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**Figure 1.** **Experimental design and analytical framework to study the response of mouse gut microbiome to dietary fiber intervention.**

**A**. Schematic diagram of experimental design. Dots indicate the days on which longitudinal fecal samples, microbiome and metabolomics data were collected.

**B**. Cartoon illustration of our computational approaches to infer the ecological and metabolic processes underlying dietary fiber intervention.

**C**. Baseline gut microbiota composition of isogenic mice purchased from different vendors.

**D**. Principal coordinate analysis (PCoA) of the aitchison distance matrix of baseline microbiota in **C**.

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**Figure 2.** **Dynamical responses of short-chain fatty acid (SCFA) metabolism and gut microbiome to dietary fiber intervention.**

1. Temporal changes in fecal concentration of three major SCFA within one month’s intervention of two dietary fibers (inulin and resistant starch). Stacked bands represent averages of SCFA concentration.
2. Compositional shifts in the predominant bacterial species of the inulin- and resistant starch-fed mice during the observation period.
3. Total bacterial density measured by quantitative PCR. Lines represent mean and shading areas represent standard error of the mean.
4. Distinct gene abundance profiles of inulin-fed mice between short- (day 5) and long-term (day 31) intervention. Principal coordinates analysis (PCoA) was based on Bray-Curtis distance of metagenomic gene abundances.

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**Figure 3.** **A visualization and non-parametric statistical testing method for individuality of dietary fiber-induced longitudinal responses.**

1. Inulin-induced vendor-specific shifts in short-chain fatty acid (SCFA) metabolism. Each symbol represents a mouse (dots: cellulose group, crosses: inulin group) and all mice data from the same vendor under the same dietary fiber treatment was to fit to an eclipse when possible (non-zero variability in both dimensions). For each vendor, an arrow was drawn from the eclipse center o f the vendor under cellulose treatment (adjusted to the origin) to that under the inulin treatment. Factor 1 and 2 were extracted using sequential non-negative matrix factorization and P-value was calculated by PERMANOVA (permutational multivariate analysis of variance) test on the first two factors across different vendors. The values in the parenthesis of the x- and y-labels represent the explanatory power of each individual factor.
2. Individuality of the inulin-induced responses in the absolute abundance of the seven taxa in B.
3. Individualized gut bacteria (at the species level) responses in their relative abundance or absolute abundance following inulin treatment. B1-B7 represent seven taxa with the highest averaged relative abundance across all inulin-group samples.

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**Figure 4. Ecological inference of keystone** **bacterial responders to inulin intervention**

1. Inferring ecological processes from complex microbiota dynamics using generalized Lotka-Volterra (gLV) model.
2. Temporal expression of inulinase genes. Each dotted line represents an individual mouse. \*: p≤0.05; \*\*: p≤0.01; \*\*\*: p≤0.001.
3. Posterior distribution of five species-level taxa with significant growth responses to inulin treatment. For C, D and L, significance was determined when 95% credible interval does not include 0.
4. Core ecological network constituted by significant inter-taxa interactions (self-interactions not shown). Point and blunt arrows represent positive and negative interactions respectively. The arrow thickness is proportional to the posterior mean of the corresponding interaction coefficient.
5. Relative abundance of the five inulin responders in C. The figure legend also applies to H and I.
6. Explanatory model for individualized responses in total bacterial density.
7. Spearman correlation between total bacterial density and relative abundance of the five inulin responders in C.
8. Scatter plots and linear regression lines (shading area: standard error of the mean) illustrating the relationship between relative abundance of *Bacteroides acidifaciens* and *unclassified Muribaculaceae* and total bacterial density.
9. Scatter plots and linear regression lines (shading area: standard error of the mean) illustrating the relationship between baseline relative abundance of the most correlated (positive or negative) species-level taxa and the time-averaged relative abundance of the two inulin responders in H.
10. Principle coordinate anlaysis (PCoA) of baseline human gut microbiota (Bray-Curtis distance matrix of 16S or shallow shotgun metagenomics) in four cohorts of literature studies with inulin intervention.
11. Relative abundance of two major bacterial phyla in the same samples shown in J.
12. Significant positive inulin responders identified from the four literature studies in J.