**Intestinal enrichment of oral-typical bacteria in feces reflects depletion of gut commensals**

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**SUMMARY**

The association of gastrointestinal diseases with relative enrichment of oral bacteria in human feces can be explained by two alternate hypotheses: it may indicate an increased population density of ectopic oral bacteria in the gut (the expansion hypothesis) or a depleted gut commensal bacterial load (the marker hypothesis). Through mouse experiments and human microbiome data analysis, we found that the quantitative abundance of oral-typical bacteria in the intestine remains stable as opposed to the marked reduction in the gut bacterial load following antibiotic treatment, thus supporting the marker hypothesis. Our mathematical model indicates that the stable oral bacterial population is maintained by a balance between direct antibiotic inhibition and indirect ecological competitive release due to depleted gut commensals. Recognizing that the relative enrichment of oral bacteria does not reflect an ectopic bloom, but results from a depleted gut bacterial population, critically informs the interpretation of microbiome compositional data and interventions to restore healthy gut microbiomes.

**INTRODUCTION**

The healthy persons harbor distinct microbiome communities at different body sites (Costello et al., 2009; The Human Microbiome Project Consortium, 2012). The translocation of oral-associated bacteria to the lower gastrointestinal tract and their intestinal enrichment have been linked to a number of digestive system disorders such as inflammatory bowel disease (IBD) (Read et al., 2021) and colorectal cancer (CRC) (Komiya et al., 2019). Compared to the hematogenous route (oral-blood axis) (Abed et al., 2020), the enteral route (oral-gut axis) is a natural and more studied pathway of oral bacterial dissemination (Jin et al., 2022; Kitamoto et al., 2020). For an average person, ~1011 oral-resident bacterial cells are transported to stomach via saliva, food and liquid daily (Segata et al., 2012) but they rarely colonize the healthy gut. Gastric acids, alkaline biles and antimicrobial peptides kill many of those, and survivors face competition from gut-resident bacteria due to colonization resistance (Jin *et al.*, 2022). This is supported by DNA-based surveys that detect very low abundances of oral-resident bacterial DNAs in the feces of health individuals (typically <2%) (Rashidi et al., 2021; Schmidt et al., 2019).

Broad spectrum antibiotics such as ampicillin can weaken the oral-gut barrier by depleting gut anaerobes and promote colonization of translocated oral bacteria (Atarashi et al., 2017). Other than antibiotics, diets, aging, and gut inflammation may also disrupt gut colonization resistance (Kitamoto *et al.*, 2020). All these factors jointly contribute to the clinical associations between ectopic colonization of oral pathobionts and a variety of digestive diseases (e.g., Crohn’s disease (Gevers et al., 2014), ulcerative colitis (Schirmer et al., 2018), CRC (Kostic et al., 2013), liver cirrhosis (Qin et al., 2014)). However, nearly all those association studies were based on relative microbiome profiling and thus inconclusive regarding whether the relative enrichment of oral-typical bacteria reflects their active expansion and bloom in the gut. The technical limitation has hampered our ability to associate quantitative microbiome features with disease and led to artificial interpretations from relative microbiome analyses (e.g., trade-off between *Bacteroides* and *Prevotella*) (Vandeputte et al., 2017).

By definition, the relative enrichment of oral bacteria following perturbations can be explained by two alternative hypotheses (Fig. 1). The expansion hypothesis proposes that the active expansion of translocated oral bacteria in the gut outweighs the depletion of gut-resident bacteria in determining the relative enrichment. By contrast, the marker hypothesis states the opposite, i.e., the relative enrichment is an artifact caused by loss of gut commensals. The two hypotheses have distinct implications for human health and pathologies: While the expansion hypothesis indicates that the ingested oral bacteria can directly drive or exacerbate digestive diseases, the marker hypothesis indicates indirect effects of microbiome on disease onset and progression due to the loss of gut bacteria. Though largely ignored, bacterial load is itself an important variable in microbiome-disease associations and influences host physiology, metabolism, and immunity (Contijoch et al., 2019; Tang et al., 2019; Zarrinpar et al., 2018). In the following, we will distinguish the two hypotheses by quantifying the load of oral-typical bacteria in the gut microbiome of mice and humans.

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**Fig. 1| Expansion versus marker hypotheses to explain the relative enrichment of oral bacteria in human microbiome.** The density of oral-typical bacteria colonizing the human intestine is synergistically determined by a basal transmission influx from the oral cavity, biomass loss due to natural death and fecal excretion, and ecological interactions between bacteria of oral and gut origins. Perturbations such as antibiotics may substantially increase the relative abundance of oral-typical bacteria in the human gut (fecal) microbiome by two alternative mechanisms. The expansion hypothesis proposes that the relative enrichment measures its absolute abundance (i.e., active expansion of the oral populations), while the marker hypothesis views it as an artifact caused by reduction in the gut bacterial density.

**RESULTS**

**Antibiotic-treated mouse gut microbiome supports the marker hypothesis**

Detection of bacterial translocation events requires identification of sequence-level features (e.g., marker genes, single nucleotide polymorphisms) in samples collected from multiple body sites of a host (Coker et al., 2018; Schmidt *et al.*, 2019). However, paired oral and gut samples in mice are extremely rare in the literature (Greenberg et al., 2022). To detect translocation from gut microbiome alone, we compiled a reference collection of marker genes that represent bacteria typically inhabiting mouse oral cavity. The 16S rRNA sequences in the Mouse Oral Microbiome Database (MOMD) (Joseph et al., 2021) were used as the starting point for gathering oral-typical sequences (Fig. S1A). We filtered MOMD by removing gut-colonizing sequences closely matching to those in two large-scale mouse gut bacterial collections (Lagkouvardos et al., 2016; Liu et al., 2020) and added oral-typical sequences absent in the MOMD from a small but rare set (n=11) of paired oral-gut samples from pregnant mice (Theis et al., 2020); see STAR Methods. The resulted collection has 149 full length 16S rRNA sequences (Table S1) from diverse genera (Fig. S1B). Given the collection, we can classify whether an amplicon sequence variant (ASV) is oral-typical or -atypical by exactly matching the sequences in the collection. On average, 4.5% ASVs in the distal gut microbiome of the 11 pregnant mice were found to be oral-typical. In 10 out of the 11 mice, >85% of the total fractions of the oral-typical ASVs in the gut were contributed by those present in the oral cavity of the same mice (Fig. S1C).

Having established the reference marker gene collection, we sought to test the expansion vs. the marker hypothesis in mice. We first reanalyzed a public study (Reese et al., 2018) that treated mice with an antibiotic cocktail (Ampicillin-Vancomycin-Neomycin-Metronidazole) for 5 days (Fig. 2A). The oral populations, mainly consisting of three ASVs from the genera *Lactobacillus*, *Proteus* and *Escherichia-Shigella*, are enriched in relative abundance after two days’ exposure (Fig. 2B). However, we did not observe an active expansion of the potentially translocated oral populations compared to the control group by tracking the longitudinal changes of the mean oral bacterial loads (total bacterial loads multiplied by fractions of oral-typical ASVs) (Fig. 2C, left). By contrast, the antibiotic cocktail reduced the averaged gut-resident (i.e., oral-atypical) bacterial density by more than 2 orders of magnitudes (Fig. 2C, right). The differential responses of the oral vs. gut populations clearly support the marker hypothesis: the high relative abundances of oral-typical bacteria in feces simply indicate the depletion of gut commensals. Interestingly, the oral bacterial fractions are linearly correlated (r = -0.52, P = 3.5e-17) with the total bacterial loads on the log scale (Fig. 2D). It is likely that the dominant ASVs (Fig. S2A) in the outlier samples (those with low total fractions of oral-typical ASVs and low total bacterial loads; see the red box in Fig. S2) were oral-derived but undetected by filtered-MOMD. Since these outliers were collected between day 1-6 (Fig. S2B), the underestimated total fractions of oral-typical bacteria may explain the abrupt and unexpected falls of the total oral bacterial fractions (Fig. 2B) and loads (Fig. 2C) after day 2 during the antibiotic exposure.

The same conclusions were drawn by reanalyzing another public data from bone-marrow-transplanted mice that received different mono-antibiotic prophylaxis (Staffas et al., 2018). Ampicillin but not Streptomycin, Aztreonam, or Vancomycin consistently depleted gut bacterial biomass (Fig. S3A). The oral bacterial loads were stable throughout the experiments for all four antibiotics including ampicillin (Fig. S3B). A log-log linear relationship (r = -0.75, P = 5.5e-11) between oral bacterial fractions and total bacterial loads was shown (Fig. S3C).

The reanalysis of the two public datasets were limited by the lack of paired oral-gut samples, which prevented us from showing translocation of bacterial DNAs from the oral cavity to the gut under antibiotic treatment. We therefore conducted a simple yet dedicated mouse experiment where paired oral-gut samples were collected prior to antibiotic treatment (Fig. 2E). The premise of the experiment is that, if antibiotics facilitate massive transmission of oral bacteria to the gut, we expect to see higher similarity of the post-antibiotic gut microbiome to the pre-antibiotic oral microbiome than to the pre-antibiotic fecal microbiome. Indeed, the fecal samples at day 8 shared more identical ASVs (Hamming distance) with the oral samples at day 0 and were also compositionally similar (Bray-Curtis distance) in 2 out of the 3 mice (Fig. 3G). Most importantly, 10%-20% of ASVs (the majority from 6 members; Fig. S4A) found in the post-antibiotic feces were only detected in the pre-antibiotic oral microbiome (Fig. 2H), suggesting antibiotic-induced oral-gut transmission of those ASVs. Despite the small number of mice, the oral bacterial loads mildly decreased (Fig. S4B) but the total bacterial loads reduced by ~4 orders of magnitudes (Fig. S4C), again supporting the marker hypothesis.

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**Fig. 2| Oral-gut bacterial translocation in antibiotic-treated mice.** (**A-D**) Reanalysis of a public study (Reese *et al.*, 2018). (**A**) Experimental design. Mice were treated with either water (the control group; n=11) or an antibiotic cocktail of ampicillin-vancomycin-neomycin-metronidazole (AVNM) (the antibiotic group; n=10) for five days. (**B**) Compositional dynamics of oral bacterial ASVs during and after antibiotic cocktail treatment. (**C**) Total loads of ASVs classified as of oral (left) and gut (right) origin averaged across mice in the control and antibiotic groups. Lines and dots: mean; shading: 95% confidence interval (CI). (**D**) Linear relationship between total bacterial loads and oral bacterial fractions in the log-log space. Line: linear regression; shading: 95% CI. (**E-I**) New mouse experiments in this study. (**E**) Experimental design. Three mice (M1, M2, M3) were treated with ampicillin-vancomycin-neomycin (AVN) for a week. Paired oral (oral\_d0) and fecal (fecal\_d0) samples were taken at day 0 prior to antibiotic cocktail treatment and post-antibiotic fecal samples (fecal\_d8) were collected at day 8. (**F**) Gut microbiome compositions of all pre- and post-antibiotic samples. (**G**) The Hamming and Bray-Curtis distances between the pre- and post-antibiotic microbiome compositions. (**H**) Sources of ASVs in the post-antibiotic gut microbiomes and their per-source total fractions.

**Oral-typical bacterial DNAs in humans**

To identify 16S rRNA genes for oral-typical bacteria colonizing humans, we leveraged the Human Microbiome Project (HMP) that sequenced paired oral-gut microbiome samples from 237 healthy volunteers (The Human Microbiome Project Consortium, 2012). Distinct bacterial communities were found inhabiting the two body sites (Fig. 3A), which provides the pragmatic basis for distinguishing oral-typical from oral-atypical ASVs. We adopted a similar criteria used before (Thomas et al., 2019) for ASV filtering: the mean relative abundance and prevalence of oral-typical ASVs must be greater than 0.01% and 5% respectively among all oral samples, and no greater than the same cutoffs among all fecal samples (Fig. 2B,C). The filtering step left 178 ASVs (Table S2) that belong to a variety of genera including *Prevotella*, *Streptococcus*, *Leptotrichia*, and *Haemophilus* (Fig. 2D). Using those ASVs as references, we found that 219 out of 280 HMP stool samples have undetectable oral-typical ASVs. Among the remaining 61 samples, the identified oral-typical ASVs in 53 samples were all present in at least one paired oral cavity sample of the same persons (Fig. 2E). The average total fractions of oral-typical bacteria in the HMP stool samples is as low as 0.05%, which are consistent with previous literature findings (Rashidi *et al.*, 2021; Schmidt *et al.*, 2019).

We next show that the 178 oral-typical ASVs identified from healthy people in the HMP study can be generalized to patients who might have different oral sequence signatures. To this end, we reanalyzed paired oral-gut microbiome samples from patients with inflammatory bowel disease (IBD) and their own healthy controls. The mean total fractions of oral-typical ASVs in the gut of the non-IBD healthy controls remains low at 1.1%. As expected (Read *et al.*, 2021), the total oral bacterial fractions in the patients with Crohn’s disease (CD) and ulcerative colitis (UC) increased ~4 folds on average up to 4.2% and 4.3% respectively. Among 81 out of 101 samples, the proportions of oral-typical ASVs in the feces that were also present in the paired oral samples were no less than 85%. Using the same IBD cohort, we demonstrated that the estimated total fractions of oral-typical bacteria in the feces are robust against the cutoff thresholds used to filter HMP (Fig. S5). These computational tests suggest that the oral-typical ASVs we compiled from the HMP study can robustly estimate the total fractions of oral-typical bacteria in other healthy or patient cohorts.

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**Figure 3. Identification of bacterial DNAs typically found in the human oral cavity but not the intestine.** (**A**) An overview of the 4,354 microbiome samples from The Human Microbiome Project (HMP). T-distributed stochastic neighbor embedding (tSNE) (Van der Maaten and Hinton, 2008) collapses all samples (dots) into distinct clusters based on their compositions. (**B, C**) The average relative abundance (B) and prevalence (C) of ASVs (dots) among all HMP oral cavity samples (x axis) and the stool samples (y axis). 178 ASVs were identified as oral-typical and highlighted in orange (see the main text or STAR methods for the filtering criteria). (**D**) Genus-level distribution of the 178 oral-typical ASVs. (**E, F**) The total fractions of oral-typical ASVs in the human fecal samples (circles) and their proportions present in the paired oral samples. (E) Healthy individuals in HMP. (F) Patients with inflammatory bowel disease and their own healthy controls (n=101) (F). HC: healthy control; CD: Crohn’s disease; UC: ulcerative colitis. Data sources: panel A-E (The Human Microbiome Project Consortium, 2012); panel F (Imai et al., 2021).

**Validation of maker hypothesis in patients receiving antibiotic prophylaxis**

Allogeneic hematopoietic cell transplantation (allo-HCT) is the only potentially curative therapy for patients with malignant hematopoietic disorders. The initial conditioning regimen (e.g., chemo- or radio-therapy) depletes malignant and healthy hematopoietic cells, weakens the immune system, and receive antimicrobial prophylaxis to avoid infections. The antibiotic adminsitraiton were found to cause intestinal epithelial tissue damage and marked loss of bacterial diversity and composititional. In the allo-HCT recipients from MSKCC, the remaining 45% of samples were dominated by ectopic bacteria, including 18% of samples that were highly abundant in oral bacterial genera such as *Streptococcus* and *Actinomyces* (**Fig. 3A**). By co-occurrence analysis, we found 32 distinct combinations of oral bacterial ASVs that co-occurred in feces more than expected by chance (**Table S3**), supporting that the fecal enrichment of oral bacteria in these allo-HCT patients is driven by their collective transmission from oral to gut.

The relative abundance of oral bacteria in these fecal samples was bimodally distributed (**Fig. 3B**), which is consistent with our model prediction (**Fig. 1C**). The distribution was heavily skewed toward 0, but 383 samples from 182 unique patients were composed of 95% oral bacteria. Even single bacterial ASVs (**Fig. S2C**) could dominate these samples by ≥30%, with dominations of *Streptococcus* (ASV8 and ASV16) among the most frequent domination states. Shotgun-sequenced samples showed that the two ASVs contained a variety of *Streptococcus* species, mostly *S. thermophilus*. Some of these *Streptococci* could be alive and replicating in the fecal sample, as evidenced by peak-to-trough ratio (i.e., the ratio of reads mapped to oriC to terminus) calculated by iRep (Brown et al., 2016) analysis (**Table S2**).

To validate the proposed quantitative relationship (**Fig. 1D**), we measured the total bacterial density in the feces (16S rRNA copies per gram of feces) by qPCR (Liao et al., 2021). The timing of antibacterial prophylaxis (**Fig. 3C**, lower panel) corresponded to the period in which gut-resident bacteria declined in both relative (upper panel) and absolute (middle panel) abundances. Consistent with our model prediction, the mean absolute abundance of oral bacteria (both habitat 1 and 2) remained constant despite antibiotic exposure, explaining their increased relative abundances (**Fig. 3C**). As a result, the proportion of bacteria from oral habitats 1 and 2 had the strongest negative correlations with the total bacterial density (Slope=-0.34 and -0.39, *P*<0.001) among all five habitats (**Fig. S3A-E**). When combined, the two oral populations showed an even stronger association (Slope=-0.49, *P*<0.001; **Fig. 3D**, bottom row). We determined 3.4% as the threshold percentage of oral bacteria in feces above which the linear fitting is nearly optimal (middle row) and the best-fit slope matches the predicted value -1 (top row). This threshold delineates the dynamic range of our model: the negative association becomes less apparent or even obscured by noise at oral bacteria fraction below this threshold.

**Theoretical population ecology model**

The human gut lumen is an ecosystem with rhythmic food intake and fecal excretion (Goyal et al., 2018). Assuming the transient ecological dynamics induced by these cyclic events have short time scales, we approximated its long-term dynamics and quasi-steady state by a continuous, coarse-grained model of oral-derived (]) and gut-resident (]) bacteria (**Fig. 1A**)

Eq. (1)

Eq. (2)

Here is the oral-gut transmission rate due to saliva, food, and liquid intake, is the fecal excretion rate constant, and are the host carrying capacities, and and are the maximum growth rates as a proxy of population fitness. Our model focuses on antibiotic perturbations—the major disruptor of gut microbiome (Ramirez et al., 2020)—and represents the impacts of antibiotics on the fitness of both types of bacteria.

The model makes two predictions on the fraction of oral bacteria in feces () at steady state. First, its value changes abruptly from low (nearly absent) to high (very abundant) when the perturbation exceeds a threshold (**Fig. 1B**, red line). The ultrasensitive response to the perturbation strength suggests that a unimodal distribution of the perturbation effects can generate a bimodal distribution in the relative oral bacteria abundance (**Fig. 1C**). The mathematical result indicates that humans with perturbed gut bacteria may constitute two subpopulations with very low or very high relative abundance of oral bacteria in their feces. We find evidence for this model prediction in the fecal microbiota of healthy Western adults, which show bimodal distributions of *Prevotella* species commonly found in the oral cavity (Lahti et al., 2014; Tett et al., 2021). We further derived that is inversely proportional to the total bacterial density () in the gut lumen regardless of antibiotic-induced perturbations

Eq. (3)

This implies a negative linear relationship in the log-log space between the fraction of oral bacteria and the total bacterial density in the gut, irrespective of the perturbations (**Fig. 1D**).

**Quantifying oral bacteria in feces**

Quantifying the fraction of oral bacteria in feces is a microbial source tracking problem (Knights et al., 2011; Shenhav et al., 2019). Paired oral and gut microbiome samples are generally unavailable for most literature studies. To circumvent this limitation, we developed a new computational approach that mathematically models any bacterial population—including those in the fecal and oral samples—as a mixture of stereotypical bacterial communities inhabiting different body sites of a typical average person. We identified five habitats from Human Microbiome Project (HMP) (Human Microbiome Project Consortium, 2012): All 4,587 HMP samples collected from five major body sites (GI tract, oral cavity, nasal cavity, skin, and urogenital tract) of 235 healthy individuals clustered into five habitats of similar compositions that match roughly, though not exactly, their collection sites (**Fig. 2A**). The nasal cavity and skin clustered together, and the oral cavity formed two clusters, each corresponding to different oral cavity subsites (Lamont et al., 2018; Segata et al., 2012).

We extracted the typical composition of each habitat from the HMP samples using non-negative matrix factorization (Lee and Seung, 1999) (**Fig. 2B**, upper panel; **Fig. S1A,B**). This revealed that each habitat had one or a few dominant bacterial genera (**Fig. 2C**). For instance, *Streptococcus* (54%) and *Prevotella* (20%) were the most abundant genera in the oral cavity habitat 1 (e.g., saliva) and 2 (supra-/sub-gingival plaques) respectively. The unmixing step also quantified the proportions of oral bacteria in HMP samples. We compared our approach to two alternative methods based on Random Forest classifier (RFC) (Ho, 1995) and SourceTracker 2 (Knights et al., 2011), both showing Pearson’s correlation coefficients > 0.6 (**Fig. S1C**). The predicted fractions confirmed the general notion that oral bacteria are rarely abundant in the feces of healthy people (Costello et al., 2009; Human Microbiome Project Consortium, 2012) (**Fig. 2D**). Although the majority of HMP samples are composed of bacteria typically inhabiting their collection body sites, 37 (11.5%) fecal samples have 10 % oral genera (**Fig. 2D**, violet box) such as *Veillonella* (**Fig. 2E**, upper panel) and *Prevotella* (**Fig. 2E**, lower panel). This finding supports the purpose of unmixing: even healthy people can have significant proportions of oral bacteria in their feces.

**Validation of model predictions**

The typical composition of the five habitats allowed us to estimate the proportion of oral bacteria in any fecal microbiome sample—without the need of paired oral sample—by using a simple constrained regression (**Fig. 2B**, lower panel). We applied this method to a large-scale dataset containing >10,000 fecal microbiome samples from >1,000 patients (Liao et al., 2021). All patients in this dataset (MSK cohort) had hematological diseases including leukemias, lymphomas, and myeloma and underwent allo-HCT at Memorial Sloan-Kettering Cancer Center. We validated the predicted oral bacterial fractions using RFC (**Fig. S2A**).

Compared to the AVNM-treated mice in the public study (Fig. 2D), the total bacterial loads in our AVN-treated mice are 2 orders of magnitude higher prior to antibiotic treatment but an order of magnitude lower after antibiotics, suggesting higher potency against gut anaerobes. Since our experiment used smaller doses, this might be explained by longer antibiotic treatment (7 days vs. 5 days).

Interestingly, the total bacterial loads and the oral bacterial fractions in the feces are negatively associated (Pearson’s r = -0.52, P=) on the log scale and follow a linear relationship with slope -0.70 (Fig. 2D). The outliers (samples with low oral bacterial fractions and low total bacterial loads; enclosed by the red box in Fig. S2) were all collected between day 1-6, which correspond to the reduction in the oral bacterial abundance during the same time period (shown in Fig. 2B,C). We suspect that these outliers were artificial due to the unrecognized ASVs of orally translocated bacteria but not covered by filtered-MOMD.

**Associations with stool consistency, antibiotic exposure and allo-HCT patient outcomes**

Stool consistency was looser in allo-HCT patients with higher relative abundance of oral bacteria (**Fig. 3E**). We further identified two antibacterial antibiotics that were significantly associated with an increased fraction of oral bacteria in fecal samples above 30% (Taur et al., 2012): oral vancomycin and piperacillin/tazobactam (**Fig. 3F**). Intravenous vancomycin showed no association, likely because it fails to reach the GI tract. Piperacillin/tazobactam, a combination of beta-lactam and beta-lactamase inhibitor that can reach the GI tract and have a broad spectrum against many gut bacteria (Morjaria et al., 2019), had the strongest association. This association was not only apparent in adults receiving allo-HCT but also seen in an independent cohort of pediatric patients (Bekker et al., 2019) (**Fig. S4**).

Regarding hematopoietic cell transplant outcomes, the allo-HCT patients with high oral bacteria during the pre-engraftment period had lower overall survival compared to those whose microbiome was mainly composed of gut-resident bacteria (**Fig. 3G**). Although the mechanism underlying this association is unclear, existing evidence suggest against bloodstream infections (BSIs) by ectopic oral bacteria: Oral-typical bacteria only caused 5 infection cases (all *Streptococcus spp.*) in 5 patients during transplantation and none were preceded by intestinal *Streptococcus* domination (**Table S3**). The loss of gut bacteria may actually preclude microbiota dominations by true pathogens—such as *Enterococcus*—and reduce the risk for the development of BSI caused by gut-to-blood transmission (Tamburini et al., 2018) (**Fig. 3H**). Unlike oral bacteria domination states, *Enterococcus* dominations represent true blooms since a high relative abundance positively correlates with a high total bacterial density (**Fig. S3F**).

Finally, the fecal samples with higher proportion of oral bacteria tended to have higher fungal densities (**Fig. 3I**, **S3G**), suggesting that fungi could expand to fill the niche left open by the loss of gut bacteria. The gut colonization and overgrowth of fungal pathogens such as *Candida parapsilosis* typically occurs when gut bacteria are depleted, consistent with the finding that gut-resident bacteria can protect against fungal blooms and infection (Rolling et al., 2021; Zhai et al., 2020).

**Generalization to other patient cohorts**

Supporting the *marker* hypothesis, another key characteristic of IBD besides the relative enrichment of oral bacteria is the reduced density of the gut bacterial population. This observation suggests that the apparent rise in relative abundance of oral bacteria in human feces may simply indicate a loss of the gut bacterial density.

We next validated the quantitative relationship between oral bacteria in feces and gut bacterial density for three GI diseases (Crohn’s disease (CD), Ulcerative colitis (UC), and *Clostridioides difficile* infection (CDI)) using the Mount Sinai cohort (Contijoch et al., 2019) and the LUMC cohort (Bekker et al., 2019) which had measurements of microbiome density. Previous studies reported, separately, relative expansion of oral bacteria in the gut microbiome and lower microbiome density in both CD and UC patients (Contijoch et al., 2019; Read et al., 2021; Vandeputte et al., 2017). Our study links the two signatures by showing a negative interdependence between each other (slope=-0.26, *P*<0.001 for the Mount Sinai cohort; slope=-0.25, *P*=0.04 for the LUMC cohort) using data with oral bacteria 3.4% (**Fig. 4A**,**B**). Oral bacteria from habitat 1 but not habitat 2 significantly contributed to the correlation (**Fig. S5**). Notably, the negative association remained significant (slope=-0.22, *P*=0.018) after excluding patients with prior antibiotics or an unclear antibiotic history in the Mount Sinai cohort (**Fig. S6A**), indicating the relationship is independent of antibiotic exposure.

We also assessed the generality of the associations of oral bacterial fraction in feces with disease status, antibiotic exposure, and gut fungal growth in patients with the three GI diseases. Re-analyzing multiple case-control cohort studies confirmed known associations between the fecal proportion of oral cavity bacteria and disease status, including CD (*P*=0.029) and UC (*P*=0.037) patients in the PRISM, LifeLines DEEP and NLIBD cohorts (Franzosa et al., 2019) (**Fig. 4C**), CDI patients in the UMH cohort (Schubert et al., 2014) (*P*<0.001; **Fig. 4D**) and pediatric CD patients in the RISK cohort (Gevers et al., 2014) (*P*<0.045; **Fig. S7A**). Notably, these associations were much stronger for bacteria from oral cavity habitat 1 than habitat 2 (**Fig. S8**). More interestingly, all associations for subsets of (pediatric) IBD patients who have not previously received antibiotics became insignificant (**Fig. S6B**), suggesting that the relative enrichment of oral bacteria in feces is not a signature of IBD but, instead, reflects collateral damage of antibiotic treatment. Finally, the percentage of oral bacteria increased with disease severity in pediatric UC patients from the PROTECT cohort (Schirmer et al., 2018) (*P*<0.001; **Fig. 4E**). Although similar associations with disease severity were not found in the pediatric CD patients enrolled in the UPenn cohort (**Fig. S7B**), those patients with enriched oral bacteria had a significantly higher percentage of fungal DNA in stool samples (**Fig. 4F**).

**DISCUSSION**

Most of the quantitative human gut microbiome studies to date (Contijoch *et al.*, 2019; Jian et al., 2020; Rao et al., 2021; Schluter et al., 2020; Vandeputte *et al.*, 2017; Vieira-Silva et al., 2019) have focused on amplicon-based profiling in the absence of paired oral samples.

A general tenet of theoretical ecology holds that population density impacts ecosystem function as much as the population composition. Yet almost all studies of human gut microbiome identify the associations of ectopic oral bacteria in the gut with specific diseases based on bacterial compositional changes (Kitamoto et al., 2020a; Read et al., 2021; Schmidt et al., 2019) and neglect variations in population density (Rao et al., 2021; Vandeputte et al., 2017). For example, >10 different oral bacterial species (e.g., *Streptococcus spp.*, *Veillonella parvula*, *Fusobacterium nucleatum*) were reportedly enriched in the intestine of IBD patients by 12 studies, where 10 drew conclusions based on bacterial relative abundances estimated from 16S amplicon sequencing (Read et al., 2021). Mouse experiments show the possibility that the enriched oral bacteria in feces may be oral pathobionts (Atarashi et al., 2017; Kitamoto et al., 2020b), the driver hypothesis, but this remains to be demonstrated in humans. Here we favor an alternative interpretation, the marker hypothesis: oral bacteria in feces neither correspond to absolute expansions of oral pathogens in the gut nor do they reflect species- or disease-specific biological differences. Rather, they simply indicate a shared decline of gut bacterial density (Duvallet et al., 2017).

**Figure 1.** **Ecological modeling links relative abundance of oral bacteria to total bacterial density in fecal samples.** (**A**)The marker hypothesis and its ecological model. The human gut lumen has a constant inflow of oral bacteria (at rate ) and a first-order outflow of bacteria of both oral and gut origins (at rate constant ). Perturbations such as antibiotics, which impact the fitness of bacteria in the gut, can reduce total bacterial density and relatively increase the abundance of oral bacteria detected in human feces. (**B**) Predicted response of the fecal proportion of oral bacteria to the perturbation level that impacts bacterial fitness. The compositional switch is more sensitive when is lower. (**C**) Bimodal distribution of the relative abundance of oral bacteria in feces results from its ultrasensitive response to a unimodal distribution of the perturbed fitness (). P.d.f.: probability density function. (**D**) Predicted linear relationship in log-log space between relative abundance of oral bacteria and total bacterial density in feces.

**Figure 3. Oral bacteria in feces of MSK allo-HCT patients are associated with bacterial density, stool consistency, antibiotic use, and transplant outcomes.** (**A**)Relative abundances of bacteria represented by their habitat origins (first row) and taxonomy (second row). Each thin column is a sample and all samples are clustered by their most abundant sources of origin (labeled above each cluster). (**B**) Bimodal distribution of oral bacteria in feces.(**C**) Dynamics of relative or absolute abundances of bacterial populations from the gastrointestinal tract and the two oral cavity habitats. (**D**) Negative relationship between fraction of oral bacteria in feces and total bacterial density. Red and blue lines (associated shading area: 95% confidence interval) in the scatter plot represent the best linear fits using data within the dynamic range (oral bacteria 3.4%, orange shading) and the entire range of data respectively. R2 and the fitted slopes were determined stepwisely by varying the range of data included in the linear regression. (**E**) Fraction of oral bacteria in feces stratified by stool consistency. (**F**)Hazard ratio and 95% confidence intervals of antibacterial antibiotic predictors for gut microbiome domination by oral bacteria (30%). (**G**)Overall survival curves of allo-HCT patients stratified by the dominant bacterial sources in their gut microbiome pre-(bone marrow) engraftment. The two oral cavity habitats are combined. *P*-value: Wald test. (**H**)Hazard ratio and 95% confidence interval of oral bacteria domination (30%) as a predictor for *Enterococcus* bloodstream infection. (**I**)Fraction of oral bacteria in feces stratified by fungal cultivability. cfu: colony-forming unit. In panels (E) and (I), the numbers represent the percentages of data above the thresholds indicated by dashed lines. \*\*\**P*<0.001; Kruskal-Wallis test. ns, not significant.

**Figure 4. Oral bacteria in feces indicates gut microbiome density, disease status and severity, and intestinal fungal growth in patients with gastrointestinal diseases.** (**A**,**B**) Quantitative relationship between proportion of oral bacteria and microbiome density (as a proxy of bacterial density) in the Mount Sinai cohort (A) and the LUMC cohort (B). Red and blue lines and associated shading areas represent best linear fits and 95% confidence intervals using data within the gray shaded area (oral bacteria 3.4%) and the entire range respectively. Abbreviations: healthy control (HC); Crohn’s disease (CD); ulcerative colitis (UC); *Clostridioides difficile* infection (CDI); recurrent *Clostridioides difficile* infection (rCDI); ileal pouch-anal anastomosis (IPAA); fecal microbiome transplantation (FMT); primary sclerosing cholangitis (PSC). (**C**-**F**) Fractions of oral bacteria in feces are associated with disease status (C,D), severity (E) and fungal DNA fraction (F). Each dot represents a sample. Median and interquartile range are indicated by colored circles and bars respectively. The numbers above dashed lines indicate the percentage of samples with 3.4% oral bacteria. Data sources: CD and UC (the PRISM, LifeLinesDEEP and NLIBD cohorts), CDI (the UMH cohort), pediatric UC (the PROTECT cohort), and pediatric CD (the UPenn cohort). \*\*\**P*<0.001; \**P*<0.05; Kruskal-Wallis test.

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**AUTHOR CONTRIBUTIONS**

Conceptualization, C.L., T.R. and J.B.X; Public microbiome dataset analysis, C.L; Methodology, C.L.; Investigation, C.L. and T.R; Writing – Original Draft, C.L., T.R.; Writing – Review and Editing, T.M.H., J.B.X., J.U.P., B.Z., and M.R.M.v.d.B; Supervision, J.B.X. and T.M.H.

**DECLARATION OF INTERESTS**

J.U.P. reports research funding, intellectual property fees and travel reimbursement from Seres Therapeutics and consulting fees from DaVolterra, CSL Behring and from Maat Pharma. He has filed intellectual property applications related to the microbiome (reference nos. 62/843,849, 62/977,908 and 15/756,845). M.R.M.v.d.B. has received research support from Seres Therapeutics; he has consulted, received honorarium from or participated in advisory boards for Seres Therapeutics, WindMIL Therapeutics, Rheos, Frazier Healthcare Partners, Nektar Therapeutics, Notch Therapeutics, Forty Seven Inc., Priothera, Ceramedix, Lygenesis, Pluto Immunotherapeutics, Magenta Therapeutics, Merck & Co., Inc. and DKMS Medical Council (Board); and he has IP Licensing with Seres Therapeutics, Juno Therapeutics and stock options from Seres and Notch Therapeutics. T.M.H. has participated in a scientific advisory board for Boehringer-Ingelheim Inc.

**STAR METHODS**

**KEY RESOURCES TABLE**

|  |  |  |
| --- | --- | --- |
| **REAGENT or RESOURCE** | **RESOURCE** | **IDENTIFIER** |
| **Deposited Data** | | |
| Human Microbiome Project | Human Microbiome Project Consortium, 2012 | SRA study PRJNA48489 |
| MSK cohort | Liao et al., 2021; Yan et al., 2021 | SRA studies PRJNA394877, PRJNA607574, PRJNA606262, PRJNA548153, PRJNA545312 |
| PRISM, LifeLines DEEP and NLIDB cohorts | Franzosa et al., 2019 | SRA study [PRJNA400072](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA400072/) |
| UMH cohort | Schubert et al., 2014 | mothur.org/CDI\_MicrobiomeModeling/ |
| RISK cohort | Gevers et al., 2014 | SRA study SRP040765 |
| Belgium PSC/IBD cohort | Vieira-Silva et al., 2019 | European Genome-phenome Archive  EGAS00001003600 |
| PROTECT cohort | Schirmer et al., 2018 | SRA study PRJNA436359 |
| Mount Sinai cohort | Contijoch et al., 2019 | SRA study PRJNA413199 |
| LUMC cohort | Bekker et al., 2019 | SRA study PRJEB28845 |
| UPenn cohort | Lewis et al., 2015 | SRA study SRP057027 |
| **Databases** | | |
| SILVA v138 | Quast et al., 2013 | www.arb-silva.de |
| MicrobiomeHD | Duvallet et al., 2017 | [doi.org/10.5281/zenodo.840333](https://doi.org/10.5281/zenodo.840333) |
| **Softwares** | | |
| Python v3.7.9 | Python | python.org |
| Scikit learn v0.24.0 | Pedregosa et al., 2011 | scikit-learn.org |
| Non-negative matrix factorization | Lee and Seung, 1999 | scikit-learn.org |
| t-distributed stochastic neighbor embedding | van der Maaten and Hinton, 2008 | scikit-learn.org |
| Random Forest classifier | Ho, 1995 | scikit-learn.org |
| Lifelines v0.25.6 | Davidson-Pilon, 2019 | github.com/CamDavidsonPilon/lifelines |
| SourceTracker2 | Knights et al., 2011 | github.com/biota/sourcetracker2 |
| iRep | Brown et al., 2016 | github.com/christophertbrown/iRep |
| Cutadapt v3.4 | Martin, 2011 | github.com/marcelm/cutadapt |
| Naive Bayesian classifier | Wang et al., 2007 | rdp.cme.msu.edu |
| DADA2 | Callahan et al., 2016 | benjjneb.github.io/data2 |
| Bhatt lab workflow | Siranosian et al., 2021 | github.com/bhattlab/bhattlab\_workflows |
| MEGAHIT | Li et al., 2015 | github.com/voutcn/megahit |
| MetaBAT 2 | Kang et al., 2019 | bitbucket.org/berkeleylab/metabat/src/master/ |
| CONCOCT | Alneberg et al., 2014 | github.com/BinPro/CONCOCT |
| DAS Tool | Sieber et al., 2018 | github.com/cmks/DAS\_Tool |
| PATRIC | Davis et al., 2020 | www.patricbrc.org |
| Kraken2 | Wood et al., 2019 | github.com/DerrickWood/kraken2 |

**RESOURCE AVAILABILITY**

**Lead contact**

Further information and requests for resources should be directed to and will be fulfilled by the lead contact, Joao B. Xavier (xavierj@mskcc.org)

**Materials Availability**

This study did not generate new unique reagents.

**Data and code availability**

* All raw sequences of the microbiome datasets analyzed in this study are public available with accession numbers listed in the key resource table.
* All processed data supporting the findings of this study are available within the article and its supplementary materials.
* Customized Python scripts for all analyses included in this study are available on Github (https://github.com/liaochen1988/Source\_codes\_for\_oral\_microbiome\_contamination).

METHOD DETAILS

**Ecological modeling**

Our model (Eq. (1)-(2) in the main text) describes several key ecological processes associated with the oral-derived and gut-resident bacterial populations: transmission of oral bacteria to the gut lumen (zero-order kinetics), excretion of both populations in feces (first-order kinetics), population growth, and intra-/inter-population competition for resources (Lotka-Volterra-type (Stein et al., 2013)). The host effects such as gut inflammation are not explicitly modeled. We focus on antibiotic-induced perturbations and assume that antibiotics inhibit growth of both types of bacteria equally. If the averaged inhibitory effects between oral and gut bacteria are proportional and differ by a constant, the coefficients representing the unequal inhibitory effects (Carr et al., 2020) can be absorbed into the growth rates ( and ). Since oral cavity would be only briefly exposed to antibiotics during swallowing (Carr et al., 2020), we assume that ϵ does not affect . Antibiotics may also change dilution rate (e.g., inducing diarrhea) but this effect is indirect and generally mild (Polage et al., 2012). The details of model derivation and analytical solutions are available in **Supplemental Information**. Unless otherwise noted, the model parameters are assigned to their default values: , , , , , .

**Quantifying oral bacteria fraction in microbiome samples**

A similar approach using the Human Oral Microbiome Database (HOMD) has been previously employed to classify oral bacteria (Coker *et al.*, 2018; Hu et al., 2022).

We model the bacterial community in any microbiome sample as a linear combination of five source communities, corresponding to the typical communities of the five bacterial habitats revealed by the HMP dataset in the tSNE plot. Our approach is based on two assumptions: (1) bacteria translocate among different body sites (O’Boyle et al., 1998) within individuals and (2) each human body site is a distinct habitat that selects for a particular microbiome composition, such that the microbiome composition at a specific body site in one person can be approximated by the typical composition shared among the entire population. The second assumption is supported by findings that microbiome compositions vary more between body sites within the same individuals than between the same body site but in different individuals (Chu et al., 2017; Human Microbiome Project Consortium, 2012; Segata et al., 2012).

We simultaneously obtained the typical compositions of these habitats () and their mixing proportions () in HMP samples by decomposing the HMP relative abundance table () using Non-negative Matrix Factorization (NMF). The following objective function was minimized by NMF under the constraints that both and are non-negative: , where is the element-wise L1 norm, is the Frobenius norm, and is the Kullback-Leibler distance. Both (a constant that multiplies the regularization term) and (a regularization mixing parameter) are set to zero because the decomposition error (i.e.,) is optimized without regularization (see **Fig. S1A**). We normalized such that each row sum equals to 1 (i.e., the relative abundance for each community sums up to 1) and is updated accordingly to keep their product () the same. Given the microbiome relative abundances of new test samples (), the mixing proportions of these samples () can be similarly solved by minimizing where is obtained in the previous step and fixed here. Unless otherwise specified, our approach sums up the fractions of oral bacteria from both oral cavity habitat 1 and 2 to compute “oral bacteria in feces”.

We choose to collapse bacterial taxa at the lowest classified level up to genus for two reasons: (1) the interindividual variability in gut microbiome is lower in higher taxonomic ranks (Eckburg et al., 2005; Human Microbiome Project Consortium, 2012) and (2) higher taxonomic rank reduces batch effects when comparing results across multiple studies (DeSantis et al., 2006). Since the test samples may be classified using any taxonomic database, its relative abundance table () needs to reconstructed to match the taxonomic labels assigned to HMP sequences () using the GreenGenes taxonomy (DeSantis et al., 2006). When a taxon is not a GreenGenes taxonomy, it will be mapped to the lowest classified taxonomy in GreenGenes along the lineage of the taxon until the rank kingdom. Non-bacterial sequences are removed from all relative abundance tables.

**Alternative oral bacteria quantification approaches**

We adopted two well-established microbial source tracking methods to validate our approach. A Random Forest classifier (1,000 trees with maximum tree depth 5) was trained on all HMP samples to predict sample collection body sites from bacterial composition. The prediction is probabilistic with probabilities calculated as the number of trees voting for each body site divided by the total number of trees in the forest. For new test samples, the proportion from each body site is therefore an average of the relative abundance of all bacterial taxa weighted by the probabilities that they come from the body site.

SourceTracker 2 (Knights et al., 2011) uses a Bayesian approach to estimate the mixing proportions of all source communities into a sink community. For any fecal sample as a sink, we used all other samples from different body sites of the same individuals as sources. Rarefaction is performed at 100 sequences/sample for both sources and sinks. The total fraction of oral bacteria in feces is the sum of mean proportions from all oral cavity samples (from different subsites).

**Identifying co-occurring ASVs**

The algorithm for computing co-occurrence is described in detail elsewhere (Machado et al., 2021). Briefly, it begins with ASV pairs and iteratively identifies co-occurring ASVs of larger combination sizes. In the next iteration, larger combinations are created by extending all co-occurring groups identified in the current iteration with one new ASV. The presence/absence of an ASV is determined by a relative abundance cutoff of 0.001. A combination of ASVs must satisfy the following criteria to be considered as co-occurring: (1) they must co-occur in at least 200 patients and 500 samples; (2) they must co-occur at least twice more than expected by chance, which is estimated by assuming each ASV is observed independently and its number of observation can be modeled by a binomial distribution; (3) the (false discovery rate) FDR-corrected *P*-values for the independent observation hypothesis must be less than 0.05. An oral group is a co-occurring group of oral ASVs. In this analysis, ASVs assigned to the following genera are considered to have an oral origin: *Actinomyces*, *Leptotrichia*, *Campylobacter*, *Fusobacterium*, *Neisseria*, *Corynebacterium*, *Rothia*, *Treponema*, *Veillonella*, *Prevotella*, *Streptococcus*, *Capnocytophaga*, *Haemophilus*. This list is a conservative enumeration based on the overlaps between principal bacterial genera found in the healthy oral cavity (Deo and Deshmukh, 2019) and the major signature taxa (relative abundance 1%) of the oral cavity habitat 1 and 2 of the HMP samples.

**16S rRNA gene amplicon sequencing data analysis**

Generally, we prefer to adopt the metadata, OTU/ASV abundances and taxonomy used in the original studies if provided. This helps us contrast our results with their findings by minimizing the technical differences in processing their 16S sequences. Sample metadata, OTU table (including taxonomy) and sequences of the HMP cohort were downloaded from the HMP website (https://www.hmpdacc.org/HMQCP/all/). Sample, subject and clinical metadata, taxonomy and counts of ASVs, 16S/18S quantitative PCR data, and binarized fungal CFU counts of the MSK cohort (Liao et al., 2021; Yan et al., 2021) were downloaded from Figshare (https://figshare.com/collections/Compilation\_of\_longitudinal\_microbiome\_data\_and\_hospitalome\_from\_hematopoietic\_cell\_transplantation\_patients/5271128). Subject and clinical metadata, and microbial species relative abundance profiles of the PRISM, LifeLines DEEP and NLIBD cohorts were downloaded from the supplementary material of Franzosa et al., 2019. Subject and clinical metadata, OTU taxonomy and counts of the UMH (Schubert et al., 2014) and RISK (Gevers et al., 2014) cohorts were downloaded from the MicrobiomeHD database (<https://zenodo.org/record/569601#.YTqb8y9h1TY>). Subject metadata and genus-level quantitative microbiome profiling matrix of the Belgium PSC/IBD cohort were downloaded from the supplementary material of Vieira-Silva et al., 2019. Sample, subject and clinical metadata as well as the OTU table of the PROTECT cohort were downloaded from the supplementary material of the associated publication (Schirmer et al., 2018). Sample, subject, clinical metadata as well as other microbiology data of the Mount Sinai cohort (Contijoch et al., 2019), the LUMC cohort (Bekker et al., 2019), and the UPenn cohort (Lewis et al., 2015) were downloaded from the supplementary material of the associated studies.

For samples whose relative microbiome profiles are not provided (the Mount Sinai cohort and LUMC cohort), their 16S reads were downloaded and analyzed using an in-house processing pipeline (Liao et al., 2021). Briefly, ASVs were identified using the Divisive Amplicon Denoising Algorithm (DADA2) pipeline including filtering and trimming of the reads (Callahan et al., 2016). Reads were trimmed to the first 180 bp or the first point with a quality score Q<2 (Martin, 2011). Reads were removed if they contained ambiguous nucleotides (N) or if two or more errors were expected based on the quality of the trimmed read. We assigned taxonomy to ASVs using the naive Bayesian classifier (Wang et al., 2007) and the SILVA 138 database (Quast et al., 2013).

**Shotgun metagenomic sequencing data analysis**

The Shotgun data in Lewis *et al.* 2015 was analyzed using the taxonomic classification services provided by the Pathosystems Resource Integration Center (PATRIC (Davis et al., 2020)). PATRIC can take the SRA accession number of each sample as an input without downloading or transferring the sequencing files, and output the taxonomic classification of metagenomic DNA sequences included in the sample. The default algorithm is Kraken2 (Wood et al., 2019), which uses exact k-mer matches to achieve high accuracy and fast classification speeds.

We used iRep (Brown et al., 2016) to determine the replication rates of *Streptococcus spp.* that dominate stool samples in the MSK cohort. We first identified 33 Shotgun samples with at least 10% ASV\_8 or ASV\_16 based on their relative abundances in the 16S samples. We adapted a recently published pipeline (Siranosian et al., 2021) to assemble the contigs from short reads using MEGAHIT (Li et al., 2015) and then bin the contigs into Metagenome-assembled genomes (MAGs) using two different methods: Metabat2 (Kang et al., 2019) and CONCOCT (Alneberg et al., 2014). The results were then aggregated to produce an optimized, non-redundant set of MAGs by DAS Tool (Sieber et al., 2018). The high-quality MAGs (75% complete, 175 fragments/Mbp sequence, and 2% contamination) classified as *Streptococcus spp.* by Kraken2 (Wood et al., 2019) were analyzed by iRep. The iRep value of a MAG represents the average number of replication events over different subpopulations of the MAG weighted by their relative abundances.

**Statistical analysis**

Pairwise Kruskal-Wallis test was used exclusively for multiple comparisons. The raw *P*-values were adjusted for multiple testing using Benjamini-Hochberg correction to control the FDR and associations with post-correction *P*<0.05 were considered significant. When different stratified fecal sample groups are compared for their oral bacteria fractions, we replaced values less than 0.034 with 0.034 in the test. This is because comparing oral bacteria fractions below this threshold is meaningless for detecting significant differences in the total bacterial density between the groups (see **Fig. 3D** in the main text). The Student’s t-test was used to assess the significance of slopes of linear fits in the scatter plots between bacterial relative abundance and total bacterial or microbiome density.

We used the Cox’s time-varying proportional hazard model to regress fecal dominations of oral bacteria (relative abundance30%) as a microbial endpoint of interest against antibiotic administration (aminoglycosides, aztreonam, piperacillin/tazobactam, linezolid, sulfamethoxazole/trimethoprim, cephalosporins, oral vancomycin, intravenous vancomycin, amoxicillin clavulanate, quinolones, metronidazole, doxycycline, clindamycin, macrolide derivatives, carbapenems, tigecycline, other antibiotics) as multivariable predictors. Although the enrichment of oral species in gut microbiome has been linked to liver cirrhosis (Dubinkina et al., 2017; Qin et al., 2014), liver dysfunction such as altered bile acid secretion is less likely a causal factor for allo-HCT patients since the collateral damage on liver caused by the pretransplant regimen is not as severe and patients with severe liver disease would not undergo transplantation. Next, we again examined domination of oral bacteria in fecal samples, this time as a univariable predictor of *Enterococcus* infection using the same time-varying Cox’s hazard model. Penalty was not added for all Cox hazard calculations. The oral domination states in missing samples were imputed as the same as their nearest preceding samples within 4 days and assumed false if their nearest preceding samples are 5 or more days earlier. For survival analysis of mortality, we looked at the most common likely origin of fecal samples collected between day 0 and engraftment, as the exposure. Outcome analysis started at engraftment. To compare overall survival Kaplan-Meier curves were plotted and between-group *P*-values were calculated using Wald test.

All statistical analyses were performed using Python v3.7.9. Information on the statistical tests and simulations can be found in the figure legends and in the corresponding Method Details.

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