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Conference Abstract A5

Epidemiology of Gram-Positive (G+ bacteria) Bloodstream Infections in Patients After Allogeneic Hematopoietic Stem Cell Transplantation (allo-HSCT)

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Background

Bloodstream infections (BSIs) caused by Gram-positive (G+) microorganisms remain a significant problem in patients after allogeneic hematopoietic stem cell transplantation (allo-HSCT), leading to severe infectious complications and prolonged hospitalization.

Aim

To study local epidemiology, risk factors, and mechanisms of antibiotic resistance.

Materials and Methods

The study included 212 patients over 18 years old that received their first allo-HSCT between January 2023 and December 2024 at the Gorbacheva Institute. Patients who received a second allo-HSCT or those with localized/systemic infections requiring antibacterial therapy (ABT) at the time of transplantation were excluded (37 patients). Outcomes were evaluated in 175 patients.

The median age at transplantation was 42 years (range: 18–75); 49% were male (n=86). Patient characteristics are presented in Table 1.

Vancomycin-resistant enterococci (VRE) colonization prior to allo-HSCT was observed in 10.3% (n=18). Among G+ BSI cases, VRE colonization was present in 28.7% (n=5).

Results

The incidence of G+ BSI within the first 30 days after allo-HSCT was 25.1% (n=44). The median day of onset of bloodstream infections (BSI) was 6 days (range 2–27 days) after allo-HSCT. The BSI were caused by the following etiological agents:

Staphylococcus epidermidis — 79.5% (n=35)
Staphylococcus haemolyticus — 2.3% (n=1)
Staphylococcus hominis — 2.3% (n=1)
Corynebacterium jeikeium — 2.3% (n=1)
Enterococcus faecium — 4.5% (n=2)
Streptococcus mitis — 2.3% (n=1)
Staphylococcus aureus — 2.3% (n=1)
Streptococcus epidermidis — 2.3% (n=1)

Antibiotic susceptibility patterns are presented in Table 2.

In 25.9% of cases (n=13), central venous catheter (CVC) replacement was performed, with a median time of 2 days (range 0–13) from BSI confirmation to replacement.

In 13.6% of cases (n=6), Gram-positive bloodstream infections (G+ BSI) were preceded by bloodstream infections caused by Gram-negative (G–) bacteria, with a median onset day of 8 (range 1–28). In 11.4% of cases (n=5), G– BSI developed after G+ BSI (median onset day = 6, range 1–13). In 4.5% of cases (n=2), BSIs were caused by both G+ and G– pathogens.

First-line therapy was administered in 43.2% of cases (n=19) — median initiation on day 11 from BSI onset. Second-line therapy was used in 36.4% (n=16), third-line in 20.5% (n=9).

Risk factors (univariate analysis): Severe mucositis grade 3–4 (p=0.01) was significantly associated with G+ BSI. Diarrhea, GVHD (grades 3–4), and neutropenia duration showed no statistically significant correlation. Multivariate analysis revealed no independent predictors of G+ BSI (p>0.05). Severe mucositis was borderline significant (p=0.08), requiring validation in a larger cohort.

Thirty-day overall survival (OS) was 100%. Median OS was not reached. All deaths occurred in patients with G– BSI during or after G+ BSI.

Conclusions

The incidence of G+ BSI in patients after allo-HSCT was 32.5%. The predominant pathogen was Staphylococcus epidermidis. Fatal outcomes were recorded among patients with G– BSI developing against the background of G+ BSI. In univariate analysis, severe mucositis (p=0.01) and duration of neutropenia (p=0.035) were associated with G+ BSI.

Table 1. Patient characteristics and allo-HSCT

Characteristics	Study group
	% n=175
Study period	01.2023 – 12.2024
Median age	42 (18-75)
Male	49%(86)
Main diagnosis	
AML	57% (99)
ALL	13%(23)
CMPD	10%(18)
LH and nHL	4.6%(8)
AA	5.7%(10)
MDS	9.7%(17)
Relapse/progression	14%(24)
Type of transplantation **MRD** **MUD** **MMUD** **Gaplo-HSCT**	 17%(30) 26%(46) 28%(49) 29%(50)
Conditioning regimen **MAC**	 39.4%(69)

Table 2. Antibiotic susceptibility of isolated strains

Bacteria	**Sensitivity %, (n)**			
	Clindamycin	**Vancomycin**	**Linezolid**	**Tigecycline**
Staphylococcus epidermidis (n=35)	25,7%	85,7%	97,1%	100%
Staphylococcus haemolyticus (n=1)	0%	100%	100%	100%
Staphylococcus hominis (n=1)	0%	100%	100%	100%
Staphylococcus aureus (n=1)	100%	100%	100%	100%
Streptococcus epidermidis (n=1)	0%	100%	100%	100%
Streptococcus mitis (n=1)	0%	100%	100%	0%
Corynebacterium jeikeium (n=1)	0%	100%	0%	0%

Enterococcus faecium (n=2)	0%	100%	100%	100%