Metabolites of Gut Microbiome Are Associated With Glucose Metabolism in Non-diabetic Obese Adults: A Chinese Monozygotic Twin Study

Ke Yu
Capital Medical University
Cai-Guo Yu
Capital Medical University
Xing-Qi Yin
Capital Medical University
Zong-Wei Wang
Capital Medical University
Xiao-Bo Wang
Capital Medical University
Li-Li Wang
Capital Medical University
Shuang Guo
Capital Medical University
Ya-Xin An
Capital Medical University
Dong Zhao (zhaodong@ccmu.edu.cn)
Capital Medical University

Research Article

Keywords: Gut microbiome, glucose metabolism, twin study, obesity

Posted Date: June 30th, 2021

DOI: https://doi.org/10.21203/rs.3.rs-661792/v1

Abstract

Background

Evidence suggests gut microbiome is associated with diabetes. However, it's unclear whether this association remains in non-diabetic subjects. We conducted a monozygotic twin study, in which the participants are without diabetes, and are not taking any medications, to explore the potential association.

Methods

Nine pairs of adult monozygotic twins were enrolled and divided into two twin-pair groups (a and b). Clinical and laboratory measurements were conducted. Visceral adipose tissue (VAT) was assessed. Fecal samples were collected to analyze the microbiome composition by 16S rDNA gene amplicon sequencing. Liquid chromatography mass spectrometry was performed to detect the metabolites.

Results

The participants aged 53 years old averagely, with 8 (88.9%) pairs were women. All the participants were obese with VAT higher than 100 cm^2 (152.2±31.6). There was no significant difference of VAT between the twin groups (153.6±30.4 cm^2 vs. 150.8±29.5 cm^2, p=0.54). Other clinical measurements, including BMI, lipid profiles, fasting insulin and blood glucose, were also not significantly different between groups ($p \geq 0.056$), whereas HbA1c level of group a is significantly higher than group b(5.8±0.3 % vs. 5.6±0.2 %, p=0.008). The number and richness of OUTs are relatively higher in group a, and 13 metabolites were significantly different between two groups. Furthermore, several of the 13 metabolites could be significantly linked to special taxons. The potential pathway involved drug metabolism-other enzymes, Tryptophan metabolism and Citrate cycle.

Conclusion

Gut microbiome composition and their metabolites may modulate glucose metabolism in obese adults without diabetes, through Tryptophan metabolism, Citrate cycle and other pathways.

Background

Increasing evidence suggests the gut microbiome is associated with metabolic diseases, especially obesity and type 2 diabetes (T2D) [1-4]. However, the subjects of most previous studies [5-10] are diabetic or pre-diabetic patients, with different genetic background, and taking different kinds of anti-diabetic drugs, which may have confounding effects on the gut microbiome composition and fecal metabolites [11-13]. Thus, it's unclear whether this association remains in healthy or early subclinical status without obvious confounding factors. Monozygotic twins shared the same genotype and early environmental exposures, and thus, potentially similar gut microbiome composition [14]. We searched in PubMed using keywords as "gut microbiome" and "Twin", there were less than 35 results, among which only three are

relevant to the research issue addressed in this manuscript. Thus, in this Chinese monozygotic (MZ) twin study, in which the twins grow up in the same family, are without known diabetes, are not taking antibiotics or other medications that may influence the gut microbiome, we explore the potential association of gut microbiome with glucose metabolism in healthy obese subjects.

Methods

Study participants

Nine pairs of adult MZ twins who were native residents in Tongzhou District of Beijing were enrolled in our study. The twin pairs grow up in the same family, are without diagonsed diabetes, and are not taking antibiotics or other medications that may influence the gut microbiome in the last two weeks before they came to hospital. The twin pairs were excluded as long as one of them is pregnant, or with tumor history, or with mental disease, or with recent history of diarrhea or intestinal infection.

All participants signed the informed consent. The study complied with the Helsinki Declaration for investigation of humans. The Ethics Committee of Capital Medical University, China, approved the protocols of this study.

Clinical and laboratory measurements

The nurses first administered questionnaires, inquiring into each participant's medical history, smoking and drinking habits, and intake of medications. Then, venous blood samples were obtained after 8 to 10 hours of fasting. Blood samples were analyzed for serum levels of glucose, insulin, triglycerides, total low-density lipoprotein (LDL) and high-density lipoprotein (HDL) cholesterol, glutamic-pyruvic transaminase enzyme (ALT), glutamic-oxaloacetic aminotransferase(AST), gamma-glutamyltransferase(GGT), and serum creatinine. Physical examinations were also performed, including, body weight, body height, waist and hip circumference. Visceral adipose fat (VAT) were evaluated for each participant (Inbody 770, Biospace Co. Ltd.).

Blood samples were also obtained and sent to Beijing Genomics Institute to extract DNAs and identify the egg type. Short tandem repeats were applied to identify and confirm the egg type.

Microbiome composition analysis

Total genome DNA from fecal samples was extracted using Soil DNA Kit according to manufacturer's protocols. DNA concentration was monitored by Qubit® dsDNA HS Assay Kit.

20-30ng DNAs was used to generate amplicons.V3 and V4 hypervariable regions of prokaryotic 16S rDNA were selected for generating amplicons and following taxonomy analysis. The concentration of DNA library was validated by Qubit3.0 Fluorometer. Quantify the library to 10nM, DNA libraries were multiplexed and loaded on an Illumina MiSeq or NovaSeq instrument according to manufacturer's

instructions (Illumina, San Diego, CA, USA). Sequencing was performed using paired-end. Image analysis and base calling were conducted by the Control Software embedded in the instrument.

The effective sequences were used in the final analysis. Sequences were grouped into operational taxonomic units (OTUs) using the clustering program VSEARCH（1.9.6） against the UNITE ITS database (https://unite.ut.ee/) pre-clustered at 97% sequence identity. The Ribosomal Database Program (RDP) classifier was used to assign taxonomic category to all OTUs at confidence threshold of 0.8. The RDP classifier uses the UNITE ITS database which has taxonomic categories predicted to the species level.

Fecal metabolites analysis

We detected metabolites, including methanol, acetonitrile, 2-chlorophenylalanine, formic acid, ammonium formate and ddH_2O, based on liquid chromatography mass spectrometry (LC/MS) in faecal samples.

Fecal samples were thawed at 4℃. 100 μL of each sample was transferred into 1.5 ml centrifuge tubes, and 400μL of methanol (pre-cooled at -20℃) were added to each tube and vortex for 60 s. Then, the mixtures were centrifuged for 10 min at 12 000 rpm 4℃ and all supernatant in each tube was transferred into another 1.5 mL centrifuge tube, and samples were blow-dried by vacuum concentration. The processed supernatant was dissolved with 150μL 2-chlorobenzalanine (4ppm) methanol aqueous solution (4℃),and filtered through a 0.22 μm membrane to obtain the prepared sample extracts for LC-MS.

Chromatographic separation was accomplished in an Thermo Ultimate 3000 system equipped with an ACQUITY UPLC® HSS T3 (150×2.1 mm, 1.8 μm, Waters) column maintained at 40℃. The temperature of the autosampler was 8℃. Gradient elution of analytes was carried out with 0.1% formic acid in water (C) and 0.1% formic acid in acetonitrile (D) or 5mM ammonium formate in water (A) and acetonitrile (B) at a flow rate of 0.25mL/min. Injection of 2μL of each sample was done after equilibration. An increasing linear gradient of solvent B (v/v) was used as follows: 0~1 min, 2% B/D；1~9 min, 2%~50% B/D; 9~12 min, 50%~98% B/D；12~13.5 min；98% B/D；13.5~14 min；98%~2% B/D; 14~20 min, 2% D-positive model (14~17 min, 2% B-negative model).

The ESI-MSn experiments were executed on the Thermo Q Exactive Focus mass spectrometer with the spray voltage of 3.8 kV and -2.5 kV in positive and negative modes, respectively. Sheath gas and auxiliary gas were set at 45 and 15 arbitrary units, respectively. The capillary temperature was 325 ℃. respectively. The Orbitrap analyzer scanned over a mass range of m/z 81-1 000 for full scan at a mass resolution of 70 000. Data dependent acquisition (DDA) MS/MS experiments were performed with HCD scan. The normalized collision energy was 30 eV. Dynamic exclusion was implemented to remove some unnecessary information in MS/MS spectra.

Statistical analysis

Database management and statistical analysis were done using SAS 9.4 software (Cary, NC). The central tendency (spread) was represented by the arithmetic mean (SD). To compare means and proportions, we applied paired t-test and the c2-statistic, respectively. Significance was a 2-tailed a-level of 0.05 or less.

Table 1. Characteristics of Participants

Characteristic	Different Twin Pairs		
	Group a	Group b	*P* Value
Number	9	9	
Number (%) with characteristic			
Women	8 (88.9)	8 (88.9)	/
Current drinking	1(11.1)	1(11.1)	/
Current smoking	1(11.1)	1(11.1)	/
Mean of characteristic			
Age, years	53.0±8.6	53.0±8.6	/
Body mass index, kg/m2	29.7±3.4	28.8±3.2	0.056
Visceral fat, cm^2	153.6±30.4	150.8±29.5	0.54
HbA1c, %	5.8±0.3	5.6±0.2	0.008†
Plasma glucose, mmol/L	5.82±0.71	5.58±0.34	0.29
Serum insulin, mU/L	11.7±4.4	12.0±3.0	0.77
Triglyceride, mmol/L	1.66±0.63	1.53±0.54	0.60
Total cholesterol, mmol/L	5.15±1.22	4.21±0.97	0.16
HDL cholesterol, mmol/L	1.25±0.23	1.23±0.11	0.76
LDL cholesterol, mmol/L	3.34±0.96	2.90±0.50	0.27
ALT, U/L	24.9±11.1	21.8±10.2	0.074
AST, U/L	20.6±7.6	20.1±11.4	0.82
GGT, U/L	21.9±8.8	20.3±8.4	0.13
Serum creatinine, μmol/L	63.0±8.2	64.8±9.1	0.21

Abbreviations: HDL, high-density lipoprotein; For continuously distributed variables, reported values are arithmetic (±SD). Significance of the difference with the adjacent left column: * $P \leq 0.05$; † $P \leq 0.01$; ‡

$P \leq 0.001$.

Results

Characteristics and glucose levels of participants

Nine obese twin pairs without diabetes were enrolled in this study, aged 53 years old averagely, with 8 (88.9%) pairs were women. The twins were divided to two groups (a vs. b) during analysis. All of the participants were obese with VAT higher than 100 cm^2 (152.2±31.6), and there was no difference between the twin groups (153.6±30.4 cm^2 vs. 150.8±29.5 cm^2, P=0.54). However, the HbA1c levels is significantly different, averaged 5.8±0.3 % *vs.* 5.6±0.2 % (P=0.008). Fasting blood glucose and body mass index averaged 5.82±0.71 vs. 5.58±0.34 mmol/L (P=0.29), 29.7±3.4 vs. 28.8±3.2 (P=0.056), respectively. The other characteristics of participants were described in Table 1.

Differences of gut microbiome composition

Two hundred and seventy-nine OTUs were detected in all samples. The twin groups shared 249 same OTUs, with 18 unique OTUs for group a and 12 for group b (Figure 1, panel A). Thirty OTUs with the highest richness in each participant were displayed in the clustered heatmap, with the depths of colors representing the richness (Figure 1, panel B). The corresponding top five taxons were k__Bacteria, p__Firmicutes, c__Clostridia, o__Clostridiales and f__Lachnospiraceae.

Differences of fecal metabolite profiles

Thirteen metabolites were significantly different between two groups (Figure 2), which includes anabasine, DDAO, lumazine, S-Allyl-L-cysteine, citric acid, alloxan, indoleacetic acid, mercaptopurine, methyl jasmonate, N-methyl-L-glutamic acid, N-Methyldioctylamine, n-Pentadecylamine, and Salicylic acid. The first four metabolites were significantly lower in gourp a, while the others were significantly higher.

We preformed correlation analysis between the above 13 metabolites with Pearson Correlation Coefficient. 19 significant correlations were detected between each two metabolites. Four significant correlations were detected for n-Pentadecylamine, three for alloxan, anabasine and DDAO and two for mercaptopurine (Figure 2).

Pathway impacts were also performed, and we found seven potential pathway related with gut microbiome and the metabolites. Three with greatest impacts were Drug metabolism -other enzymes, Tryptophan metabolism and Citrate cycle, with impacts from 0.048 to 0.11 (Figure 3).

Correlation analysis of gut microbiome and metabolites

We performed correlation analysis to explore the potential associations of significantly different metabolites with special taxons. Twenty significant associations were found at family levels, with five

were found for o__Coriobacteriales_Unclassified (with N-methyl-L-glutamic acid, Alloxan, Mercaptopurine, Citric acid and Anabasine) (Figure 4).

Discussion

In this study, we aimed to explore whether the gut microbiome composition and the metabolites are associated with the glucose metabolism in nine obese MZ twin parirs without history of diabetes. The twins were divided into group a and group b. There was no significant differences for VAT or BMI or other characteristic between these two groups, whereas the level of HbA1c is significantly higher in group a. 16S rDNA-based high-throughput sequencing and LC/MS were performed in 18 fecal samples from these nine MZ twin pairs. Analysis showed that the number and richness of OUTs are relatively higher in group a, and 13 metabolites were significantly different between two groups. Furthermore, several of the 13 metabolites were significantly associated with special taxons, which indicated that the gut microbiome may modulate the glucose metabolism through the gut microbiome composition and their metabolites. The potential pathway involved Drug metabolism -other enzymes, Tryptophan metabolism and Citrate cycle.

Previous studies performed in diabetic patients with different ethnicities mostly suggested the gut microbiome composition changes are associated with the onset or the development of the disease. However, the differential communities or taxons are in consistent. Three Chinese studies were conducted in participants at different stages of glucose intolerance status: normal glucose tolerance (NGT), prediabetes (Pre-DM), and T2DM patients. Zhang et al. [5] analyzed 121 subjects: 44 NGTs, 64 Pre-DMs and 13 newly diagnosed T2DM. Results showed that Verrucomicrobiae had a significantly lower abundance in both the pre-DM and T2DM groups. Zhao et al. [8] performed analysis T2DM patients with or without complications, and the healthy controls. Results suggested higher abundance of Proteobacteria and higher ratio of Firmicutes/Bacteroidetes in T2DM patients. Zhong et al. [7] explored the gut metagenomics and metaproteomics signatures in Pre-DMs, T2DMs without treatment and NGTs. They found a significantly higher abundance of Megasphaera elsdenii (MLG-1568) in both T2DMs and Pre-DMs than in NGTs. A recent African study [10] also revealed that gut microbiota composition is associated with T2DM, with identification of higher richness of Desulfovibrio piger, Prevotella, Peptostreptococcus, and Eubacterium in T2DM group. Bhute et al. [6] assessed gut microbial diversity in 49 Indian participants who were also divided into three groups: New-DMs, Known-DMs and healthy subjects. Results indicated that microbial dysbiosis may not be just limited to eubacteria in diabetes, which may also extend into other two domains leading to trans-domain dysbiosis in microbiota. Another recent study conducted by Gaike et al. [9] suggested that gut microbial diversity of newly diagnosed T2DMs is significantly different from that of NGTs, whereas this difference was not observed between the Pre-DM group and NGT group. The inconsistent microbiota composition results from these above studies indicate the complexity of gut microbiome changes in human subjects. On the other hand, it may also indicate the potential interference of various confounding factors, such as the genotype, the different environment exposures and the ethnity.

A Korean MZ twin study [15] conducted gut microbiome analysis in 20 MZ twins nor obese or diabetic, with 36 fecal samples collected. They analyzed the association of changes in microbiome composition with different factors, such as BMI and glucose levels, in all 36 fecal samples. Results suggested the decrease in Akkermansia muciniphila may occur prior to the onset of diabetes, and strain-level differences in composition was observed despite of species-level similarities in the twin pairs.

The potential mechanisms of the gut microbiota and glucose metabolism mainly involves several metabolites [16], including beneficial metabolites, such as short-chain fatty acids (SCFAs), sulfur-containing amino acids, bile acids, and indole derivatives, and also potentially harmful metabolites, such as branched-chain amino acids(BCAAs) and lipopolysaccharide (LPS).

In the current study, anabasine, DDAO, lumazine, S-Allyl-L-cysteine were identified to be lower, while citric acid, alloxan, indoleacetic acid, mercaptopurine, methyl jasmonate, N-methyl-L-glutamic acid, N-Methyldioctylamine, n-Pentadecylamine, and Salicylic acid were higher in group a with higher HbA1c levels. And some of the above metabolites could be linked to special taxons, which indicated that the impaired glucose metabolism may be associated with gut micorbiome composition and their metabolites.

In comparison with previous studies, our current study was performed in MZ twins. The participants shared same genetic background and grow-up environment, and none of them was taking any medications when enrolled in this study, which can eliminate the effect of medications on gut microbiome. Thus, the design of our study is more favorable to identify the unique microbial changes and to explore the potential taxons and their metabolites associated with the development or prevention of impaired glucose metabolism. Nevertheless, our current findings must be interpreted within the context of their limitations. First, the sample size is relatively small. Second, most of the participants are female, the gender bias cannot be excluded. Third, the study design is cross-sectional, which cannot make causal explanations.

Conclusion

Results of our study indicate that the higher levels of HbA1c in the twin pairs may be associated with some metabolites of the gut microbiome, including anabasine, DDAO, lumazine, S-Allyl-L-cysteine, citric acid, alloxan, indoleacetic acid, mercaptopurine, methyl jasmonate, N-methyl-L-glutamic acid, N-Methyldioctylamine, n-Pentadecylamine, and Salicylic acid. And some of the above metabolites could be significantly linked to special taxons, which indicated that the impaired glucose metabolism may be associated with gut micorbiome composition and their metabolites. The potential pathway involved Drug metabolism -other enzymes, Tryptophan metabolism and Citrate cycle.

Declarations

Ethics approval and consent to participate

The Ethical Committee of Beijing Luhe Hospital, Capital Medical University granted ethical approval to of this study. Written informed consent was obtained from all patients included in the study.

Consent for publication

Not applicable.

Availability of data and materials

The data of this study is available on request.

Competing interests

The authors have no conflicts of interest.

Funding

No funding was received for this work.

Authors' contributions

Dong Zhao and Ke Yu designed and conducted the study. Ke Yu and Cai-Guo Yu analyzed the data and drafted the manuscript. Xing-QI Yin, Li-Li Wang, and Shuang Guo collected and collated clinical and laboratory data. Zong-Wei Wang and Xiao-Bo Wang completed the clinical laboratory tests. Ya-Xin An reviewed the manuscript.

Acknowledgements

The authors gratefully acknowledge the study participants and nursing staff involved in this study.

References

1. Clemente JC, Ursell LK, Parfrey LW, Knight R. The impact of the gut microbiota on human health: an integrative view. Cell. 2012;148(6):1258–70.

2. Jackson MA, Verdi S, Maxan ME, Shin CM, Zierer J, Bowyer RCE, et al. Gut microbiota associations with common diseases and prescription medications in a population-based cohort. Nature communications. 2018;9(1):2655.

3. Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, et al. A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature. 2012;490(7418):55–60.

4. Karlsson FH, Tremaroli V, Nookaew I, Bergstrom G, Behre CJ, Fagerberg B, et al. Gut metagenome in European women with normal, impaired and diabetic glucose control. Nature. 2013;498(7452):99–103.

5. Zhang X, Shen D, Fang Z, Jie Z, Qiu X, Zhang C, et al. Human gut microbiota changes reveal the progression of glucose intolerance. Plos one. 2013 ;8(8):e71108.

6. Bhute SS, Suryavanshi MV, Joshi SM, Yajnik CS, Shouche YS, Ghaskadbi SS. Gut Microbial Diversity Assessment of Indian Type-2-Diabetics Reveals Alterations in Eubacteria, Archaea, and Eukaryotes. Frontiers in Microbiology. 2017;8:214.

7. Zhong H, Ren H, Lu Y, Fang C, Hou G, Yang Z, et al. Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. EBioMedicine. 2019;47: 373–83.

8. Zhao L, Lou H, Peng Y, Chen S, Zhang Y, Li X. Comprehensive relationships between gut microbiome and faecal metabolome in individuals with type 2 diabetes and its complications. Endocrine, 2019; 66(3):526-37.

9. Gaike AH, Paul D, Bhute S, Dhotre DP, Pande P, Upadhyaya S, et al. The Gut Microbial Diversity of Newly Diagnosed Diabetics but Not of Prediabetics Is Significantly Different from That of Healthy Nondiabetics. mSystems. 2020;5(2):e00578-19.

10. Doumatey AP, Adeyemo A, Zhou J, Lei L, Adebamowo SN, Adebamowo C, et al. Gut Microbiome Profiles Are Associated With Type 2 Diabetes in Urban Africans. Front Cell Infect Microbiol. 2020;10:63.

11. Wu H, Esteve E, Tremaroli V, Khan MT, Caesar R, Mannerås-Holm L, et al. Metformin alters the gut microbiome of individuals with treatment-naive type 2 diabetes, contributing to the therapeutic effects of the drug. Nat Med 2017;23(7):850–58.

12. Moreira GV, Azevedo FF, Ribeiro LM, Santos A, Guadagnini D, Gama P, et al. Liraglutide modulates gut microbiota and reduces NAFLD in obese mice. J Nutr Biochem 2018;62:143-54.

13. Liao X, Song L, Zeng B, Liu B, Qiu Y, Qu H, et al. Alteration of gut microbiota induced by DPP-4i treatment improves glucose homeostasis. EBioMedicine 2019;44:665-74.

14. Turnbaugh PJ, Hamady M, Yatsunenko T, Cantarel BL, Duncan A, Ley RE, et al. A core gut microbiome in obese and lean twins. Nature. 2009;457(7228):480-84.

15. Yassour M, Lim MY, Yun HS, Tickle TL, Sung J, Song YM, et al. Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. Genome Med. 2016;8(1):17.

16. Khan MT, Nieuwdorp M, Backhed F. Microbial modulation of insulin sensitivity. Cell Metab. 2014;20(5):753–60.

Figures

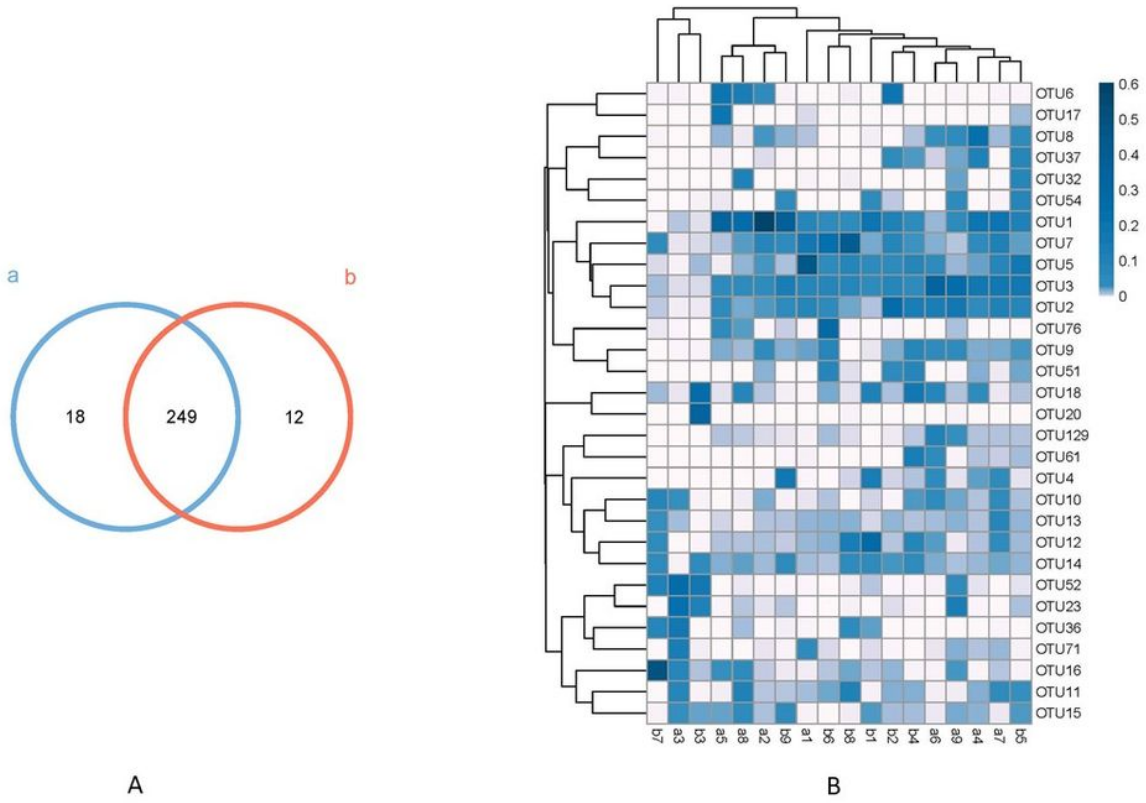

Figure 1

OTUs in groups and participants. In Panel A, different colors of circles represent different group, and the numbers represent the shared and unique OTUs for two groups. In Panel B, 30 OTUs with the highest richness in each participant were displayed in the clustered heatmap. The depths of colors representing the richness of OTUs. The row name is OUT ID, and the column name represents each participant in different twin groups.

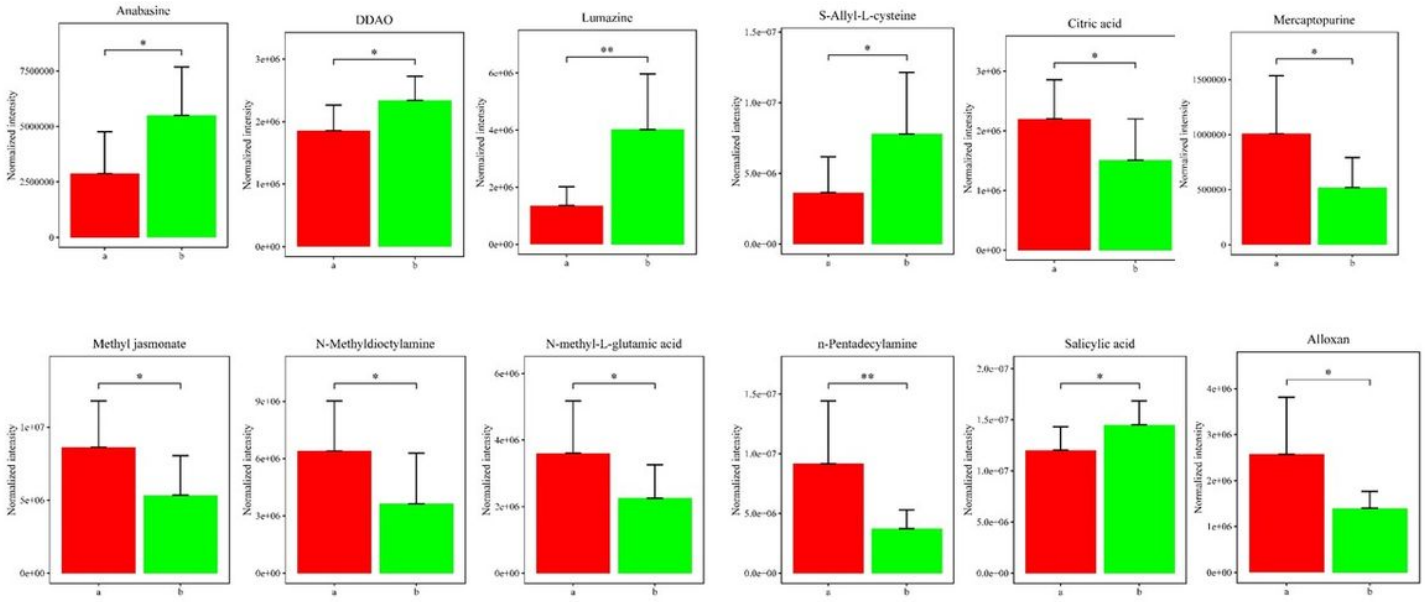

Figure 2

Fecal metabolites with significantly differences between groups (a vs. b). * P ≤ 0.05.

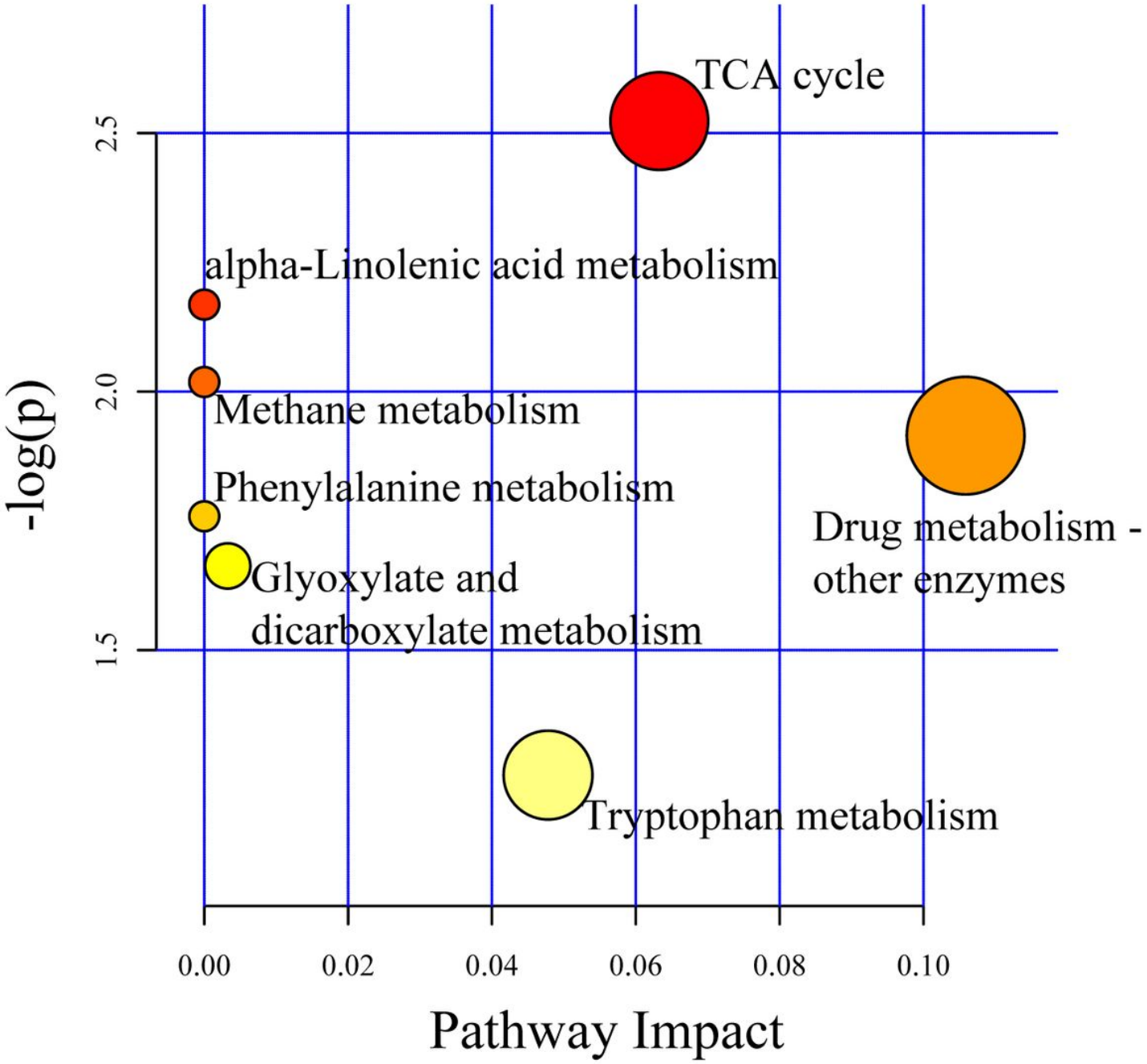

Figure 3

Pathway impact factors of seven potential metabolic pathways. The X-axis is the impact factor for each pathway, and the Y-axis is the log transformation of p value.

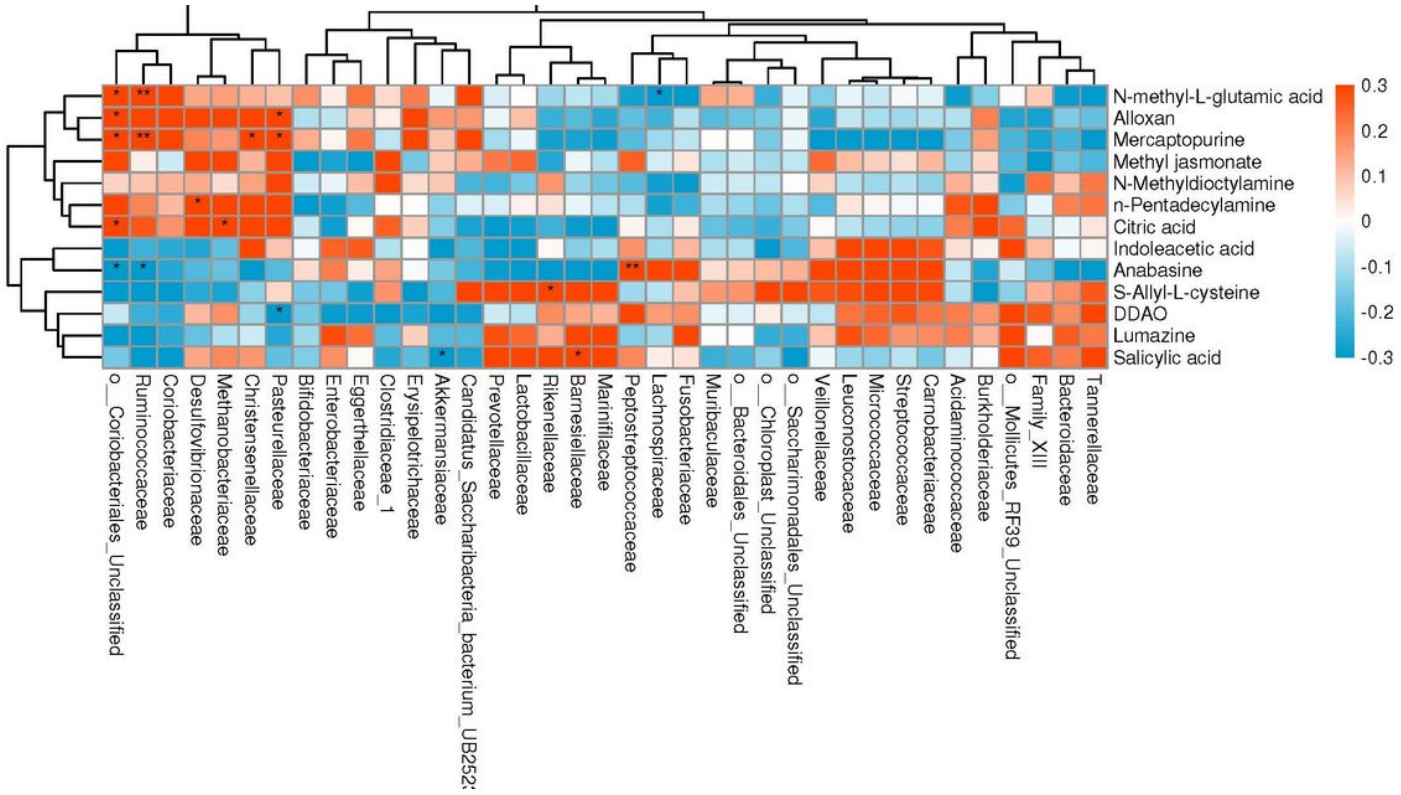

Figure 4

Correlation analysis of metabolites and taxons at family levels. *P ≤ 0.05, **P ≤ 0.01