

_{The Ohio State University} The oral microbiome in pediatric hematopoietic cell transplant recipients 🛸

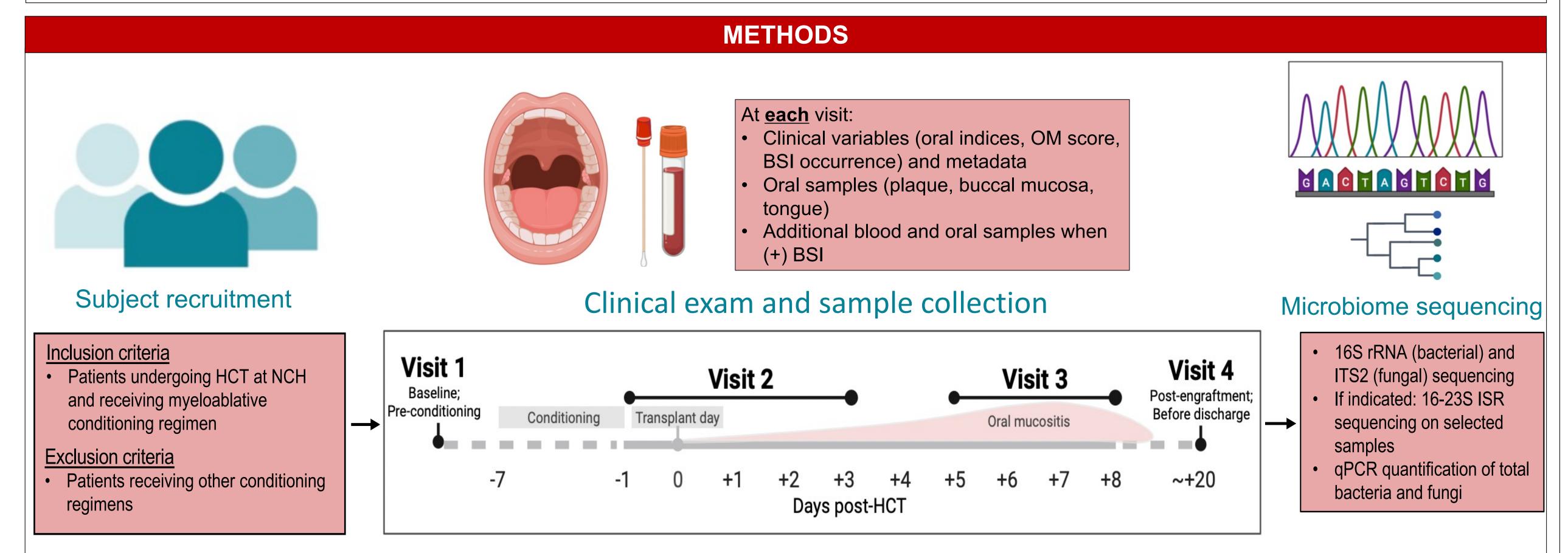
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When your child needs a hospital, everything matters.™

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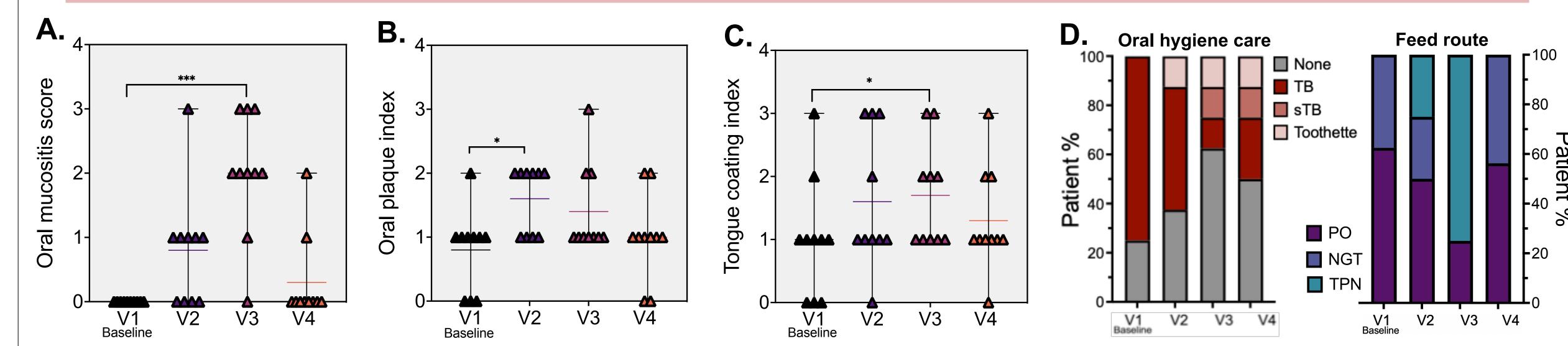
PURPOSE

Oral mucositis (OM) is a toxic side effect during hematopoietic cell transplant (HCT) and a risk factor for bloodstream infections (BSI) as the compromised mucosa becomes susceptible sites for bacterial translocation. Higher incidences of OM and BSI are observed with poor oral health and oral microbial dysbiosis is suggested to be associated with OM, but the specific role of the oral microbiome in OM and BSI pathogenesis is not fully understood. We aimed to characterize the oral microbiome in HCT recipients and investigate its role in the development and progression of OM and BSI.



RESULTS

Progression of oral mucositis and decrease in oral indices, oral care and PO intake observed post-HCT



A) Grading of oral mucositis by National Cancer Institute CTCAE: 1= asymptomatic or mild symptoms, no intervention, 2= moderate pain or ulcer that doesn't interfere with oral intake; modified diet indicated, 3= severe pain, interfering with oral intake. B) Oral plaque index: amount of tooth surface covered by debris/stain: 0 = none, $1 = \le 1/3$, 2 = > 1/3 to $\le 2/3$, 3 = > 2/3. **C)** Miyazaki tongue coating index: extent of dorsal tongue surface coating: 0= none, 1= <1/3, 2= <2/3, 3= >2/3. D) Oral hygiene care and feed route: TB: toothbrush + F toothpaste, sTB: toothbrush+ saline, Toothette with saline. PO: by mouth, NGT: Nasogastric tube. TPN: Total parenteral nutrition. Asterisk: statistically significant differences when compared to V1, baseline. * p < .05, *** $p \le .001$

FUTURE DIRECTIONS

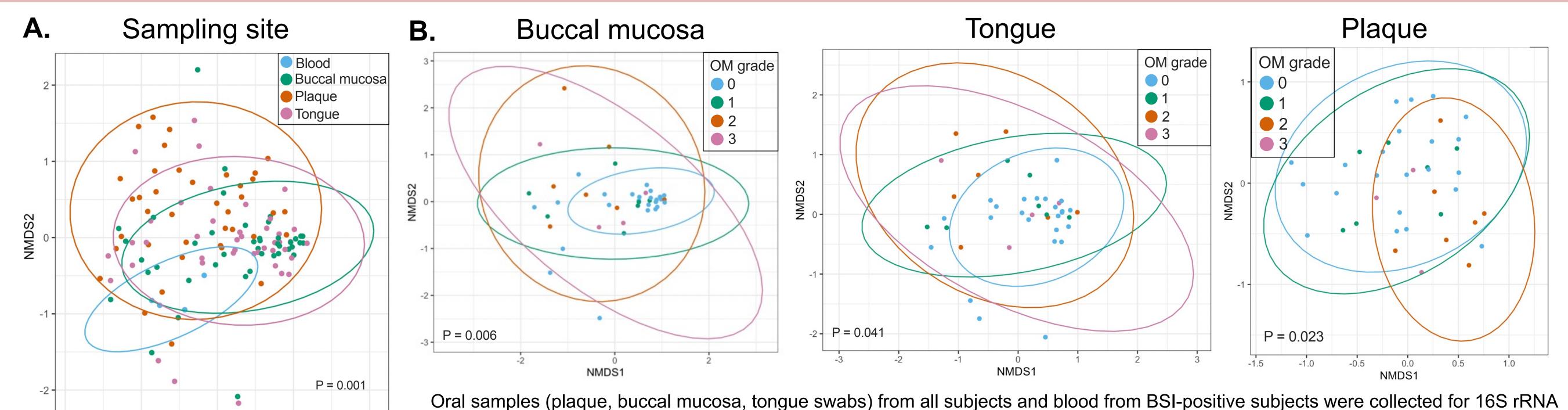
1) Expand our sample size to allow the global microbial changes to be elucidated at the species level for both bacteria and fungi, 2A) Comprehensively define the bloodstream microbial profile in children receiving HCT by longitudinally collecting blood samples from all subjects and comparing their bloodstream microbial profile when +/- BSI, 2B) Determine if the oral cavity (plaque, tongue, mucosa) is the likely source of BSI

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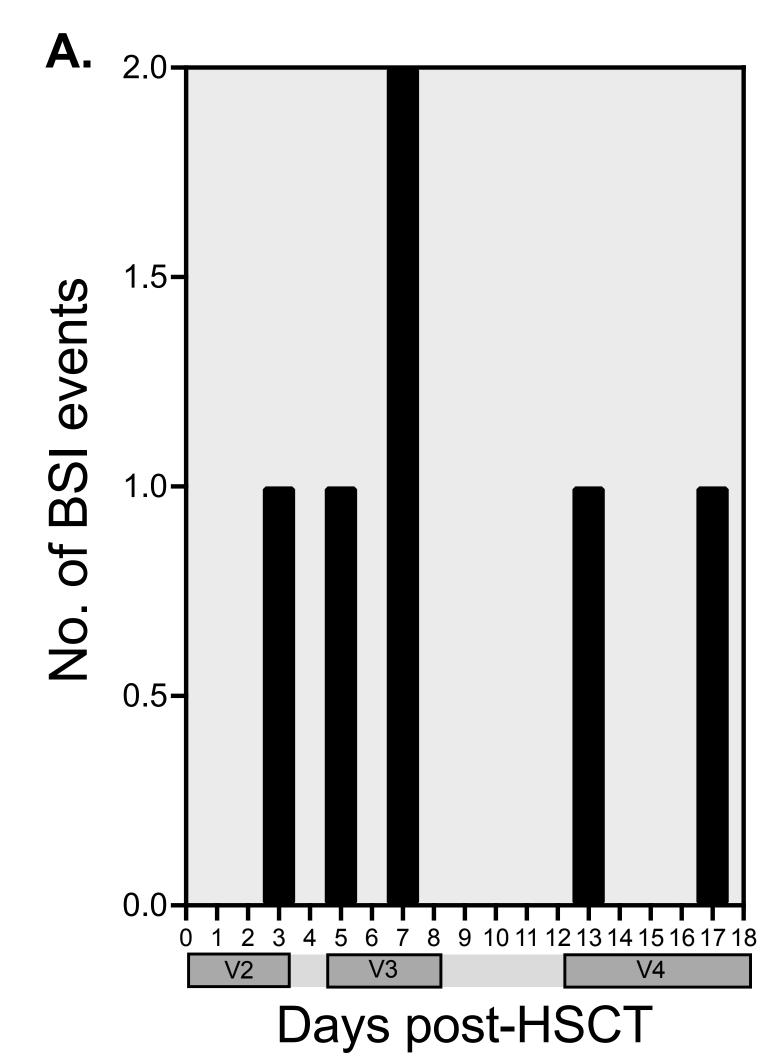
RESULTS

Site-specific microbial community changed based on oral mucositis score

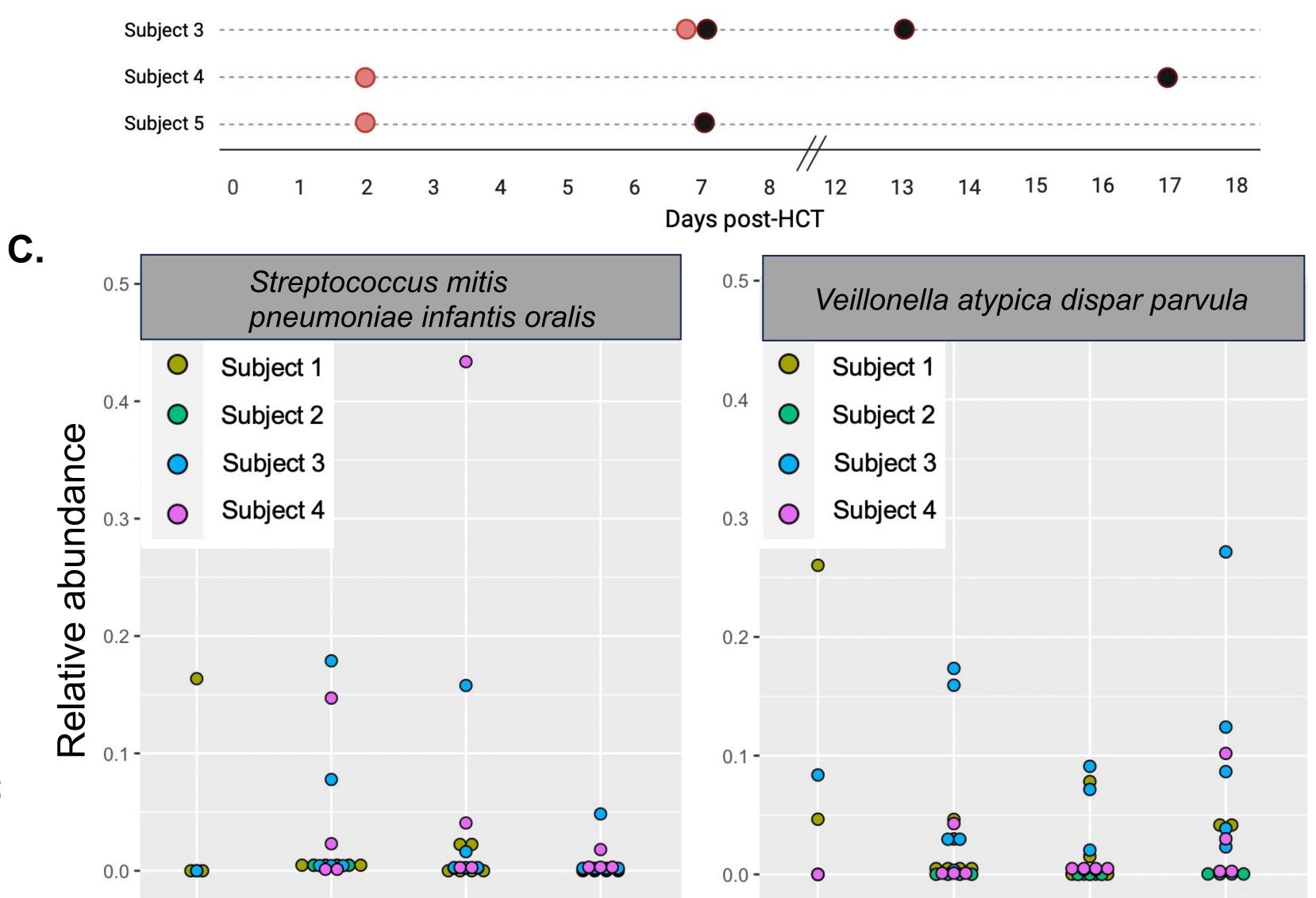


Microbial organisms potentially derived from the oral cavity identified in (+) BSI subjects

mucositis grade

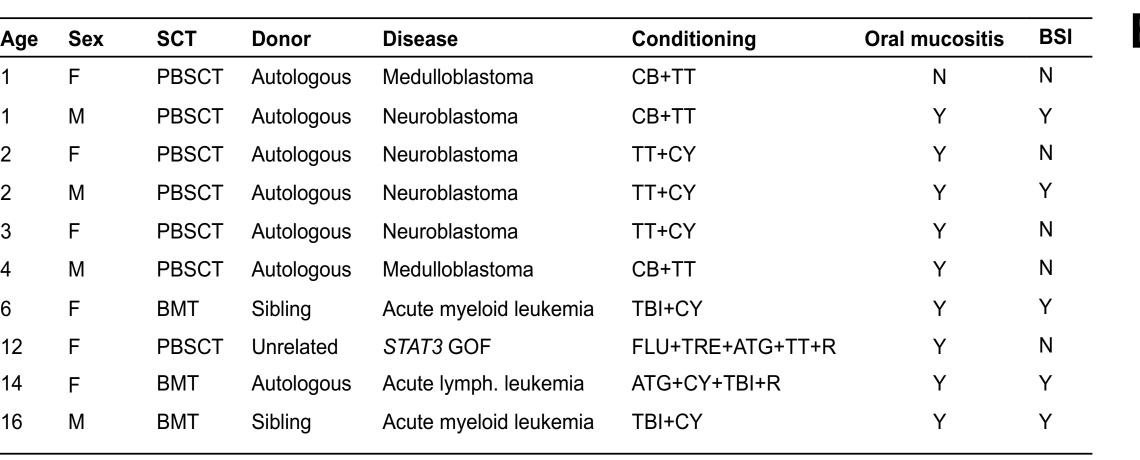


- A) Number of BSI events observed in our pilot study. V2: Day -1 to +3 post-HCT; V3: Day +5 to +8 post-HCT; V4: After engraftment/before discharge.
- B) Timeline displaying onset of OM and BSI episodes in select (+) BSI subjects.
- C) Blood microbial profile of select (+) BSI subjects. 16S rRNA sequencing was performed in blood specimens collected from (+) BSI subjects and their corresponding oral samples. For high-resolution analysis, the DADA2 algorithm was used to generate amplicon sequence variants (ASVs) that were taxonomically classified both by the SILVA database within DADA2 and by BLAST alignment to the OSU CORE database. Relative abundance of 16S ASVs of microbial species in blood and corresponding oral niches shown.
- **D)** Patient clinical data. **E)** Absolute neutrophil counts (ANC) of subjects over the course of HCT.



sequencing. Non-metric multidimensional scaling (NMDS) using Bray-Curtis dissimilarity index was used to compare beta-diversity and

PERMANOVA test was used to analyze differences in bacterial community composition among samples by (A) sampling site or (B) oral



CB, carboplatin; TT, thiotepa; CY, cytoxan; TBI, total body irradiation; FLU, fludarabine; TRE, treosulfan; ATG, antithymocyte globulin; R, rituximab.

BSI episode