



Bacteremia in Cancer and Stem Cell Transplantation (SCT), risk factors for Multidrug-Resistant Bacteria (MDRB). Preliminary Data from the First Prospective, Multicenter Study in Argentina

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BACKGROUND

There is no data published from Argentina regarding MDRB infections in patients with cancer and SCT

OBJECTIVES

To describe clinical and microbiological characteristics of episodes of bacteremia in patients with cancer and SCT, comparing MDRB bacteremia with non-MDRB, and to evaluate risk factors associated with MDRB bacteremia

METHODS

Prospective multicenter study. Episodes of bacteremia in patients with cancer and SCT were included in 8 centers, from July 2014 to May 2015. Variables with $p < .1$ in univariate analysis or clinically relevant were entered in a logistic regression model for multivariate analysis of risk factors for MDRB.

CLINICAL CHARACTERISTICS

- **254** episodes of bacteremia in 206 patients were included

- **Inclusion criteria:**

Hematological tumor: 171 (67,6%) (Acute leukemia most common)
Stem Cell Transplant (SCT): 43 (17%) (51,2% allogeneic)
Solid Tumor: 39 (15,4%)

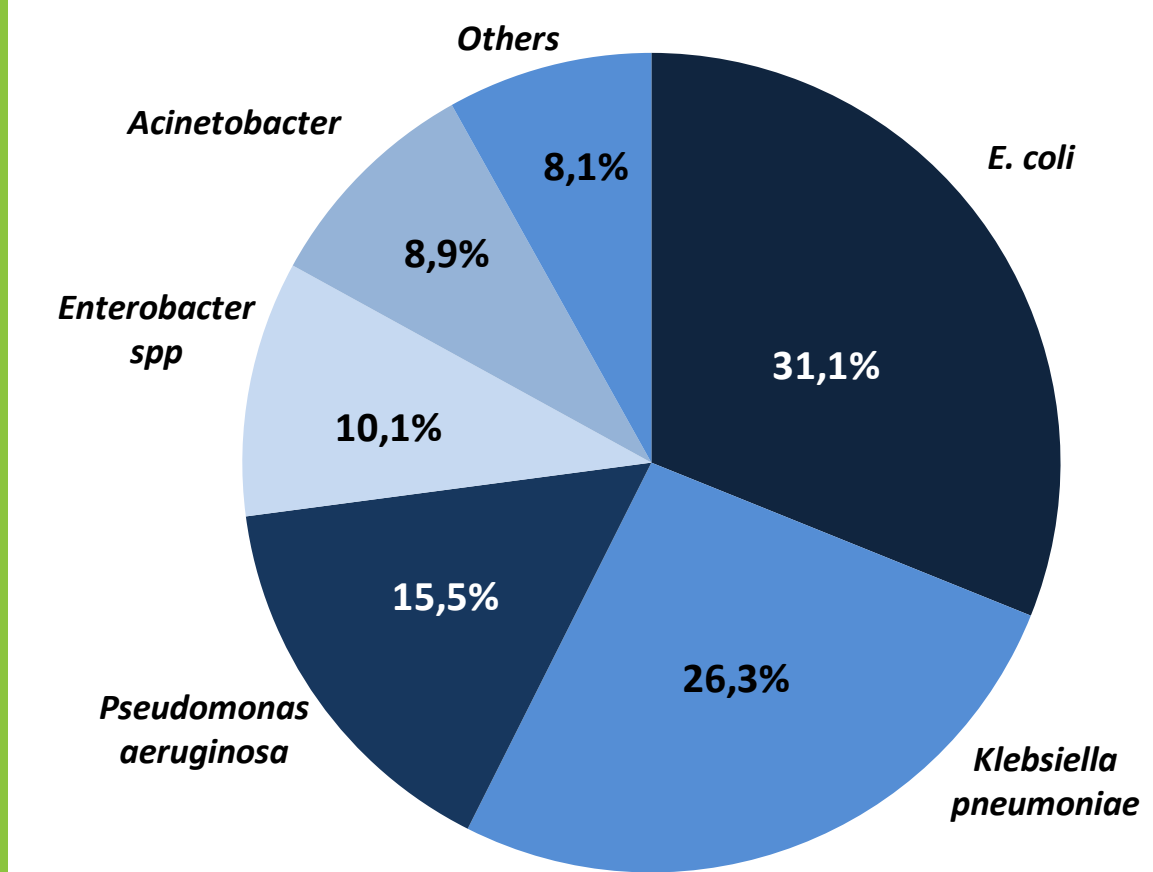
- **Neutropenia:** 169 (66,8%)

- **First episode of bacteremia:** 228 (90,1%) / Nosocomial infection: 164 (64,8%)

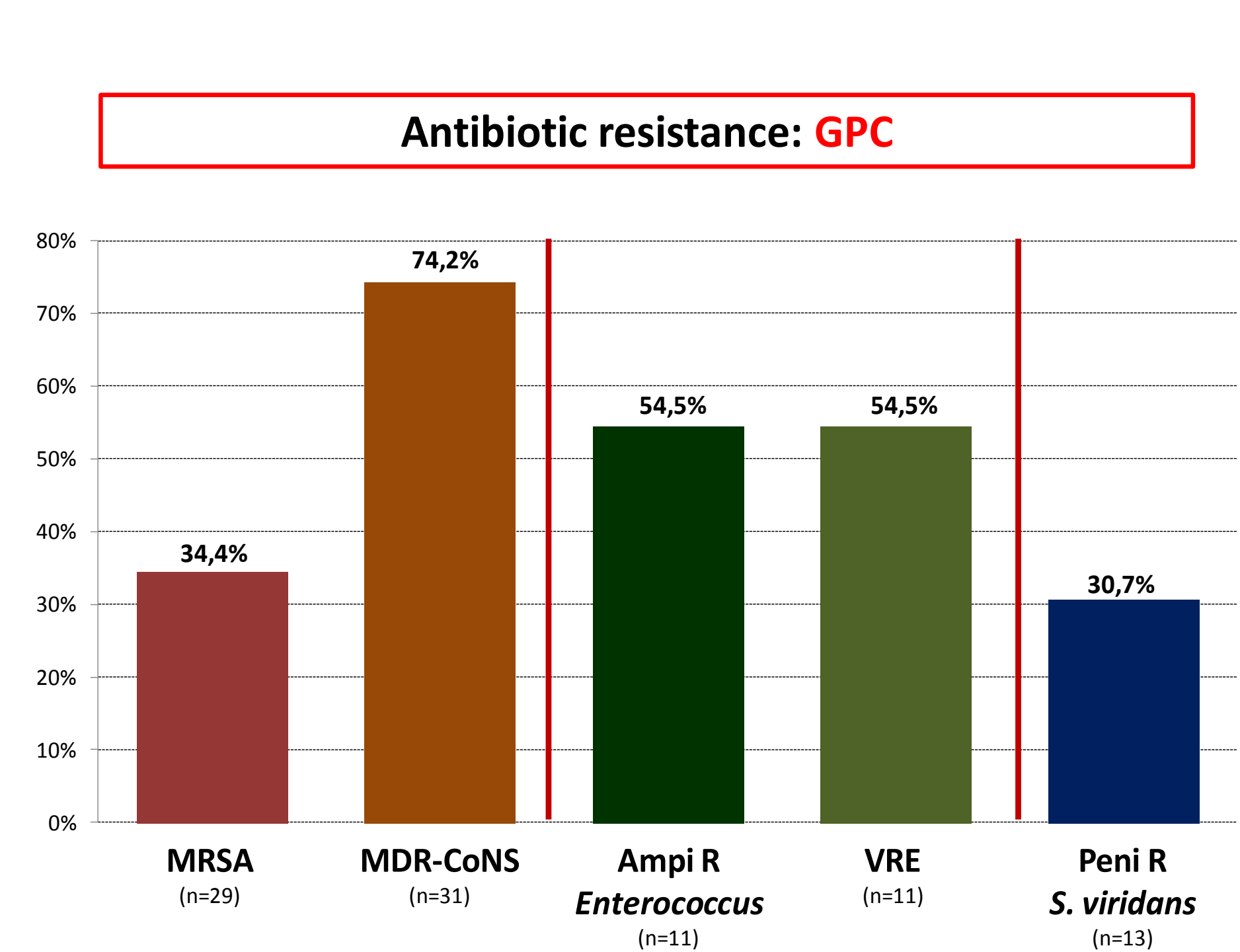
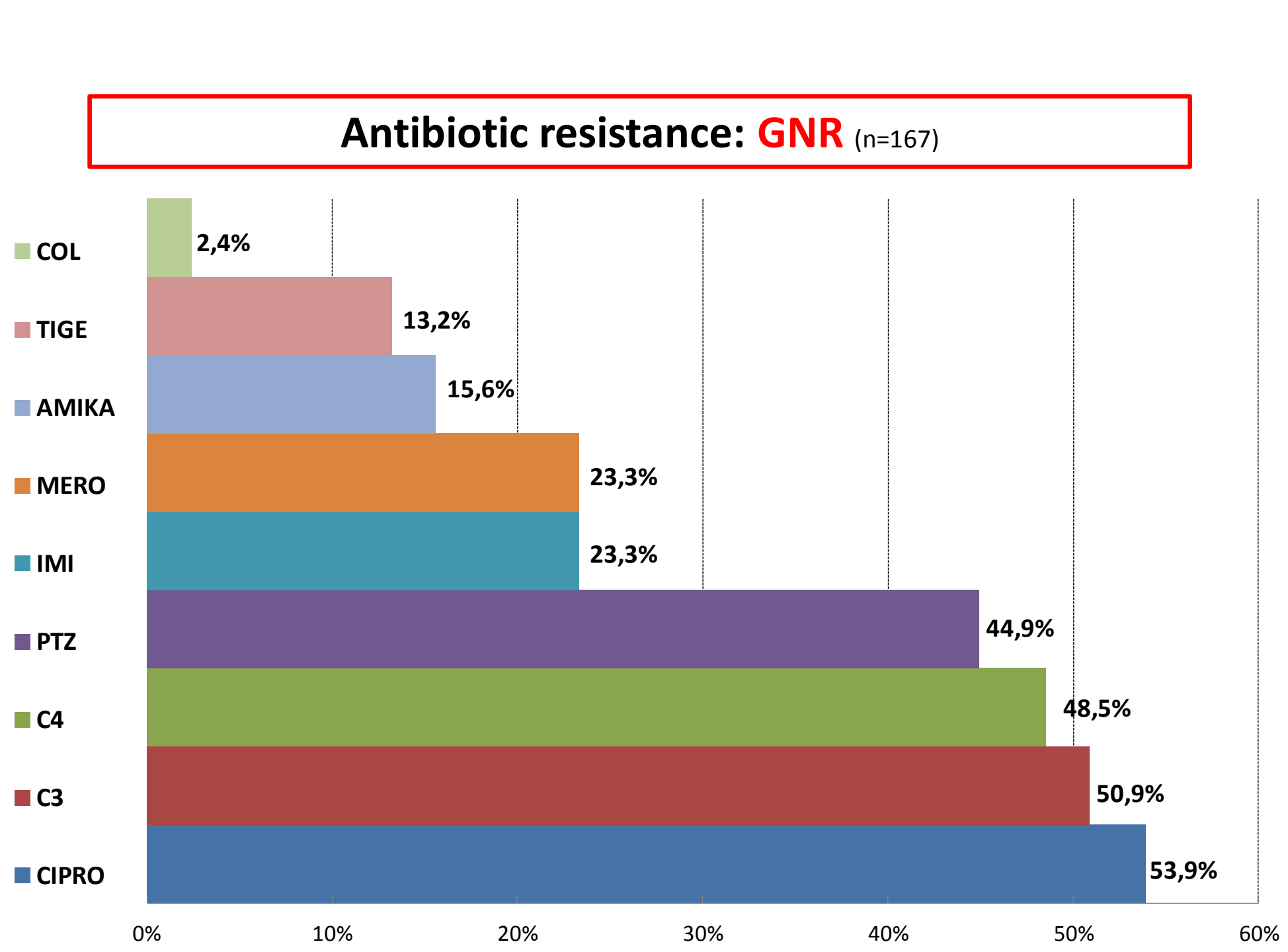
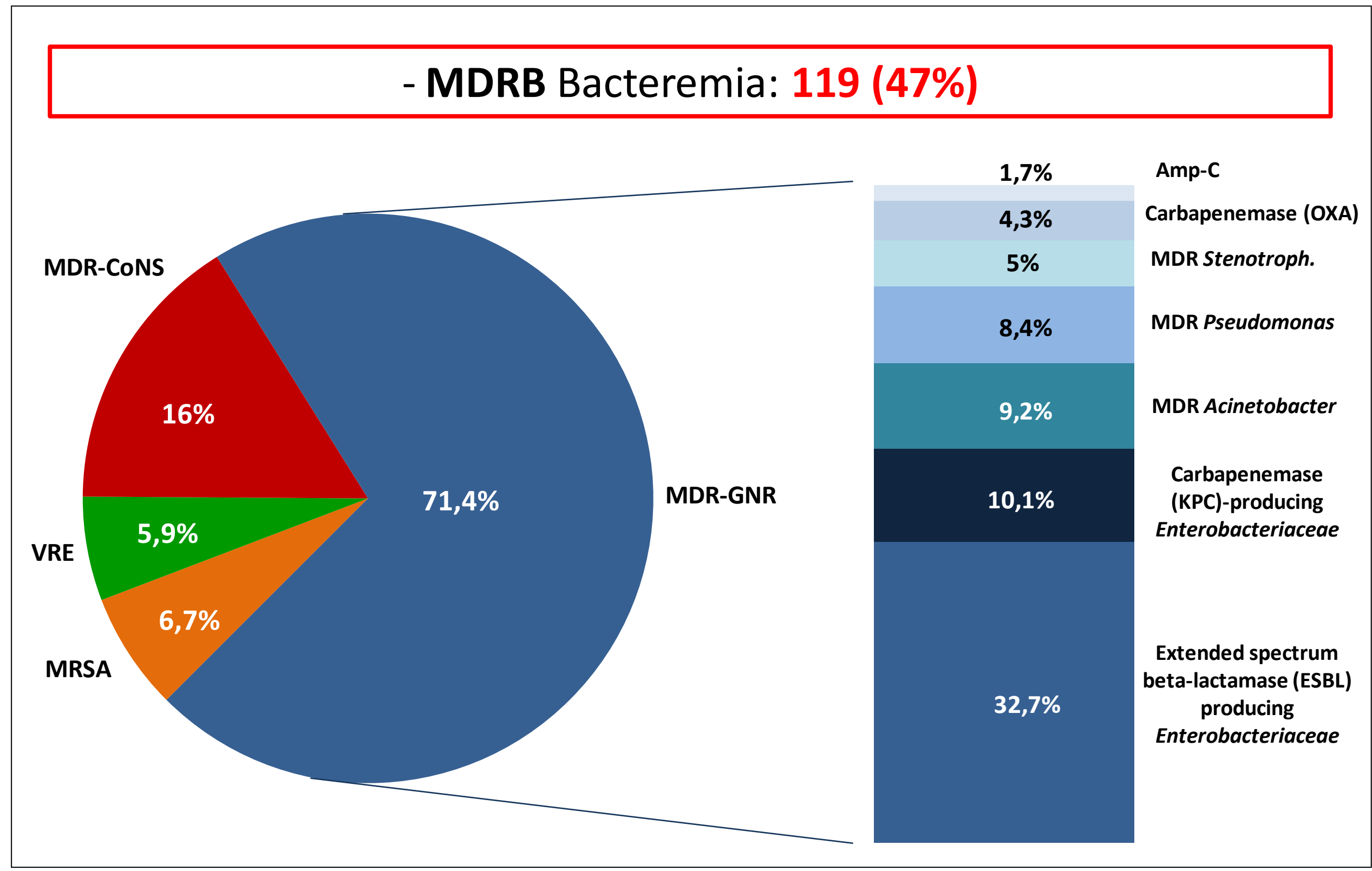
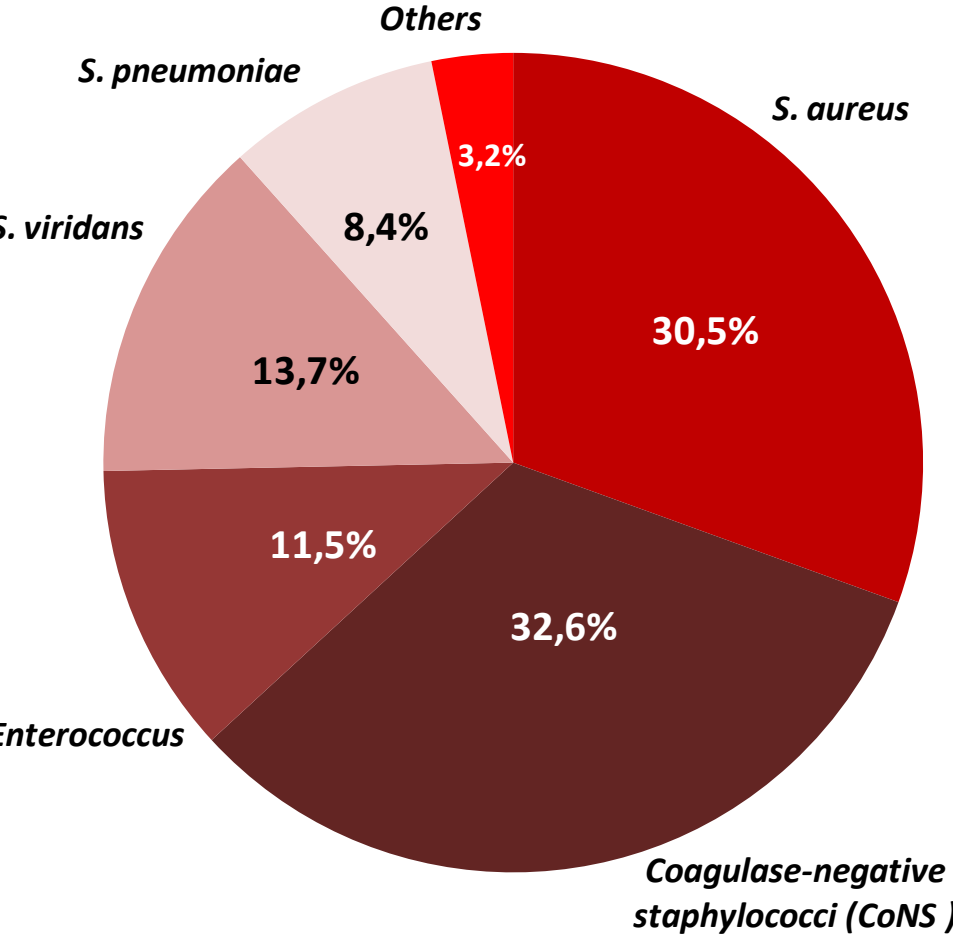
- **Hospital length of stay before bacteremia (median):** 10 days

MICROBIOLOGICAL CHARACTERISTICS

Gram negative rods (GNR): 167 (66%)



Gram positive cocci (GPC): 95 (37,5%)



Risk factors for MDRB bacteremia- MULTIVARIATE

Variable	Non-MDRB	MDRB	OR (95% CI)	p
Age	52 (33-63)	50 (33-64)	1,007 (0,99-1,024)	0,408
Solid tumor	27 (20,1%)	12 (10,1%)	1,079 (0,413-2,83)	0,876
Previous hospitalization (previous 30 days)	58 (43,3%)	69 (58%)	1,124 (0,62-2,039)	0,700
Previous MDRB colonization (previous 6 months)	11 (8,2%)	26 (21,8%)	1,739 (0,66-4,571)	0,262
Previous MDRB infection (previous 6 months)	9 (6,7%)	26 (21,8%)	1,442 (0,541-3,387)	0,464
Previous antibiotic treatment (previous 30 days)	44 (32,8%)	71 (59,7%)	2,454 (1,33-4,538)	0,004
Current MDRB colonization	12 (9%)	25 (21%)	1,152 (0,463-2,87)	0,761
>7 days of hospital stay before bacteremia	57 (42,5%)	91 (76,5%)	2,227 (1,046-4,933)	0,038
PITT Score the day of bacteremia	0 (0-2)	0 (0-3)	1,160 (0,991-1,357)	0,065
Neutropenia	74 (55,2%)	95 (79,8%)	2,46 (1,2-4,8)	0,01
Previous ICU hospitalization (previous 2 weeks)	5 (3,7%)	13 (10,9%)	1,205 (0,24-6,05)	0,821
Mechanical ventilation (previous 2 weeks)	3 (2,2%)	8 (6,7%)	0,972 (0,12-7,6)	0,978
Central venous catheter (previous 2 weeks)	69 (51,5%)	85 (71,4%)	2,09 (1,06-4,13)	0,033
Nosocomial infection	71 (53%)	93 (78,2%)	1,447 (0,74-2,8)	0,276

EMPIRICAL ANTIBIOTIC TREATMENT

Variable	Non-MDRB	MDRB	p
Combined treatment (n=252)	28 (21,1%)	51 (42,9%)	0,0001
Monotherapy (n=252)	105 (78,9%)	68 (57,1%)	0,0001
Treatment duration (days) (median, P25-P75) (n=225)	14 (10-15)	14 (8-17)	0,319

Most common monotherapies:

Piperacilin/tazobactam
Carbapenems
Quinolones / Ampicilin-sulbactam

Most common combined treatments:

Carbapenems + Colistin
Carbapenems + Amikacin
Piperacilin/tazobactam + Amikacin

OUTCOMES

Variable	Non-MDRB	MDRB	p
Breakthrough bacteremia	4 (3%)	24 (20,2%)	0,0001
Appropriate empirical treatment (AET) (n=252)	120 (90,2%)	68 (57,1%)	0,0001
Delay in AET (in hours) (median, P25-P75) (n=247)	0	0 (0-54)	0,0001
Intensive Care Unit admission (n=252)	19 (14,3%)	26 (21,8%)	0,139
Shock (n=252)	24 (18%)	33 (27,7%)	0,072
Multiorgan failure (n=252)	15 (11,3%)	25 (21%)	0,039
Clinical response at the 7 th day of treatment (n=252)	99 (74,4%)	71 (59,7%)	0,015
Overall 7-day mortality (n=251)	13 (9,8%)	23 (19,3%)	0,046
Overall 7-day mortality associated to infection? (n=35)	8 (61,5%)	21 (95,5%)	0,019
Overall 30-day mortality (n=251)	23 (17,4%)	35 (29,4%)	0,035
Overall 30-day mortality associated to infection? (n=57)	10 (43,5%)	28 (82,4%)	0,004

CONCLUSION

These data confirm that MDRB, especially GNR, are a great concern in our country, and pose a challenge regarding empirical treatment in this population. Coverage should include ESBL-producing *Enterobacteriaceae* particularly in those with the risk factors previously identified.