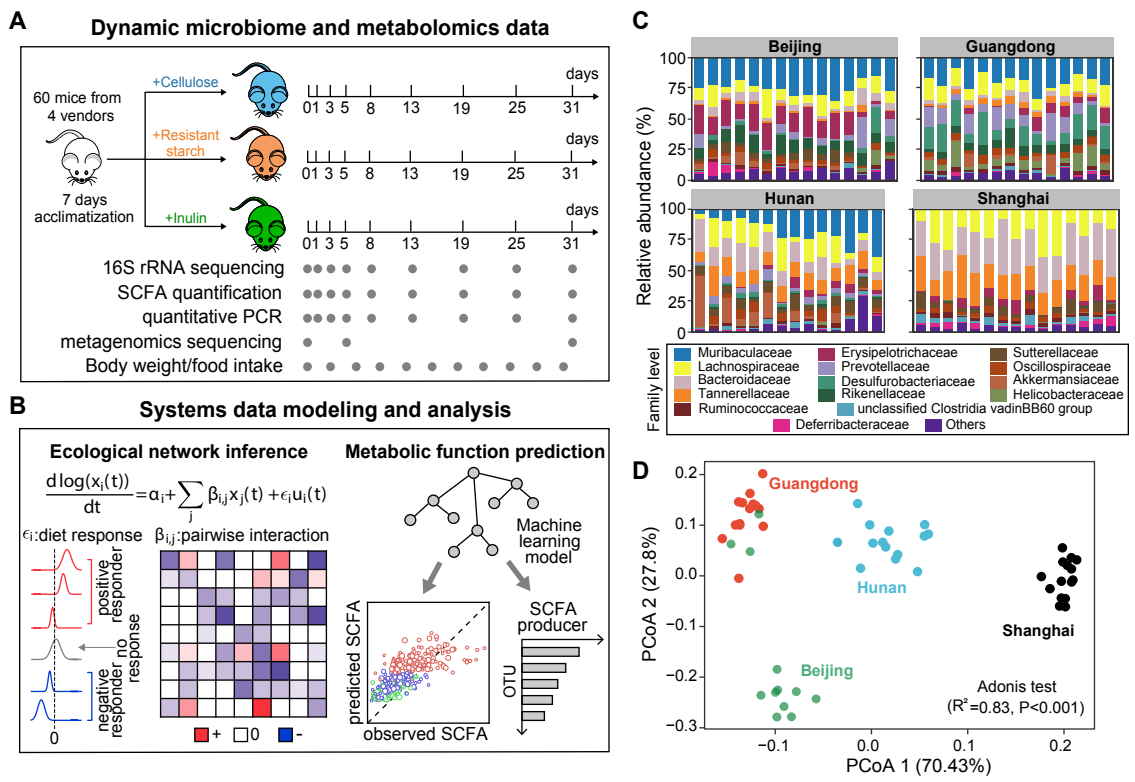
A
Dynamic microbiome and metabolomics data
60 mice from 4 vendors
7 days acclimatization
+Cellulose
+Resistant starch
+Inulin
days
01 3 5 8 13 19 25 31
16S rRNA sequencing
SCFA quantification
quantitative PCR
metagenomics sequencing
Body weight/food intake
B
Systems data modeling and analysis
Ecological network inference
Metabolic function prediction
ϵi:diet response
βi,j:pairwise interaction
positive responder
no response
negative responder
Machine learning model
SCFA producer
OTU
predicted SCFA
observed SCFA
+ 0 -
C
Beijing
Guangdong
Hunan
Shanghai
Relative abundance (%)
Family level
Muribaculaceae
Lachnospiraceae
Bacteroidaceae
Tannerellaceae
Ruminococcaceae
Erysipelotrichaceae
Prevotellaceae
Desulfurobacteriaceae
Rikenellaceae
unclassified Clostridia vadinBB60 group
Deferribacteraceae
Others
Sutterellaceae
Oscillospiraceae
Akkermansiaceae
Helicobacteraceae
D
Guangdong
Hunan
Shanghai
Beijing
Adonis test
(R2=0.83, P<0.001)
PCoA 1 (70.43%)
PCoA 2 (27.8%)