

Baseline microbiome composition impacts resilience to and recovery following antibiotics

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The gut microbiome of healthy individuals naturally undergoes temporal changes linked to the dynamics of its community components¹. These dynamics are only observable in longitudinal studies; they are particularly relevant to understanding ecosystem responses to external environment disturbances. External exposures, such as antibiotic treatment, significantly reshape the gut microbiome, impacting both pathogen and commensal microbes². The gut microbiome plays pivotal roles in digestion, nutrient absorption, and mental health, influencing immune systems, obesity, and various diseases³⁻⁶. Consequently, beyond the short-term effects on the host gut microbiome dynamics, alterations resulting from antibiotic exposure also have enduring repercussions on human health and physiological equilibrium⁷. Therefore, enhancing gut microbiome resilience during antibiotic treatment is essential, with the goal of mitigating prolonged adverse effects. Here, we explored the impact of pre-antibiotic microbial and functional profiles on resilience, suggesting that specific baseline features exhibit greater resilience to antibiotics-induced changes. Our results identified an uncultured *Faecalibacterium prausnitzii* taxon as a species at baseline associated with diminished resilience. We demonstrated that this association could be linked to the role of this *F. prausnitzii* taxon as a keystone species. Additionally, we observed the influence of other commensal bacteria, such as *Bifidobacterium animalis* and *Lactobacillus acidophilus*, as well as functional modules, such as multidrug resistance efflux pump, on resilience. This lays the foundations for designing targeted strategies to promote a resilient gut microbiome before antibiotic treatment, alleviating possible prolonged effects on human health.

Antibiotics are known to disrupt the balance of the gut microbiome and induce long-term microbiome alterations, often termed dysbiosis in the literature. Altered microbiome compositions have been linked to various health conditions like inflammatory bowel disease, obesity, and cardiovascular disease, especially the loss of producers of beneficial metabolites like short-chain fatty acids (SCFAs)^{8,9}. SCFAs play a beneficial role in health maintenance and disease development by interacting with the host immune system¹⁰. Post-antibiotic dysbiosis is characterized by diminished microbial diversity, the absence of crucial taxa, and metabolic shifts¹¹. Even brief antibiotic usage, especially in early childhood, can induce lasting changes in the gut microbiome¹². Probiotic consumption alongside or following antibiotic treatment has been proposed to alleviate antibiotic-induced disruptions. However, the existing literature lacks a consensus, presenting conflicting results¹³⁻¹⁷. Recognizing the profound effects of antibiotics on the gut microbiome is crucial to understanding the factors influencing resilience to mitigate long-term consequences and maintain overall host health.

Resilience encompasses two aspects: resistance, the ability to withstand changes upon external exposure, and recovery, the rate or time to revert to the original state (Figure 1A)¹⁸. Factors influencing resilience include host immune status, microbiome diversity, and functional redundancy¹⁹. Functional redundancy illustrates that diverse organisms across different taxa perform the same functional role in the ecosystem²⁰. High functional redundancy indicates that altering species diversity may have a limited effect on overall ecosystem functionality²¹. Here, we hypothesize that the microbial or functional composition before antibiotic treatment plays a pivotal role in resilience.

To test whether the effect of antibiotics and the recovery rate were associated, we introduced the term "fragility index" (FI). The FI reflects how vulnerable a microbial community is during exposure to external disruptions (Figure 1B). The FI is computed as follows:

$$\text{Fragility index} = \text{Estimated recovered time} \times \text{Dissimilarity upon recovery}$$

We assessed the *estimated recovered time* to the time in which the Bray-Curtis distance is the closest to zero against the baseline²². The *dissimilarity upon recovery* corresponds to the Bray-Curtis distance between the baseline and the estimated recovered time. The FI depends on the resistance and the recovery aspects; a higher fragility index indicates a less resilient microbial community when exposed to external perturbations. Henceforth, we refer to "resistance" as the "scale of perturbation", defined as the Bray-Curtis distance between before and after the antibiotic treatment. In this study, we first examined the contrast in microbial community dynamics between unperturbed states and perturbation caused by antibiotic intervention. Subsequently, we tested the hypothesis that microbial or functional profiles are crucial in determining resilience.

To quantify the microbial perturbation induced by antibiotics compared with unperturbed microbial community dynamics in healthy human individuals, we collected, reanalyzed, and compared published datasets. Our study incorporated a total of four datasets. Two datasets, from Voigt et al.²³ (hereafter Voigt) and the Human Microbiome Project Healthy Human Subjects²⁴ (hereafter HMP-HHS), correspond to healthy human cohorts tracked for temporal variation in their gut microbiome. The other two datasets, from Palleja et al.²⁵ (hereafter Palleja) and Suez et al.¹³ (hereafter Suez), correspond to antibiotic intervention studies (Figure 1C). In the Voigt study, only one participant was under antibiotic treatment. The subject, referred to as "Alien", received ceftriaxone for four days due to infection and was segregated from other participants for the analysis. The Palleja and Suez studies involved healthy human cohorts

treated with antibiotics for four and seven days, respectively. Both studies used a cocktail of broad-spectrum antibiotics and vancomycin (Extended Table 1). The antibiotic combinations ensure comparability and suitability for a combined analysis. The Palleja and Suez studies lack continuous (day-by-day) taxonomic and functional abundance data. Therefore, we employed natural cubic spline interpolation to estimate taxonomic and functional abundances at the missing time points and then calculate the estimated recovered time²⁶. Moreover, the Palleja and Suez studies have different intervention and follow-up time points. While the Suez study has a longer antibiotic intervention duration, the Palleja study has more extended follow-up time points. Hence, their respective time points were realigned to ensure comparability in the estimated recovery time between both studies (Figure 1D).

To assess the impact of antibiotics on the microbial community in comparison with the natural dynamics of a healthy microbiota, we computed the Bray-Curtis distance between each time point and the baseline for all individuals (Figure 2A, Extended Figure 1A). We employed polynomial regression to model the Bray-Curtis dissimilarity over time for antibiotic-treated and non-treated individuals. In the non-treated group, a shift occurred, reaching stability and forming a plateau around 0.4 over time (Figure 2B, Extended Figure 1B). For the antibiotic-treated group, the Bray-Curtis distance increased to 0.8 following antibiotic exposure and gradually returned to a level similar to that of the non-treated group. Notably, from day 300 to 400, the antibiotic-treated group's distance from the baseline showed no significant difference compared with the non-treated group, as indicated by overlapping confidence intervals. This shows that antibiotic exposure induced a perturbation in the gut microbiota, reaching about twice the scale of the shift in healthy individuals, and eventually returning to a level similar to the non-treated group during recovery. We observed a significant correlation between the fragility index and the scale of perturbation based on both taxonomic (genus, Spearman's correlation $p < 0.05$, $\rho = 0.49$) and functional (KEGG module, Spearman's correlation $p < 0.05$, $\rho = 0.49$) profiles (Figure 2C, 2D). This indicates that the scale of perturbation serves as a suitable proxy for the fragility index, and, in turn, is associated with overall resilience. Moreover, the scales of perturbation between taxa and functional profiles are correlated (Extended Figures 1C, 1D).

Next, our aim was to characterize the microbiome and functional profiles that are resilient upon antibiotic perturbation. First, we discovered a negative correlation (Spearman's $p < 0.01$, $\rho = -0.64$) between functional redundancy and the scale of perturbation (Figure 3A). Then, we applied the Random Forest (RF) method, an ensemble learning technique that combines independently sampled decision trees to improve model robustness and generalization performance²⁷. Utilizing RF regression models, we tested which microbial and functional features were linked to antibiotic perturbation and detected an uncultured *F. prausnitzii* as the most relevant predictor (Spearman's $\rho = 0.6$, Figure 3B). Our RF results were validated by correlation to leave-one-out cross-validation (LOOCV) (Extended Figure 2). In contrast, baseline Shannon diversity and the baseline abundance of *Blautia* sp., *Ruminococcus* sp. CAG 254, *Prevotella* sp. CAG 520, *L. acidophilus*, and *B. animalis* are negatively correlated with the scale of perturbation (Spearman's ρ s < -0.53 , Figure 3B). At the genus level (Figure 3B column 2), baseline Shannon diversity (Spearman's $\rho = -0.56$) and the abundance of Dehalococcoidales gen. incertae sedis (Spearman's $\rho = -0.56$) are significantly and negatively correlated with the scale of perturbation. We built a second RF model to predict the scale of perturbation based on the baseline functional profile, including KEGG modules and gut metabolic modules (GMMs) (Figure 3B columns 3, 4)^{28,29}. We found that multidrug resistance efflux pumps (KEGG M00645 and M00700) are among the most influential ones, contributing to functional stability. Given the relevance of a known butyrate producer like *F.*

prausnitzii to predict the scale of perturbation³⁰, it is interesting to detect that the baseline abundance of modules associated with the production of this SCFA like 4-aminobutyrate degradation (GMM MF0042) and crotonyl-coA from succinate (GMM MF0115) negatively correlated with the scale of perturbation³¹. We observed that *Bifidobacterium*, *Lactobacillus*, and MF0042 are consistent features across different models (Figure 3B, all columns). Specific functions, for example, multidrug resistance efflux pumps M00646 and M00647 in Figure 3B column 5 show positive correlations with the scale of perturbation, while M00645 and M00700 in Figure 3B column 3 exhibit a negative correlation. It is important to recognize that, although classified as multidrug resistance efflux pumps, these systems can exhibit inherent differences in their composition and functional mechanisms³². When we test which taxonomic or functional features are the best predictors of the FI, our model identified fewer significant correlations, as shown in Extended Figures 3 and 4 (e.g., only six features showed correlation significance in Extended Figure 3).

In addition to the uncultured *F. prausnitzii* taxon, other recognized SCFA producers like *B. animalis*, *L. acidophilus*, *Blautia* spp., and *Ruminococcus* sp. CAG 254 were identified as relevant taxonomic features to predict the effect of antibiotic perturbation^{33,34}. We concluded that the majority of SCFA-producing species at baseline play a protective role in preserving microbial communities against extensive perturbation induced by antibiotic treatment. Based on the relevance of uncultured *F. prausnitzii* in our models, we speculated about its potential role as a keystone species within the microbial community. A keystone species exerts a disproportionately significant influence on the other community members relative to its abundance³⁵. To test whether the uncultured *F. prausnitzii* has a significant role in the microbial community, we constructed a co-occurrence network based on significant taxa-taxa correlations (Spearman's correlations, Benjamini-Hochberg corrected $q < 0.1$) (Extended Figure 5) and used centrality measures to characterize the relevance of this taxon. In network analyses, nodes with elevated betweenness centrality (i.e., the frequency of a node acting as a bridge along the shortest path between two other nodes) may signify key connectors, while nodes with high node degrees (i.e., the number of connections a node has to other nodes) may represent hubs³⁶. Both high betweenness centrality and node degree serve as indicators for potential keystone species. We observed that uncultured *F. prausnitzii* possessed the highest network betweenness centrality (Figure 4A), confirmed by an alternative method (Extended Figures 6A, 6B). We observed a depletion of the uncultured *F. prausnitzii* after the antibiotic treatment (Spearman's correlation $p < 0.01$, $\rho = -0.78$) and a decrease in the abundances of all its associated taxa ($n=14$) based on the network analysis (Extended Figure 5) (Spearman's correlations, Benjamini-Hochberg corrected $q < 0.05$, ρ values between $-0.40 \sim -0.69$). We suggest that the decline in uncultured *F. prausnitzii* during antibiotic treatment is linked to the reduction of other associated species, consistent with a role as a keystone species.

The uncultured *F. prausnitzii* taxon corresponds to two metagenomic Operational Taxonomic Units (mOTUs), ref-mOTU-v25-06108 (hereafter referred to as *F. prausnitzii* 06108) and ref-mOTU-v25-06110 (hereafter referred to as *F. prausnitzii* 06110). To discern the relevance of these mOTUs, we ran new RF regression models using baseline mOTUs (restricted to those associated with significant species in Figure 3 column 1) to predict the scale of perturbation. Notably, our results highlight *F. prausnitzii* 06108 as the foremost influential feature, positioning it as the most crucial predictor, while *F. prausnitzii* 06110 holds a lower rank (8th) in importance. We observed that the baseline abundance of *F. prausnitzii* 06108 positively correlated with the scale of perturbation, while its delta value (before/after antibiotics) negatively correlated with the scale of perturbation (Figure 4B, 4C). The latter suggests that an increased loss of *F. prausnitzii* 06108 post-antibiotics leads to a larger scale of perturbation.

Our findings propose that the depletion of *F. prausnitzii* 06108 during antibiotic treatment precipitates the loss of other associated species. Furthermore, we examined the variations in functional profiles within the two mOTUs, delineating their distinctions using KEGG modules, pathways, and BRITE, and identified several disparate functions (Extended Figures 7–9). For example, *F. prausnitzii* 06108 was exclusively correlated with KEGG modules such as cytochrome c oxidase, cytochrome bd ubiquinol oxidase and acylglycerol degradation, and KEGG pathways such as protein digestion and absorption.

Our study explores the impact of antibiotics on the gut microbiome. Our results indicate that antibiotic-induced perturbation in the studied datasets is approximately twice the scale of natural drift in healthy individuals over the same time interval. Even in the absence of any external source of perturbation such as antibiotics, drift over time, as well as measurement variability, results in an average within-donor gut microbiome similarity over time of around 0.4 Bray-Curtis distance. This is in agreement with previous findings in a study involving fecal samples from healthy Belgian women collected over 6 weeks, where within-individual Bray-Curtis distances fell between 0.25 and 0.5¹. We detected a negative correlation between functional redundancy and the scale of perturbation, consistent with previous studies suggesting that high redundancy contributes to stable functioning in a microbiome community under external perturbation³⁷. We found a positive correlation between functional redundancy and the extent of perturbation upon antibiotics exposure and established the fragility index as a proxy to comprehensively describe resilience in a microbiome context. When we explored the predictive potential of baseline microbiome abundance, we detected several commensal SCFA producers associated with the scale of perturbation. In particular, an *F. prausnitzii* taxon was anti-correlated with resilience, consistent with a keystone species role of this commensal, which we confirmed by co-occurrence network analysis, as previously reported³⁸. Conversely, *Blautia* sp., *Ruminococcus* sp., *L. acidophilus*, and *B. animalis* at baseline were associated to higher resilience. The same applies to baseline Shannon diversity, in line with previous literature¹⁹. Lastly, several functional modules, including multidrug resistance efflux pumps and butyrate-producing pathways, emerged as predictors of the degree of community perturbation upon antibiotic exposure.

Our findings complement the conventional notion of employing probiotics based on *Bifidobacterium* or *Lactobacillus* during or after antibiotics treatment to facilitate recovery, suggesting other potential candidates for supplementation post-antibiotics. Even within the same species, we found that different strains may impact community resilience differently. Future efforts will focus on validating the resilience-enhancing capabilities of SCFA producers through experimental studies. Our results suggest a potential role of probiotics before antibiotic treatment to fortify gut microbiome resilience, which future experiments should seek to validate.

Methods

Data acquisition. Raw metagenomic sequencing data from the Palleja²⁵, Suez¹³, and Voigt²³ studies were acquired from the European Nucleotide Archive (ENA) database, using the accession numbers ERP022986, PRJEB28097, and ERP009422, respectively. Metadata for these studies was obtained from the corresponding publications. For the HMP-HHS study²⁴, sequencing data were obtained from the Human Microbiome Project (HMP) portal at <https://portal.hmpdacc.org/projects/t>. The metadata for this study were controlled-access and were retrieved from the database of Genotypes and Phenotypes (dbGaP). The individuals in the HMP_HHS study who had taken antibiotics were excluded from our analysis.

Shotgun metagenomic processing. The metagenomic shotgun sequences were subjected to processing using NGLess v1.3³⁹. Reads underwent quality filtering, with a minimum read length of 45 bp and a minimum Phred quality score of 25. Sequences meeting these criteria were subsequently mapped to the human genome (adapted from hg38), with a minimum requirement of a 45 bp match and at least 90% identity, and those mapping to the human genome were filtered out. Taxonomic classification was determined by aligning the non-human reads to metagenomic Operational Taxonomic Units (mOTUs v2.5)⁴⁰ using bwa with default parameters. Functional profiling was done by aligning non-human reads to the Global Microbial Gene Catalog (GMGC v1.0)⁴¹. Instances where reads mapped to multiple genes in the reference database were addressed utilizing the "all1" method. Next, the GMGC IDs were binned into KEGG KOs²⁸, and then further into KEGG modules or gut metabolic modules (GMM)²⁹. To mitigate the impact of differences in sequencing depth in downstream analysis, rarefaction on abundance tables was performed using RTK tool v0.93.1⁴².

Abundance interpolation. To obtain continuous data (i.e., data for every single day) from the discrete raw data, natural cubic spline interpolation was employed for both taxonomic and functional abundance data^{26,43}. This technique was utilized to estimate abundances at missing time points by constructing piece wise third-order (cubic) polynomials that pass through the known data points. The spline interpolation was performed using the R function `splinefun(method = "natural")`.

Timepoint realignment. To ensure uniformity in the estimated recovery time between the Suez and Palleja studies, their respective time points underwent realignment. Day 0 in Palleja and day 6 in Suez were designated as the baseline. Day 4 in Palleja and day 13 in Suez were regarded as the final days of intervention. Ultimately, follow-up time points were extended up to day 60 in Palleja to generate estimates of recovery time that align with the time frame of Suez.

Alpha and beta diversities analysis. Both Shannon diversity and Bray-Curtis distance were calculated using the `vegan v2.5` R package⁴⁴. The rarefied abundance table at both the species and genus levels was utilized for Bray-Curtis distance computation.

Functional redundancy. To assess functional redundancy, characterized by the presence of multiple species-specific variants within gene families, the following method was employed. A Shannon metric was computed for each individual based on the GMGC profiles corresponding to each gene family (e.g., KEGG KO). This calculation was conducted independently for each gene family. Subsequently, the average Shannon metric was determined by aggregating the values across all gene families for each individual.

Correlation analysis. Spearman's correlation tests were done using the R basic function `cor.test(method = "spearman")`. These included the correlation between taxonomic or functional profile abundances and scale of perturbation or fragility index, as well as all other instances in the figures that explicitly specified Spearman's correlation test. Benjamini-Hochberg correction of the p values was done using the function `p.adjust(method = "fdr")` in base R.

Random forest regression. Random forest regression was carried out using the Python machine-learning package `scikit-learn`⁴⁵. First, the out-of-bag error (OOB error) was employed to select optimal hyperparameters, including the maximum number of features, maximum depth, and number of estimators. Subsequently, two separate evaluations were conducted: one

using 5-fold cross-validation and the other using leave-one-out cross-validation (LOOCV). The evaluation metric for both procedures was negative mean absolute error (negative MAE)⁴⁶. Following this, permutation (n = 1000) was performed by randomly shifting the dependent variable against the independent variables, and all resulting negative MAEs were recorded. The distribution of these permuted negative MAEs was analyzed to assess the overall performance of the random forest regression.

Keystone species analysis. Spearman's correlations were computed for all species using R. Subsequently, only the statistically significant correlations (Benjamini-Hochberg corrected $q < 0.1$) were employed in constructing a co-occurrence network. The betweenness centrality and node degree were then calculated. Cytoscape v3.9.1⁴⁷ was employed for network construction, visualization, and the computation of betweenness centrality and node degree. Additionally, for independent validation, the *cooccur* R package⁴⁸, which applies the probabilistic model to assess species co-occurrence, was also employed.

Linking functional profiles to specific mOTUs for the uncultured *F. prausnitzii* taxon. From the mOTU v2.5 database, the uncultured *F. prausnitzii* fraction comprises two mOTUs, namely *ref_mOTU_v25_06108* and *ref_mOTU_v25_06110*. Genomic data and GMGC profiling for the uncultured *F. prausnitzii* were extracted, and GMGC IDs with low abundance (sum across samples < 7) were filtered out. Spearman correlation analyses were then conducted between the abundances of the two target *F. prausnitzii* mOTUs and each GMGC ID, followed by Benjamini-Hochberg (BH) correction. Correlations between GMGC and mOTUs were filtered based on significance ($q < 0.05$). GMGC IDs were binned into KEGG modules, pathways, or BRITEs categories using the KEGG database (<https://www.kegg.jp>). NA values, indicating no significant correlation of GMGC belonging to a KEGG module, pathway, or BRITE with one mOTU (but significant correlation with the other), were replaced with 0. The focus was on positive correlations between GMGC and mOTUs, excluding negative correlations, to identify co-abundant mOTUs and genes within the context of the observed uncultured *F. prausnitzii* taxon.

Visualization. Figures were generated using *ggplot2* v3.3.5⁴⁹ and the *ggpubr* v0.4.0 (<https://cran.r-project.org/package=ggpubr>) R packages (<https://rdocumentation.org/packages/ggpubr/>). Smooth curves in Figures 2A and 2B are local polynomial regressions fitted by using the function `ggplot2::geom_smooth(method = "loess")`. In Figures 2C, 2D, 3A, 4B, and 4C, as well as Extended Figures 1C and 1D, the smooth lines were derived from linear regression and fitted using `ggplot2::geom_smooth(method = "lm")`.

Data availability

For raw sequencing files, please see “data acquisition” in Methods section. Processed data are available at https://github.com/CCY-dev/Microbiome_resilience_data_code.

Code availability

Scripts are available at https://github.com/CCY-dev/Microbiome_resilience_data_code.

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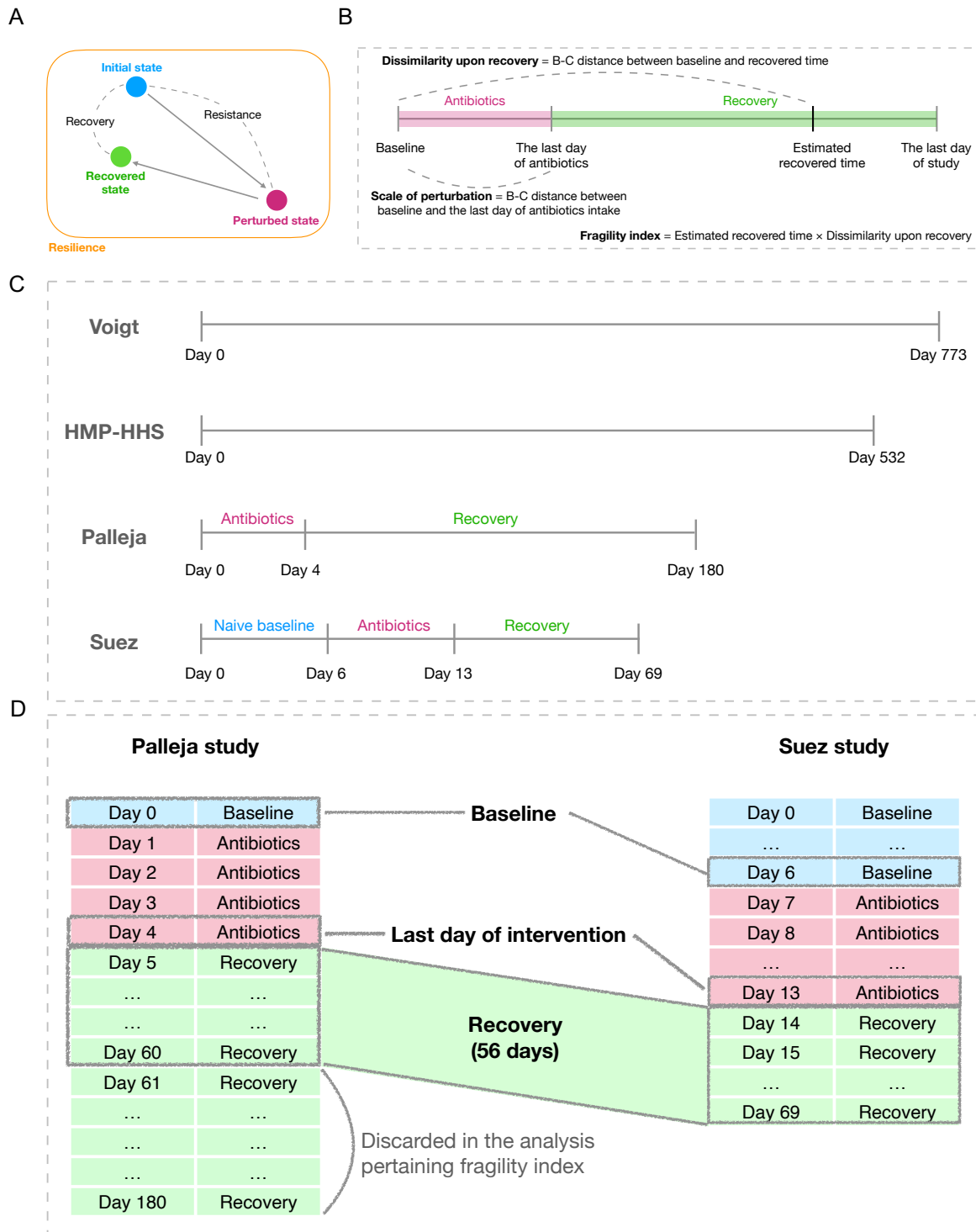


Figure 1. Study concept and design. (A) The illustration shows the concept of resistance and resilience upon antibiotics treatment. Resilience is represented as how much a microbial community change compared with its original state after the antibiotics perturbation, while recovery can be measured by how much the post-perturbation state resembles the initial state. **(B)** The figure shows the components of the fragility index, which includes the scale of perturbation, estimated recovered time and dissimilarity upon recovery. B-C is the abbreviation of Bray-Curtis. **(C)** The data included in this study are illustrated. The sample size of each study is as follows. Voigt (n = 7, including the subject “Alien”); HMP-HHS (n = 55); Palleja (n = 12); Suez before antibiotics treatment (n = 21); Suez after antibiotics treatment (n = 16). The discrepancy between the sample size of Suez before/after antibiotics is because some of the individuals underwent further post-antibiotics intervention (i.e., probiotics supplement or autologous fecal transplant) and were excluded here. **(D)** The illustration shows the alignment of time points between the Palleja and the Suez studies. Day 0 in the Palleja and day 6 in the Suez studies are taken as the baseline. Day 4 in the Palleja and day 13 in the Suez studies are the last day of intervention. The Palleja study is curtailed to day 60 so that its recovery duration is the same as that of Suez (56 days).

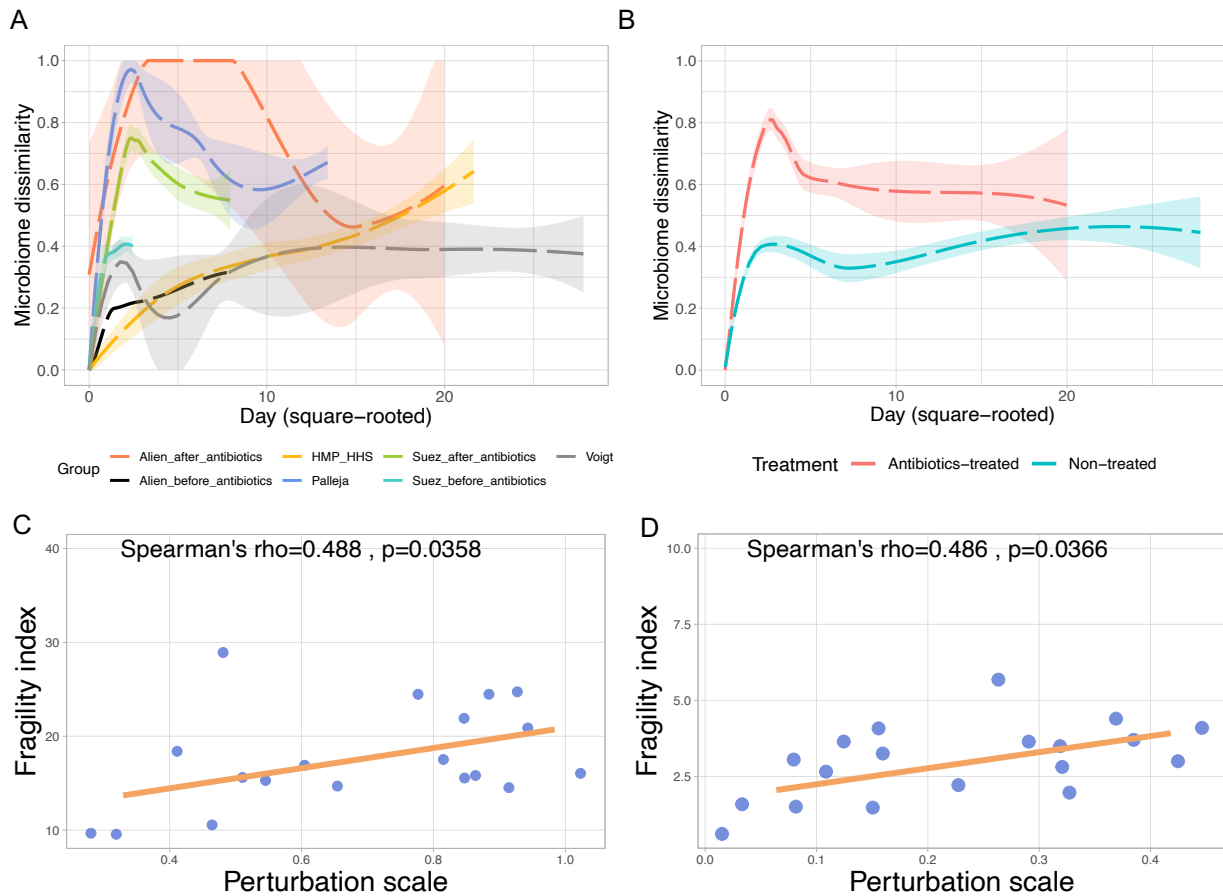
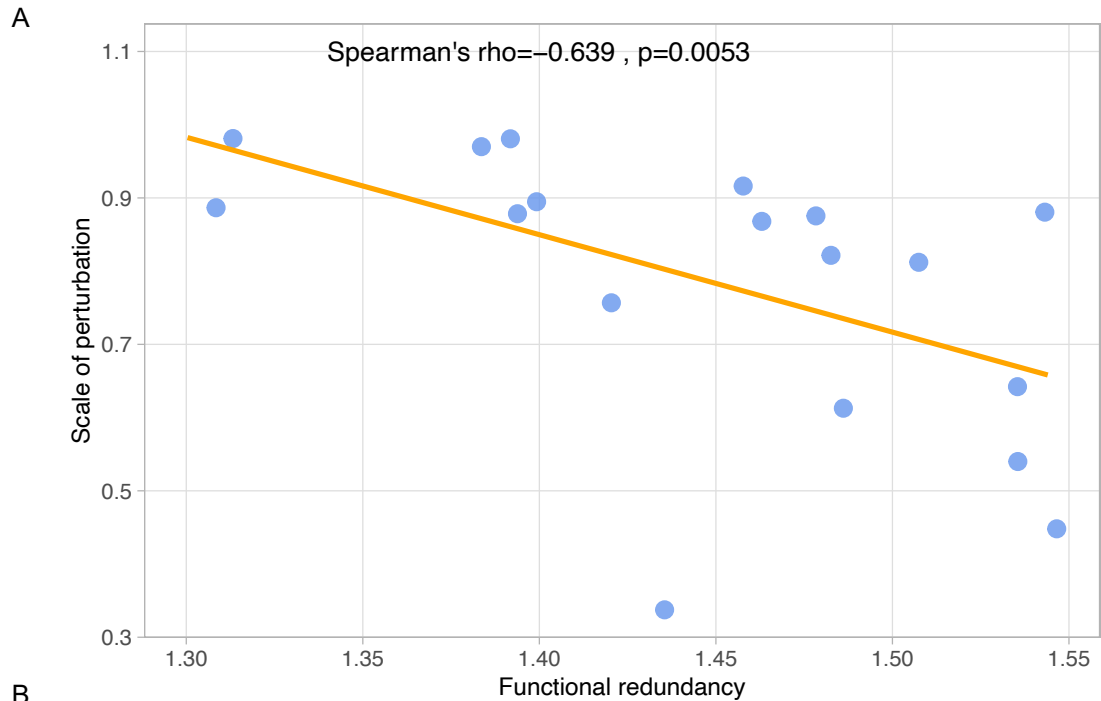


Figure 2. Gut microbiome shift is larger in antibiotics-treated group, and the scale of perturbation is correlated with the fragility index. (A, B) The line plots show the microbiome dissimilarity (Bray-Curtis distance) at species level between the baseline and each time point at subsequent days. Samples are grouped by (A) different data source, which are Alien_before_antibiotics (n = 1), Alien_after_antibiotics (n = 1), HMP-HHS (n = 55), Palleja (n = 12), Suez_before_antibiotics (n = 21), Suez_after_antibiotics (n = 16) and Voigt (n = 6), or (B) different treatment, which are non-treated (n = 83) and antibiotics-treated (n = 29). Smooth curves (dashed lines) were fitted to show the overall pattern in each group. Transparent shades indicate 95% confidence interval. The discrepancy between the sample size of Suez before/after antibiotics is because some of the individuals underwent further post-antibiotics intervention (i.e., probiotics supplement or autologous fecal transplant) and were excluded here. In (B), the significance of treatment was shown by a linear model fitting the microbiome dissimilarity as a function of treatment*day(square rooted). P-values for treatment and the interaction term treatment:day were both < 0.001 (C, D) Scatter plots showing the correlation between the perturbation scale and the fragility index are based on (C) microbial genus and (D) KEGG modules. Spearman's correlation test results are annotated on the plots. The orange solid lines are the linear regression fitted to the points to show the overall trend.



B

Number	1	2	3	4	5	6	7	8
Baseline	Species	Genus	KEGG module	Gut metabolic module	KEGG module	Gut metabolic module	Genus	Genus
Scale of perturbation	Species	Genus	KEGG module	Gut metabolic module	Genus	Genus	KEGG module	Gut metabolic module
Random Forest significance	Significant	Significant	Significant	Significant	Significant	Non-significant	Significant	Significant
Feature 1	uncultured <i>Faecalibacterium prausnitzii</i> 0.6 *	Shannon diversity -0.56 *	M00716: ArIS-ArIR two-component regulatory system -0.71 *	MF0042: 4-aminobutyrate degradation -0.48 *	M00240: Iron complex transport system 0.69 *	MF0099: Methanol conversion -0.54 *	Shannon diversity -0.26	Shannon diversity -0.37
Feature 2	Shannon diversity -0.54 *	Dehalococcoidales gen. incertae sedis -0.56 *	M00227: Glutamine transport system -0.76 *	MF0048: lactose degradation 0.59 *	M00373: Ethylmalonyl pathway 0.58 *	MF0048: Lactose degradation 0.6 *	<i>Alistipes</i> 0.64 *	<i>Bacteroides</i> 0.67 *
Feature 3	<i>Blautia</i> sp. -0.67 *	<i>Bifidobacterium</i> -0.51	M00700: Multidrug resistance efflux pump AbcA -0.61 *	MF0030: Threonine degradation -0.46 *	M00425: H/ACA ribonucleoprotein complex -0.74 *	MF0039: Lysine fermentation to acetate, butyrate 0.17	<i>Bifidobacterium</i> -0.67 *	<i>Bifidobacterium</i> -0.58 *
Feature 4	<i>Ruminococcus</i> sp. CAG.524 -0.53 *	<i>Lactobacillus</i> -0.39	M00342: Bacterial proteasome -0.7 *	MF0033: cysteine degradation -0.28	M00227: Glutamine transport system -0.61 *	MF0097: Methanogenesis - methyl-coM -0.56 *	<i>Anaerostipes</i> -0.37	<i>Anaerostipes</i> -0.49 *
Feature 5	<i>Prevotella</i> sp. CAG.520 -0.58 *	<i>Faecalibacterium</i> 0.36	M00645: Multidrug resistance efflux pump SmeABC -0.54 *	MF0019: Proline degradation -0.65 *	M00342: Bacterial proteasome -0.58 *	MF0116: Butyrate production via transferase 0.17	<i>Lactobacillus</i> -0.57 *	<i>Lactobacillus</i> -0.38
Feature 6	Dehalococcoidales species incertae sedis -0.35	<i>Bacteroides</i> 0.41	M00280: PTS system -0.78 *	MF0115: Crotonyl-coA from succinate -0.58 *	M00715: Lincosamide resistance efflux pump -0.49 *	MF0089: Entner-Doudoroff pathway I 0.56 *	<i>Bacteroides</i> 0.58 *	<i>Romboutsia</i> -0.47 *
Feature 7	<i>Lactobacillus acidophilus</i> -0.55 *	Firmicutes gen. incertae sedis -0.25	M00219: AI-2 transport system 0.56 *	MF0084: Pyruvate:ferredoxin oxidoreductase -0.47 *	M00647: Multidrug resistance efflux pump AcrAB-TolC/SmeDEF 0.47 *	MF0085: pyruvate:formate lyase -0.51 *	Firmicutes gen. incertae sedis -0.33	Firmicutes gen. incertae sedis -0.16
Feature 8	<i>Bifidobacterium animalis</i> -0.55 *	<i>Anaerostipes</i> -0.28	M00373: Ethylmalonyl pathway 0.71 *	MF0085: Pyruvate:formate lyase -0.38	M00704: Tetracycline resistance efflux pump -0.4 *	MF0042: 4-aminobutyrate degradation -0.56 *	Dehalococcoidales gen. incertae sedis -0.25	<i>Faecalibacterium</i> 0.41
Feature 9	<i>Eubacterium eligens</i> -0.36	<i>Clostridium</i> -0.33	M00425: H/ACA ribonucleoprotein complex -0.59 *	MF0011: Aspartate degradation -0.25	M00443: SenX3-RegX3 two-component regulatory system -0.67 *	MF0022: Isoleucine degradation 0.47 *	Clostridiales gen. incertae sedis 0.32	Dehalococcoidales gen. incertae sedis -0.46 *
Feature 10	<i>Ruminococcus</i> species incertae sedis -0.24	Eggerthellaceae gen. incertae -0.37	M00841: Tetrahydrofolate biosynthesis -0.69 *	MF0132: Superoxide reductase -0.51 *	M00646: Multidrug resistance efflux pump AcrAD-TolC 0.55 *	MF0030: Threonine degradation -0.44 *	<i>Faecalibacterium</i> 0.34	<i>Succinivibrio</i> -0.55 *

Spearman's rho

Figure 3. Characterization of the resilient microbiome and functional profile (A) The scatter plot shows the correlation between baseline functional redundancy and the microbiome dissimilarity (Bray-Curtis distance) of the gut microbiome at genus level between the baseline and post-antibiotics treatment. The functional redundancy is calculated as the Shannon diversity of the species-specific variants (GMGC) within each gene family (KEGG KO). Spearman's correlation test's p-value and rho of are shown in the figure. The orange solid line is the linear regression fitted to the points to show the overall trend. **(B)** This heatmap shows the result of RF regression fitting the scale of perturbation. The random forest models were trained using 5-fold cross-validation. Each column represents the scale of perturbation based on one feature predicted by the other baseline feature. RF significance is based on the permutation ($n = 1000$) result, where the negative MAE of each RF is compared to the permuted negative MAE. If a negative MAE is larger than $> 95\%$ of the permuted values, then it is regarded as significant ($p < 0.05$). Colors represent Spearman's correlation between the feature with the scale of perturbation. Text below the feature name is the Spearman's rho value. Asterisks and bold texts denote that Spearman's correlation $q < 0.1$. Benjamini-Hochberg procedure was used to adjust the p values within each column ($n = 10$).

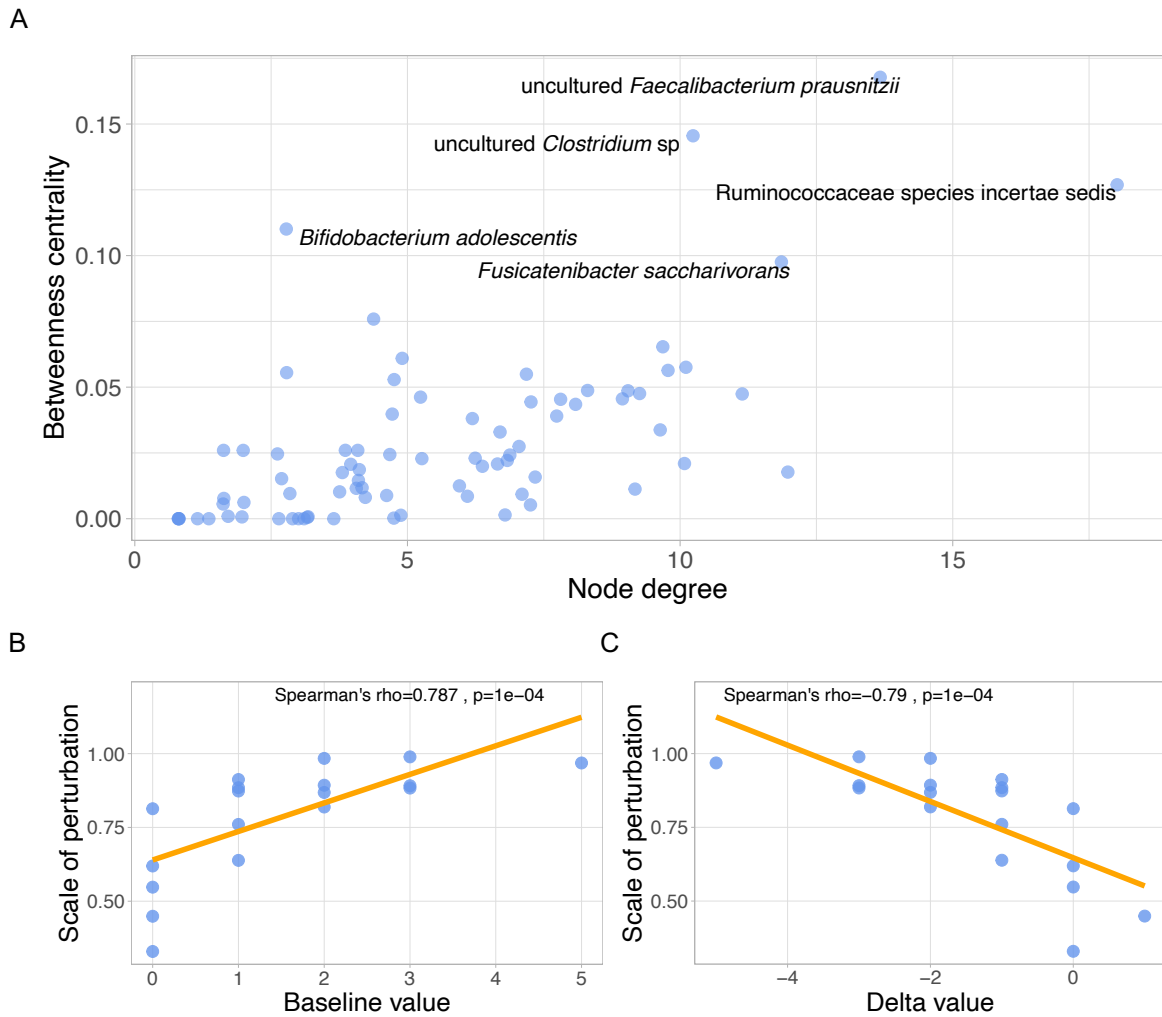


Figure 4. Uncultured *F. prausnitzii* taxon as a keystone species (A) The scatter plot shows the betweenness centrality against node degree of each species, which is the result from co-occurrence network analysis. **(B, C)** These figures plot the scale of perturbation against the (B) the abundance of *F. prausnitzii* 06108 at the baseline and (C) the difference in *F. prausnitzii* 06108 abundance between before and after antibiotics treatment (after – before). Spearman's correlation test's p-value and rho of are shown in the figures. The orange solid lines are the linear regression fitted to the points to show the overall trend.