TRANSPLANTATION AND DIALYSIS CENTER BACTERIAL PROFILE ANALYSIS: NINETEEN-YEAR REPORT (1998-2016)

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OBJECTIVES

To analyze the dynamics of the species composition of bacterial population and change the sensitivity to antibiotics in patients of transplantation and dialysis center.

METHODS

We have examined the bacteriological tests results of 1484 patients with chronic kidney disease stage 5 (hemodialysis and peritoneal dialysis patients and renal transplant recipients) in 1998-2016. Biomaterial: urine, blood, wound effluent, sputum. In all patients bacteriological tests were performed because of suspected of infection: pyelonephritis, pneumonia, catheter-associated angiosepsis, postoperative wound infection and nonspecific surgical infection.

RESULTS

The total incidence of bacterial pathogens in culture of blood, sputum, urine and wound discharge increased significantly (from 61% to 75%). The incidence of pathogens in sputum increased from 27 to 94%, from 4% to 11% in the blood, from 11 % to 39% in wound discharge and from 52% to 71% in the urine from. The results can be in some way due to the change of bacteriological research method.

We noted a monotonous increase of the gram-negative flora share – fig. 1.

However, the following trends are detected in the composition of the bacterial population: the part of Gram-positive bacteria monoculture has decreased and the parts of Gram-positive bacteria monoculture and mixed flora have increased – fig. 2.

In recent years half of the microbial associations consisted of in 22% Gram-positive and Gram-negative bacteria, in 6% of Gram-positive and fungi, in 9% of Gram-negative and fungi – fig. 3. In other cases observed ternary association. Thus, there has been a fundamental change in the nature of the microflora: the dominance of Gram-positive bacteria changed to Gram-negative, and the nature of the flora is usually mixed.
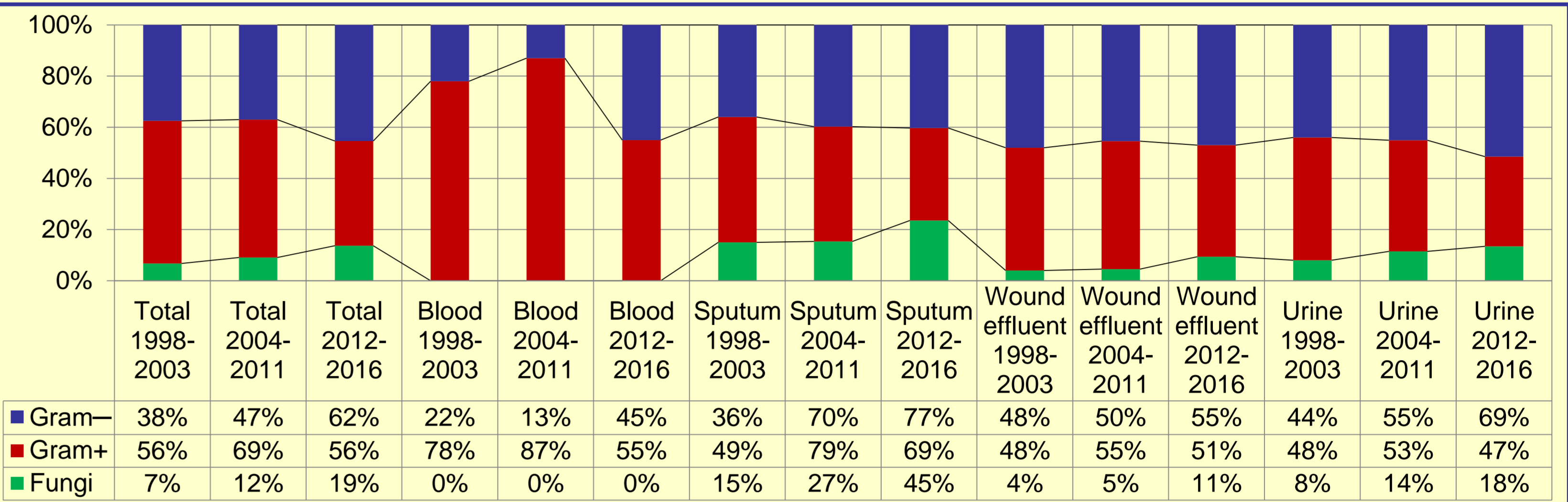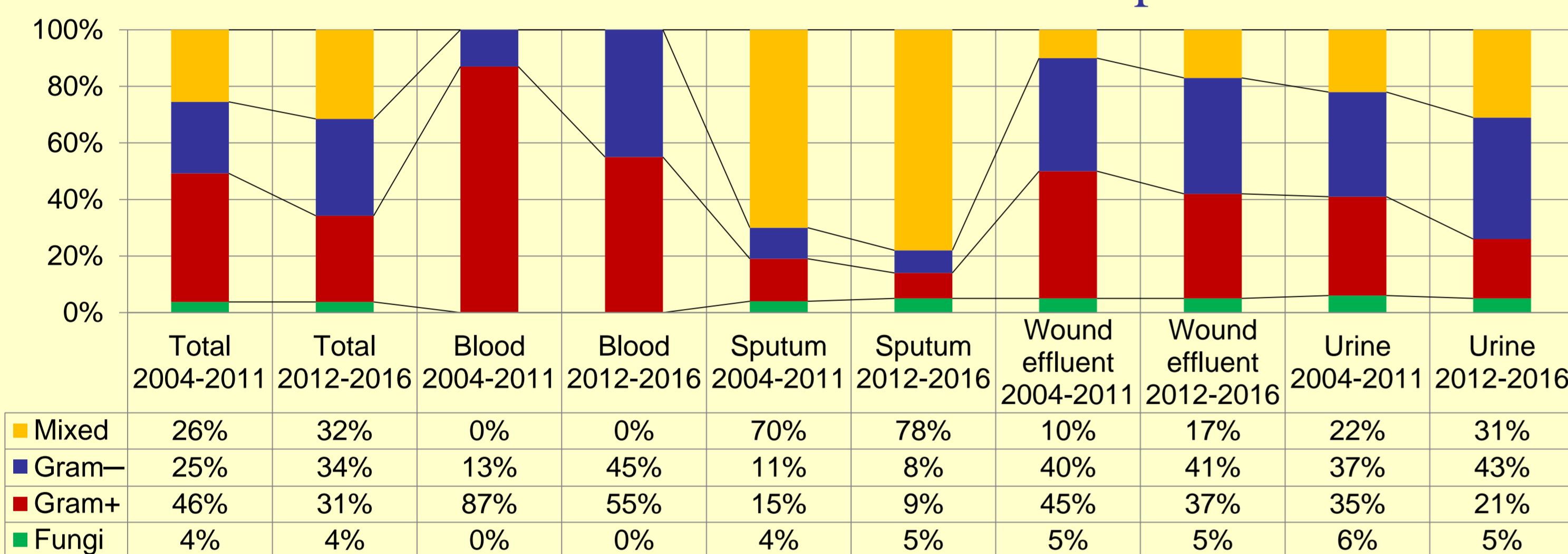

Figure 1. The overall ratio of gram-negative, gram-positive bacteria and fungi

	Total 1998-2003	Total 2004-2011	Total 2012-2016	Blood 1998-2003	Blood 2004-2011	Blood 2012-2016	Sputum 1998-2003	Sputum 2004-2011	Sputum 2012-2016	Wound effluent 1998-2003	Wound effluent 2004-2011	Wound effluent 2012-2016	Urine 1998-2003	Urine 2004-2011	Urine 2012-2016
Gram–	38%	47%	62%	22%	13%	45%	36%	70%	77%	48%	50%	55%	44%	55%	69%
Gram+	56%	69%	56%	78%	87%	55%	49%	79%	69%	48%	55%	51%	48%	53%	47%
Fungi	7%	12%	19%	0%	0%	0%	15%	27%	45%	4%	5%	11%	8%	14%	18%

Figure 2. The composition of the microflora

	Total 2004-2011	Total 2012-2016	Blood 2004-2011	Blood 2012-2016	Sputum 2004-2011	Sputum 2012-2016	Wound effluent 2004-2011	Wound effluent 2012-2016	Urine 2004-2011	Urine 2012-2016
Mixed	26%	32%	0%	0%	70%	78%	10%	17%	22%	31%
Gram–	25%	34%	13%	45%	11%	8%	40%	41%	37%	43%
Gram+	46%	31%	87%	55%	15%	9%	45%	37%	35%	21%
Fungi	4%	4%	0%	0%	4%	5%	5%	5%	6%	5%

Figure 3. Microbial associations

	Total 2004-2011	Total 2012-2016	Sputum 2004-2011	Sputum 2012-2016	Wound effluent 2004-2011	Wound effluent 2012-2016	Urine 2004-2011	Urine 2012-2016
Gram+/Gram–	24%	22%	47%	38%	10%	11%	14%	18%
Gram+/Fungi	5%	6%	11%	6%	0%	3%	4%	5%
Gram–/Fungi	3%	9%	6%	18%	0%	3%	4%	5%
Gram+/Gram–/Fungi	2%	5%	6%	13%	0%	0%	0%	3%

Gram-negative bacteria are the most common bacterial population in recent years. There are *Klebsiella pneumonia* (32%), *Acinetobacter spp.* (22%), *E. coli* (17%), *P. aeruginosa* (9%), *Enterobacter spp.* (9%) – fig. 4. *Enterococcus spp.* (50%), *Staphylococcus spp.* (44%) and *Streptococcus spp.* (6%) are found among Gram-positive bacteria – fig. 5. The incidence of *C. glabrata* and *C. krusei* increased – fig. 6.
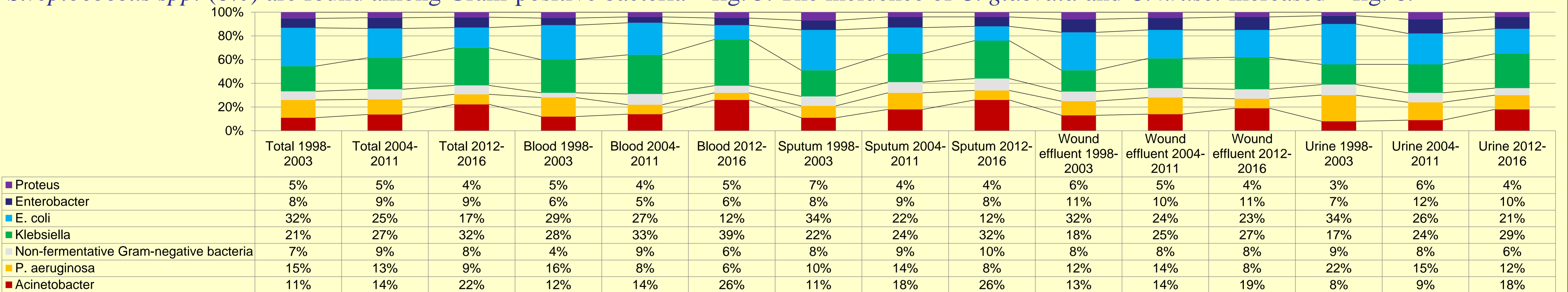

	Total 1998-2003	Total 2004-2011	Total 2012-2016	Blood 1998-2003	Blood 2004-2011	Blood 2012-2016	Sputum 1998-2003	Sputum 2004-2011	Sputum 2012-2016	Wound effluent 1998-2003	Wound effluent 2004-2011	Wound effluent 2012-2016	Urine 1998-2003	Urine 2004-2011	Urine 2012-2016
Proteus	5%	5%	4%	5%	4%	5%	7%	4%	4%	6%	5%	4%	3%	6%	4%
Enterobacter	8%	9%	9%	6%	5%	6%	8%	9%	8%	11%	10%	11%	7%	12%	10%
E. coli	32%	25%	17%	29%	27%	12%	34%	22%	12%	32%	24%	23%	34%	26%	21%
Klebsiella	21%	27%	32%	28%	33%	39%	22%	24%	32%	18%	25%	27%	17%	24%	29%
Non-fermentative Gram-negative bacteria	7%	9%	8%	4%	9%	6%	8%	9%	10%	8%	8%	8%	9%	8%	6%
P. aeruginosa	15%	13%	9%	16%	8%	6%	10%	14%	8%	12%	14%	8%	22%	15%	12%
Acinetobacter	11%	14%	22%	12%	14%	26%	11%	18%	26%	13%	14%	19%	8%	9%	18%

Figure 4. Gram-negative bacteria

	Total 1998-2003	Total 2004-2011	Total 2012-2016	Blood 1998-2003	Blood 2004-2011	Blood 2012-2016	Sputum 1998-2003	Sputum 2004-2011	Sputum 2012-2016	Wound effluent 1998-2003	Wound effluent 2004-2011	Wound effluent 2012-2016	Urine 1998-2003	Urine 2004-2011	Urine 2012-2016
Streptococcus	17%	15%	13%	17%	12%	8%	22%	18%	16%	19%	24%	21%	11%	4%	5%
Enterococcus	33%	42%	53%	40%	47%	59%	30%	34%	49%	33%	32%	44%	29%	55%	61%
Staphylococcus	50%	44%	34%	43%	41%	33%	48%	48%	35%	48%	44%	35%	60%	41%	34%

Figure 5. Gram-positive bacteria

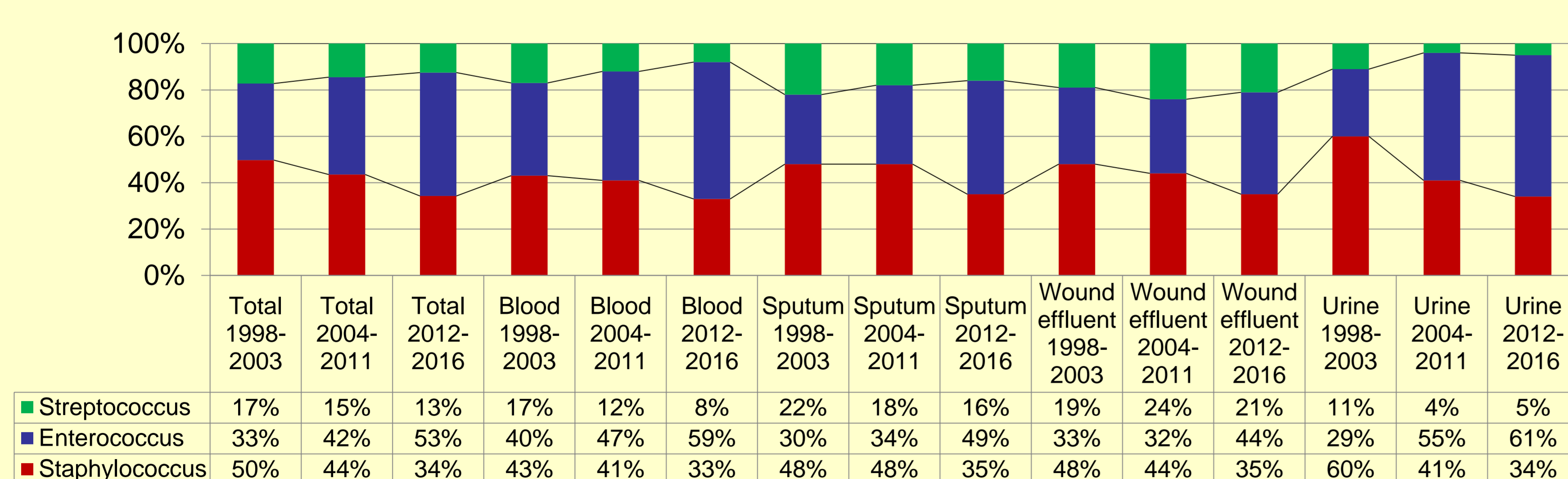|	Total 2004-2011	Total 2012-2016	Sputum 2004-2011	Sputum 2012-2016	Wound effluent 2004-2011	Wound effluent 2012-2016	Urine 2004-2011	Urine 2012-2016
Candida spp.	14%	14%	13%	14%	14%	18%	16%	10%
C. tropicalis	9%	7%	8%	8%	14%	8%	5%	4%
C. glabrata	17%	25%	21%	30%	8%	16%	22%	28%
C. krusei	9%	13%	9%	14%	9%	10%	9%	14%
C. albicans	51%	42%	49%	34%	55%	48%	48%	44%

Figure 6. Fungi genus *Candida*

The most common Gram-positive bacteria have a high sensitivity to a number of antibiotics such as vancomycin and linezolidum. The main Gram-negative bacteria is *Klebsiella spp.* We noted a growth of resistance of *Klebsiella spp.* even to modern antibiotics. Increasing of antibiotic resistance of *E. coli* was mentioned.
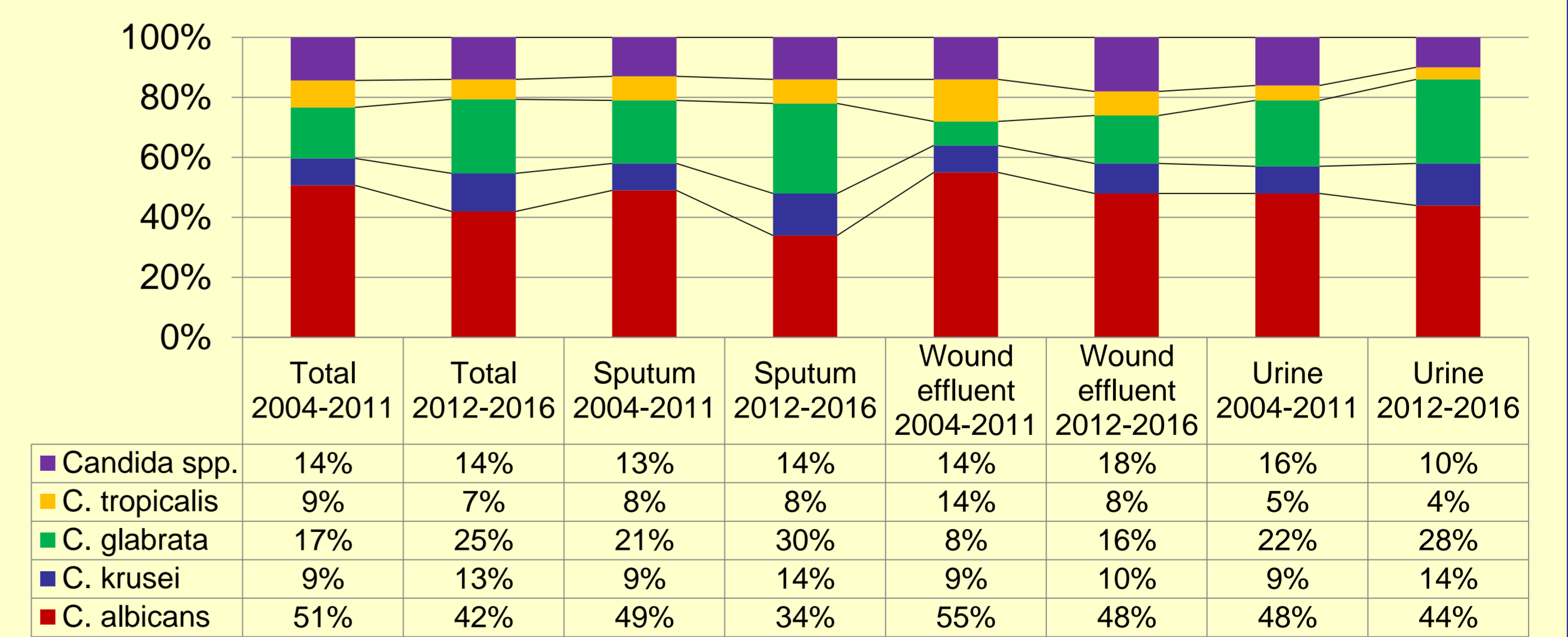
CONCLUSIONS

Bacterial profile changes significantly. Over the years, there was a great change in the nature and composition of the bacterial flora in patients of our center. This fact and the growing resistance to antibiotics dictate the need for periodic analysis of bacterial flora in order to improve treatment outcomes.