	15	14	14	14	13	15	0	32	11	10	27
<i>Proteus mirabilis</i>	60	NT	38	37	28	31	31	24	25	0	42	24	23	68

Gram-positive

	oxacillin	ampicillin	amoxicillin	amoxicillin and clavulanic acid	cefuroxime	clindamycin	ciprofloxacin	erithromycin	clarithromycin	gentamycin	vancomycin	sulphamethoxazole-trimethoprim
<i>Enterococcus faecalis</i>	NT	0	0	1	NT	IR	43	NT	NT	IR	0	IR
<i>Enterococcus faecium</i>	NT	0	100	100	NT	NT	93	NT	NT	IR	33	IR
<i>Staphylococcus aureus</i>	17	NT	NT	17	17	21	19	22	22	1	0	1