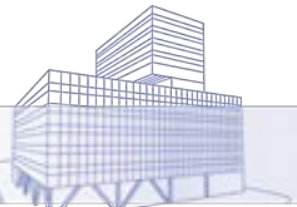


Oral microbiome and oral mucositis in autologous hematopoietic stem cell transplantation recipients

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Faculty disclosure

<input checked="" type="checkbox"/>	No, nothing to disclose
<input type="checkbox"/>	Yes, please specify:

Introduction

- Conditioning for hematopoietic stem cell transplantation (HSCT) frequently leads to oral ulcerative mucositis
- Recently more interest in role of bacteria in disease
- Goal: study the role of oral microbiome in oral mucositis in HSCT recipients

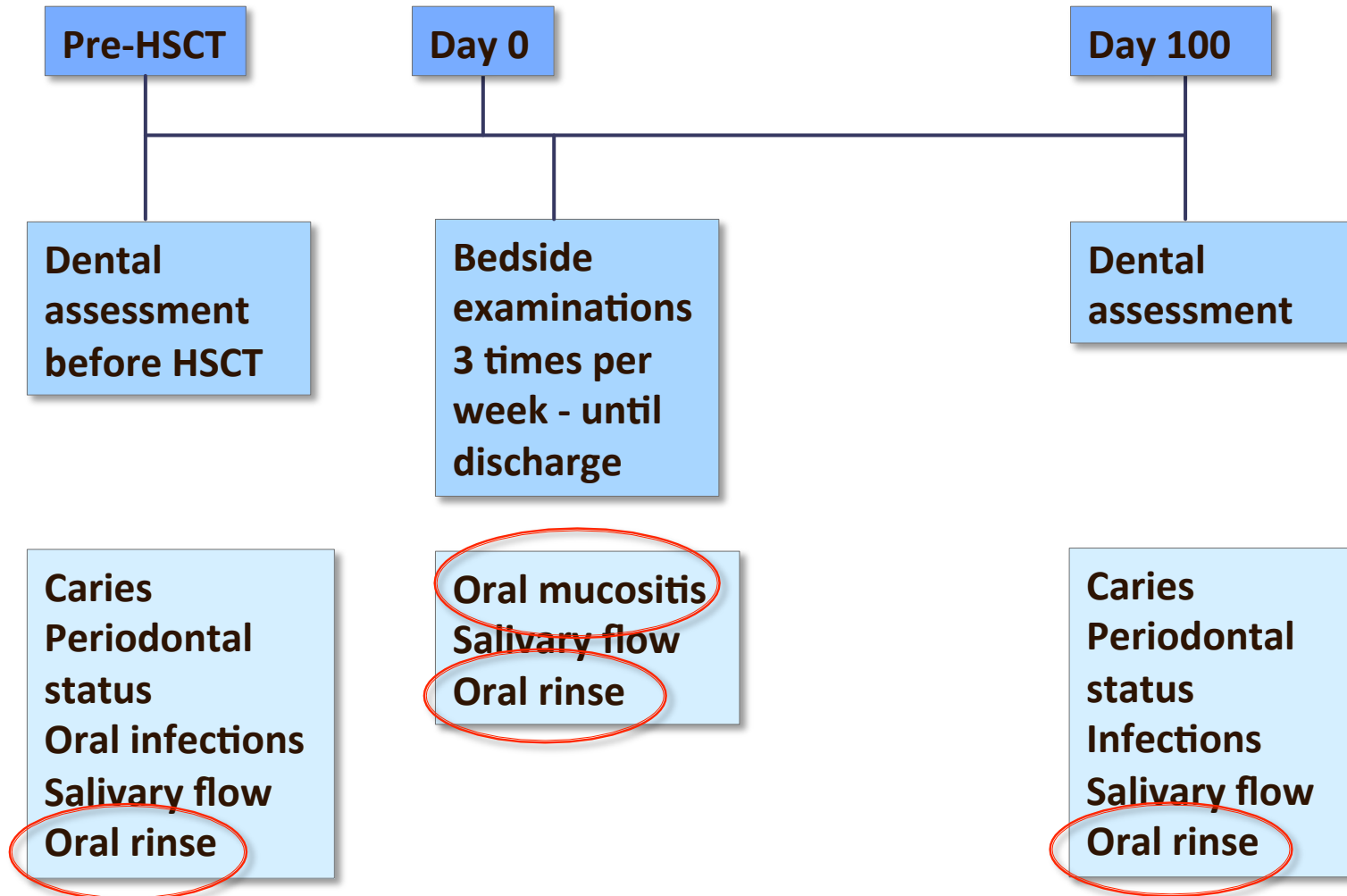


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Materials and methods

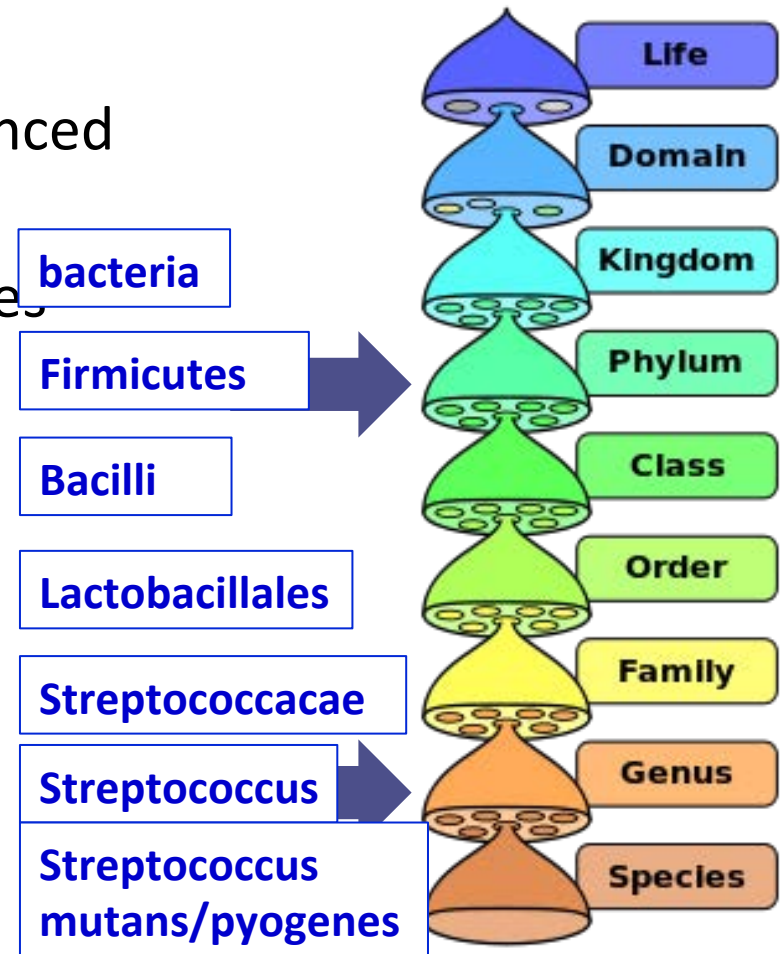
- Prospective observational multicenter study
- Autologous HSCT
- Cryotherapy
- Oral ulcerative mucositis (WHO ≥ 2)
- Oral rinse 10 ml (NaCl / PBS)
- Prophylaxis bloodstream infection
 - ciprofloxacin, feneticilline

Flow chart study



Microbiome analysis

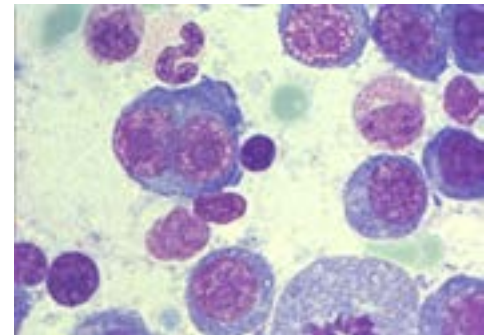
- 16S rDNA amplicons were sequenced
Illumina platform
- Reads were clustered in oligotypes
and classified in taxa
- Statistics: principal component
analysis, PERMANOVA, Shannon
diversity Index, LEfSe



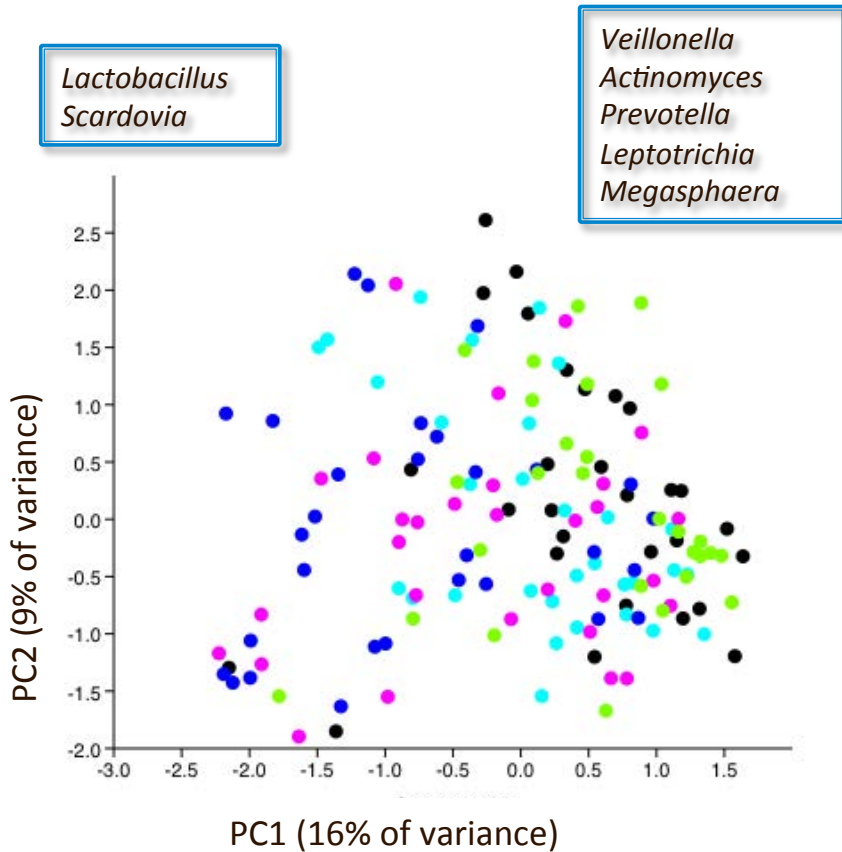
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Results

- 50 patients with multiple myeloma
- HSCT, conditioning high dose melphalan
- Age 57.4 \pm 7.3 years; 55% males
- 20 patients WHO \geq 2 (40%)
- 30 patients no ulcerative OM
- 478 oligotypes -> classified in 62 genera
- The most abundant genera:
 - *Streptococcus* (24%)
 - *Prevotella* (20%)
 - *Veillonella* (20%)

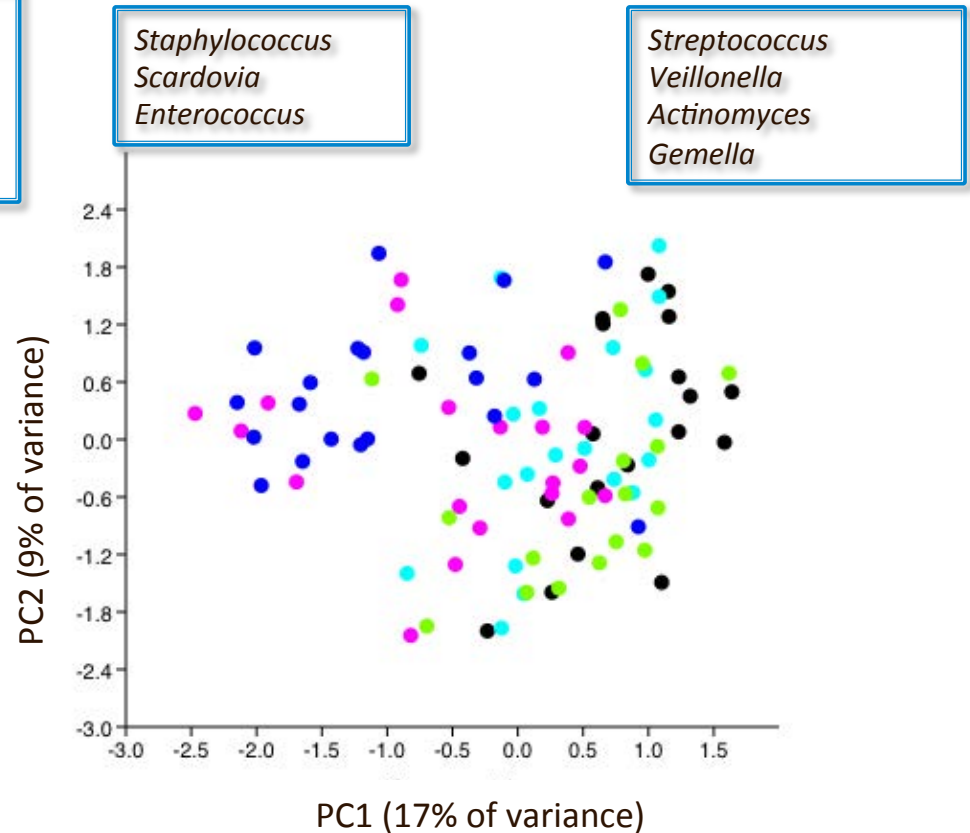


No ulcerative mucositis



PERMANOVA: $F=2.84$, $p=0.0001$

Ulcerative mucositis

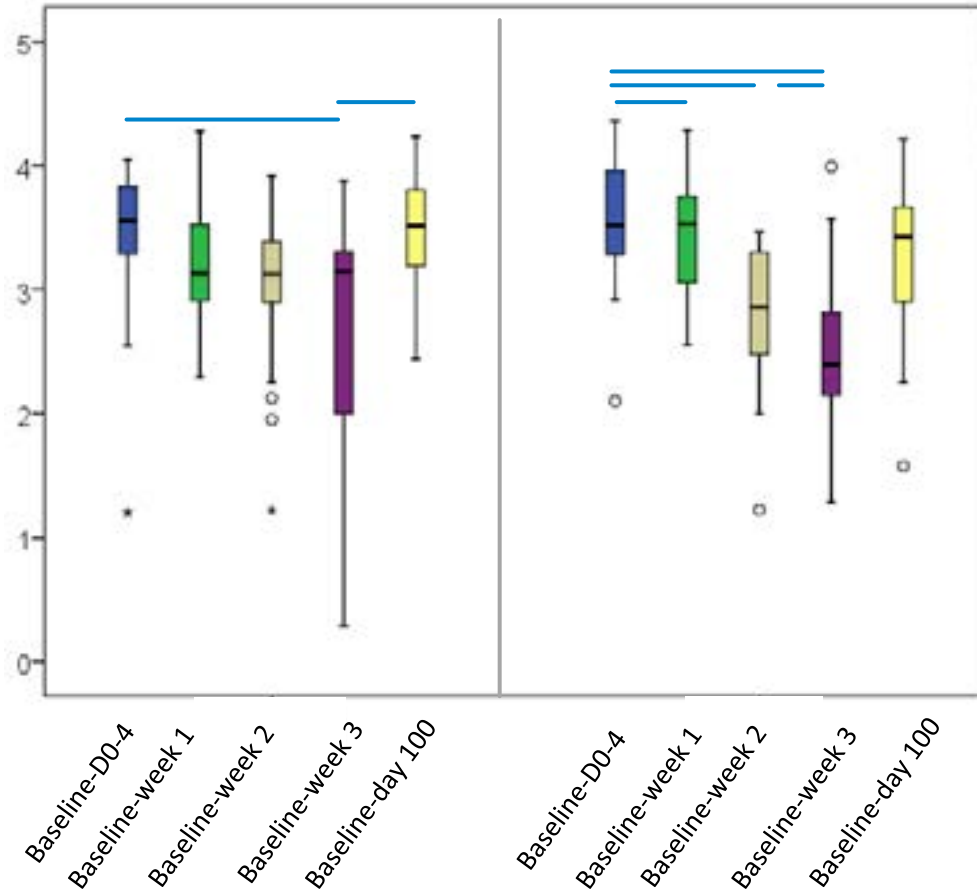


PERMANOVA: $F=2.92$, $p=0.0001$

PCA: Black – baseline, aqua – days 0-4, fuchsia – 1 week, blue – 2 weeks, green – 100 days

Shannon Diversity Index

No
ulcerative
mucositis



Ulcerative
mucositis

Lines connect statistically significant visit pairs (GLM RM test, $p < 0.001$)

Potential biomarkers for oral ulcerative mucositis

No ulcerative mucositis

- Streptococcus
- Actinomyces



Aerobes, oral flora
Early colonizers

Ulcerative mucositis

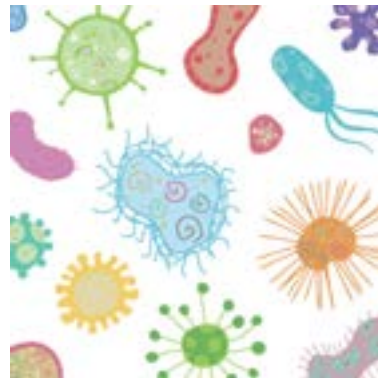
- Veillonella
- Enterococcus
- Streptococcus
- Staphylococcus
- Fusobacterium
- Prevotella

Anaerobes, skin flora
disbiosis

LEfSe: linear discriminant analysis effect size

Conclusion

- The oral microbiome shifted and diversity decreased after HSCT, independent of clinical manifestations of oral mucositis
- Shift and decrease in diversity is sooner and more severe in ulcerative mucositis patients
- Certain species present before HSCT were associated with development of oral ulcerative mucositis
- Future studies:
 - alloSCT
 - Fungi
 - Dental status and microbiome



Bray-Curtis similarity index

