Effect of Metformin on Metabolic Improvement and Gut Microbiota

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Metformin is commonly used as the first line of medication for the treatment of metabolic syndromes, such as obesity and type 2 diabetes (T2D). Recently, metformin-induced changes in the gut microbiota have been reported; however, the relationship between metformin treatment and the gut microbiota remains unclear. In this study, the composition of the gut microbiota was investigated using a mouse model of high-fat-diet (HFD)-induced obesity with and without metformin treatment. As expected, metformin treatment improved markers of metabolic disorders, including serum glucose levels, body weight, and total cholesterol levels. Moreover, Akkermansia muciniphila (12.44% ± 5.26%) and Clostridium cocleatum (0.10% ± 0.09%) abundances increased significantly after metformin treatment of mice on the HFD. The relative abundance of A. muciniphila in the fecal microbiota was also found to increase in brain heart infusion (BHI) medium supplemented with metformin in vitro. In addition to the changes in the microbiota associated with metformin treatment, when other influences were controlled for, a total of 18 KEGG metabolic pathways (including those for sphingolipid and fatty acid metabolism) were significantly upregulated in the gut microbiota associated with metformin treatment, when other influences were controlled for, a total of 18 KEGG metabolic pathways (including those for sphingolipid and fatty acid metabolism) were significantly upregulated in the gut microbiota associated with metformin treatment, when other influences were controlled for, a total of 18 KEGG metabolic pathways (including those for sphingolipid and fatty acid metabolism) were significantly upregulated in the gut microbiota associated with metformin treatment, when other influences were controlled for, a total of 18 KEGG metabolic pathways (including those for sphingolipid and fatty acid metabolism) were significantly upregulated in the gut microbiota associated with metformin 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by pathologists for pathological analysis of steatosis and inflammation (Reference Biolabs, Seoul, South Korea). Extended steatosis was diagnosed pathologically and given a score of from 0 to 3, as follows: 0 for no involvement, 1 for mild involvement, 2 for moderate involvement, and 3 for severe involvement (13). In addition, immunohistochemistry for analysis of the mucosa of the small intestine was performed by a commercial company (Reference Biolabs, Seoul, South Korea) using anti-MUC5AC antibody (LifeSpan BioSciences, Inc.).

**Metabolic and inflammatory biomarkers for the evaluation of metabolic disorders.** Hepatic AMP-activated protein kinase alpha 1 (AMPKα1), peroxisome proliferator-activated receptor alpha (PPARα), glucose transporter 2 (GLUT2), and glucose-6-phosphatase (G6Pase) levels were determined. In addition, the levels of adiponectin, leptin, mono-cyte chemoattractant protein 1 (MCP-1), tumor necrosis factor alpha (TNF-α), and interleukin-6 (IL-6) in fat pads were analyzed. The pattern of expression of the MUC2 and MUC5 genes in the ileum was analyzed. Tissues (~100 mg) were homogenized completely prior to RNA extraction. Total RNA was extracted using an Easy-Spin total RNA extraction kit (iNTRON, Sungnam, South Korea), and cDNA synthesis was performed using a high-capacity RNA-to-cDNA kit (Applied Biosystems) according to the manufacturer’s instructions. To quantify the levels of mRNA for metabolic and inflammatory biomarkers, a QuantiTect SYBR green PCR kit (Qiagen) and 7300 real-time PCR system (Applied Biosystems) were used. GAPDH (glyceraldehyde-3-phosphate dehydrogenase) was used as the internal control.

Next-generation sequencing of gut microbiota and the bioinformatics pipeline. Total DNA was extracted from frozen feces using a QIAamp DNA stool minikit (Qiagen) and a QIAcube system (Qiagen). For each sample, 16S rRNA genes were amplified using the 27F/534R primer set targeting the V1-V3 region (for 27F, forward primer 5'–AACAGCGCCAGCGCTGCTGCTGG-3'; for 534R, a reverse primer containing a unique 10-nucleotide bar code for tagging each PCR product designated NNNNNNNNNN, 5’–CATCCTACCTCCCTGCTGCTTCTCGAGAGTTTGATCCCTGGTACCTGGCTCAG-3’ [boldface nucleotides are specific sequences of 27F/534R primers]) (14). The amplified PCR products were purified using a QIAquick PCR purification kit (Qiagen). Bacterial 16S rRNA pyrosequencing was performed by a commercial company (Macrogen Inc., Seoul, South Korea) using a GS-FLX system (Roche). To analyze the 16S rRNA sequence, quality filtering, including determination of the sequence length (≥200 bp), end trimming, and determination of the number of ambiguous bases and the minimum quality score, was performed. Sequences were then assigned to operational taxonomic units (OTUs; 97% identity), followed by the selection of representative sequences using the QIME software package (Quantitative Insights into Microbial Ecology) (15). We next examined the alpha and beta diversity and performed a UniFrac analysis and a principal coordinate analysis (PCoA). Linear discriminant analysis of the effect size (LEfSe) was used to estimate taxonomic abundance and characterize differences between groups (16). The UniFrac distance between categorized samples was visualized using Cytoscape software (v2.8.3). In addition, phylogenetic investigation of communities by reconstruction of unobserved states (PICRUSt) was performed to identify functional genes in the sampled microbial community on the basis of the data in the KEGG pathway database (17).

**Cultivation of A. muciniphila in BHI with metformin.** Stool samples from the HFD-Met group were inoculated in brain heart infusion (BHI) broth supplemented with 0.1 M metformin and phenformin and incubated in an anaerobic chamber. At 3 and 6 h postincubation, total DNA was extracted using an Easy-Spin total DNA extraction kit (iNTRON, Sungnam, South Korea). Quantification of *A. muciniphila* and total bacteria was performed using SYBR quantitative PCR (qPCR) and TaqMan qPCR, respectively (18, 19).

**Statistical analysis.** All parameters were expressed as the average and standard deviation of each group. To quantify metabolic and inflammatory biomarker levels, qPCR was performed in triplicate. The 2−ΔΔCT relative quantification method, where C_T is the threshold cycle and where ΔΔCT = CT_T, target − CT_T, GAPDH/group 1 − (CT_T, target − CT_T, GAPDH/group 2), was used to assess the level of biomarker gene expression compared to the level of GAPDH expression as an internal control. Statistical significance was assessed by one-way analysis of variance, followed by Duncan’s post hoc test, with P values of <0.05 considered to indicate significance. On the basis of the relative abundance analysis using LEfSe and on the basis of the results of the Kruskal-Wallis and Wilcoxon tests, a P value of <0.05 was considered to indicate statistical significance, and the threshold on the logarithmic linear discriminant analysis (LDA) score was 3.0 to 4.0. Spearman’s correlation coefficient was calculated to identify correlations between metabolic/inflammatory biomarkers and bacterial abundance.

**RESULTS**

**Metabolic biomarker levels after a dietary change or metformin treatment.** Figure 1 shows the changes in body weight and glucose, TC, and HDL levels due to diet and metformin treatment. The body weight of mice on an HFD increased significantly over 28 weeks compared with the body weight of mice on an ND. As expected, body weight significantly decreased after a dietary change from an HFD to an ND after 18 weeks (Fig. 1A). In contrast, body weight remained constant after metformin treatment, despite continuation of the high-fat diet (Fig. 1A). The serum glucose level significantly increased in both male (*P* < 0.001) and female (*P* = 0.001) mice on an HFD, and the serum glucose level decreased after either a dietary change to an ND (*P* = 0.032) or metformin treatment (*P* = 0.016), especially in female mice (Fig. 1B). Impaired glucose tolerance, which is known to be a risk factor for T2D, was measured by OGTTs and was found to decrease significantly after a dietary change from an HFD to an ND in both male (*P* = 0.036) and female (*P* = 0.008) mice but was unaffected by metformin treatment (Fig. 1B). In addition, the homeostatic model assessment-insulin resistance (HOMA-IR), estimated on the basis of the glucose and insulin levels, showed a trend to reduced insulin resistance after a change from an HFD to an ND or metformin treatment, but these changes were not statistically significant (Fig. 1C). In addition, the homeostatic model assessment-beta cell function (HOMA-β) did not show significant differences after either a change from an HFD to an ND or metformin treatment in mice. TC levels decreased significantly after a dietary change from an HFD to an ND in both male (*P* < 0.001) and female (*P* < 0.001) mice. The effects of metformin treatment on the TC level differed depending on the gender of the mice. The TC level significantly decreased in female mice (*P* = 0.023) but not male mice (*P* = 0.875). HDL levels also significantly decreased after a change from an HFD to an ND in both male (*P* < 0.001) and female (*P* = 0.001) mice and decreased after metformin treatment in both male (*P* = 0.055) and female (*P* = 0.055) mice. Metformin treatment had no effect on the metabolic biomarker levels in the ND group.

**Effects of diet and metformin treatment on patterns of metabolic and inflammatory biomarker expression.** Figure 2 shows the relative levels of expression of various metabolic and inflammatory biomarkers in the liver and fat pads. The effects of metformin treatment and an HFD on liver tissue in mice differed according to gender. A dietary change from an HFD to an ND significantly reduced the levels of AMPKα1 (*P* < 0.001), PPARα...
(P = 0.003), and GLUT2 (P = 0.024) expression and increased those of G6Pase expression (P = 0.003) in female mice. In contrast, a dietary change from an HFD to an ND significantly reduced the level of G6Pase expression (P = 0.001) in male mice. Metformin treatment of mice on the HFD significantly decreased the levels of expression of both AMPKα(1 (P = 0.003) and GLUT2 (P = 0.013) and increased the levels of expression of PPARα (P = 0.010) in female mice. In contrast, metformin treatment and an HFD significantly reduced G6Pase expression (P < 0.001) in male mice.

In fat pads, a dietary change from an HFD to an ND significantly reduced the levels of MCP-1 (P < 0.001), TNF-α (P < 0.001), and IL-6 (P < 0.001) expression and increased the level of adiponectin expression (P < 0.001), as shown in Fig. 2B. Metformin treatment of mice on an HFD significantly reduced the level of TNF-α expression (P < 0.001) in female mice and increased the level of MCP-1 expression (P < 0.001) in male mice.

Mucin expression and histological changes in the small intestine and liver due to metformin treatment. Mucin levels were estimated on the basis of MUC2 and MUC5 expression in the small intestine. Expression of the genes for both proteins increased significantly after metformin treatment in female mice (for MUC2, P = 0.003; for MUC5, P = 0.010) but not in male mice (for MUC2, P = 0.110; for MUC5, P = 0.884) (Fig. 3A). These results are consistent with the histological data. Thickened intestinal mucosa was confirmed by immunohistochemical assays using an anti-MUC5AC antibody (Fig. 3B).

The weights of the livers of the mice in the HFD-ND and HFD-
Met groups differed significantly from the weights of the livers of the mice in the HFD group for both male mice (for the HFD-ND group, \( P = 0.036 \); for the HFD-Met group, \( P = 0.036 \)) and female mice (for the HFD-ND group, \( P = 0.095 \); for the HFD-Met group, \( P = 0.095 \)) (Fig. 3C). Severe steatosis of the liver in the HFD group was recovered by either a dietary change to an ND or metformin treatment (Fig. 3D). There was no difference in the inflammation scores between the HFD-ND and HFD-Met groups (data not shown).

**Characterization of gut microbiota.** To characterize the composition of the gut microbiota, a total of 302,689 sequences were generated from 40 stool samples. Among them, 238,522 sequences were obtained after quality filtering, with an average of 5,963 sequences being recovered per sample. Figure 4 shows differences in microbial diversity among the HFD, HFD-ND, and HFD-Met groups. The alpha diversities of the gut microbiota of these three groups decreased significantly in the order HFD group, HFD-ND group, and HFD-Met group (Fig. 4A). Unlike the HFD group, metformin treatment had no significant effect on the alpha diversity of the gut microbiota in the ND group (Fig. 4A). PCoA based on phylogenetic analysis indicated clustering of the gut microbiota within groups. PCoA of both unweighted and weighted UniFrac distances showed a clear separation of the HFD, HFD-Met, and HFD-ND groups, while no separation between the ND and ND-Met groups was observed (Fig. 4B). Furthermore, the UniFrac distance of the bacterial communities between the HFD and HFD-Met groups was considerably higher than that of the bacterial communities between the ND and ND-Met groups. In contrast, the distance between the bacterial communities of the HFD-Met and ND-Met groups was considerably higher than that between the bacterial communities of the HFD-ND and ND groups (Fig. 4C).

**Relative abundance of the gut microbiota after metformin treatment.** The composition of the phylum *Bacteroidetes* in the HFD group (43.79\% \( \pm 22.35\% \)) was significantly lower than that in the ND group (79.40\% \( \pm 10.00\% \)) (Fig. 4D). In contrast, the composition of the phylum *Firmicutes* was significantly higher in the HFD group (50.73\% \( \pm 19.20\% \)) (Fig. 4D). When metformin was administered to the HFD group, the composition of the phylum *Bacteroidetes* increased to 77.45\% \( \pm 8.73\% \), which was similar to that in the ND group (Fig. 4D). Additionally, the composition of the phylum *Verrucomicrobia* (12.44\% \( \pm 5.26\% \)) in the HFD-Met group significantly increased, unlike the effect of a dietary change from an HFD to an ND (Fig. 4D). In the HFD-Met group, the abundances of the families *Bacteroidaceae*, *Verrucomicrobiaceae*, and *Clostridiaceae* family XIII, *incertae sedis*, as well as *A. muciniphila* and *Clostridium cocleatum* changed significantly compared with those in the HFD and HFD-ND groups (Fig. 4E). Metformin treatment also affected the composition of the gut microbiota in mice fed an ND. The families *Rikenellaceae*, *Rumino cocciaceae*, and *Verrucomicrobiaceae*, as well as *Alistipes* spp., *Akkermansia* spp., and *Clostridium* spp., were more abundant in the ND-Met group than the ND group (Fig. 4F).

Differences in the gut microbiota between male and female mice were also examined. In the HFD group, the phylum *Bacteroidetes* was more abundant in female mice than male mice (Fig. 5A). In addition, the phylum *Tenericutes* was abundant in males of the HFD-ND group and *Parabacteroides* spp. were abundant in females of the ND group (Fig. 5C and D). In the HFD-Met group, *Coprobacillus* spp. were more abundant in males, while *Clostridi um* spp., *Bacteroides* spp., and members of the family *Lactobacillaceae* and the class *Bacteroidia* were more abundant in female mice (Fig. 5B). No significant difference between male and female mice in the ND-Met group was observed.

**Changes in the metabolic pathways of the gut microbiota during metformin treatment.** A total of 245 KEGG pathways were generated using the composition of the gut microbiota based on PICRUSt. PCoA plots clearly showed clustering of five groups according to diet and metformin treatment (Fig. 6A). Thirty KEGG pathways were significantly upregulated in the HFD-Met group compared with their levels of regulation in the HFD group. Among them, we excluded KEGG pathways related to a dietary change only (HFD-ND) and metformin treatment on a normal diet (ND-Met). Therefore, a total of 18 KEGG pathways were exclusively associated with the specific effects of metformin in mice receiving an HFD (Fig. 6B; see Table S1 in the supplemental material for a more detailed description of these pathways).
Statistically significant KEGG pathways for each group were additionally identified using LEfSe (Fig. 6C). After metformin treatment on an HFD, metabolic pathways, such as lipopolysaccharide biosynthesis, sphingolipid metabolism, fructose and mannose metabolism, pentose and glucuronate interconversions, and propanoate metabolism, were enriched significantly.

**Correlations between metabolic biomarkers and bacterial abundance.** *A. muciniphila* was negatively correlated with serum glucose levels (Fig. 7). *Clostridium orbiscindens* showed a negative correlation with body weight and PPARγ/H9251 and GLUT2 levels and a positive correlation with TNF-/H9251, MUC2, and MUC5 levels (Fig. 7). PPARγ and GLUT2 levels were negatively correlated with *Blautia producta* and *Allobaculum* sp. strain ID4. *Clostridium cocleatum* was positively correlated with AMPK/H9251 and TC levels (Fig. 7).

**A. muciniphila enrichment by metformin or phenformin treatment in vitro.** The composition of *A. muciniphila* in six pooled stool samples from mice in the HFD-Met group was 14.3% ± 2.6%. At 3 and 6 h postinoculation into BHI broth, the proportions of *A. muciniphila* were 3.0% ± 0.5% and 3.8% ± 1.8%, respectively. In contrast, the proportion of *A. muciniphila* in BHI broth supplemented with 0.1 M metformin significantly increased (8.8% ± 3.7% and 6.6% ± 2.8% at 3 and 6 h postinoculation, respectively) (Fig. 8). Furthermore, when BHI was supplemented with 0.1 M phenformin (another member of the biguanide class), *A. muciniphila* was further enriched (19.1% ± 4.6% and 14.7% ± 2.1% at 3 and 6 h postinoculation, respectively) (Fig. 8).

**DISCUSSION**

Recent studies reported an association between the abundance of *A. muciniphila*, obesity, and T2D (11,12), and changes in the abundance of *A. muciniphila* during metformin treatment were observed in a mouse model (11). The results of these studies were limited to an association between the gut microbiota and glucose homeostasis for a short period of time, and the association between metabolic improvement and metformin treatment due to changes in the gut microbiota remains unclear. Our results are consistent with the results of these previous studies. Additionally, we found an enrichment effect of metformin on the growth of *A. muciniphila* in vitro, which is consistent with the results obtained with an in vivo mouse model. Therefore, metformin appears to act as a growth factor for *Akkermansia* spp.

The patterns of expression of metabolic biomarkers and correlations with the composition of the gut microbiota could increase our understanding of the association between the gut microbiota and metabolic improvement. Activation of AMPK by metformin treatment is known to be the primary mechanism of improving hyperglycemia (20). Increases in cytosolic AMP by metformin were suggested to be a mechanism of AMPK activation (21). Interestingly, metabolic improvement by metformin treatment without the activation of AMPK was observed in this study (Fig. 2A). In a recent report, the effect of metformin on hepatic gluconeogenesis was determined in an AMPK-deficient mouse model (4). However, antagonism of hepatic glucagon by metformin was...
proposed to be another target for T2D improvement in a recent study (22). Moreover, hepatic PPARα, GLUT2, and AMPKα1 levels decreased significantly (Fig. 2A). Only the TNF-α level in the fat pad decreased during metformin treatment of mice on an HFD. A significant correlation between \textit{A. muciniphila} and glucose levels was observed during metformin treatment of mice on an HFD (Fig. 7). Both PPARα and GLUT2 levels were negatively correlated with \textit{B. producta}, \textit{Allobaculum sp. ID4}, and \textit{C. orbiscindens}, while the TNF-α level was positively correlated with \textit{C. orbiscindens} during metformin treatment of mice on an HFD (Fig. 7). These results suggest that OTUs of the gut microbiota are strongly associated with specific metabolic and immunological biomarkers.

Gastrointestinal mucins produced by goblet cells protect the underlying epithelium from pathogens. Recently, the degradation of mucin was reported in mice on an HFD (12) and may be associated with metabolic disorders. Mucin is degraded by specific intestinal bacteria, which may comprise 1% of the colonic microbiota (23). Among them, the effect of \textit{A. muciniphila} on metabolic improvement has recently been discussed. In addition, the increase in \textit{A. muciniphila} abundance was associated with mucus thickness (12). In this study, the abundance of \textit{A. muciniphila} increased during metformin treatment of male and female mice on an HFD. However, a significant increase in mucin gene expression and thickened intestinal mucosa were observed only in females (Fig. 3A and B). The effect of mucin on metabolic improvement may differ by gender, but the mechanisms are not fully understood. Further studies are required to explore gender differences in the role of mucin in metabolic improvement.

Bacterial diversity significantly decreased during metformin treatment and after a dietary change to an ND; metformin had a more significant effect than dietary change. The alpha diversity indicated that decreases in bacterial diversity during metformin treatment were observed only in mice on an HFD, and metformin treatment had no effect on mice fed an ND (Fig. 4A). The effects of metformin on bacterial diversity were consistent on the basis of both weighted and unweighted beta diversities and UniFrac distances (Fig. 4B and C). Therefore, metformin treatment may decrease the overall bacterial diversity, and the specific composition of the microbiota was strongly associated with metabolic improvement during metformin treatment.

The relative abundance of \textit{C. cocleatum} in the HFD-Met group was 0.1% and increased significantly during metformin treatment of mice on an HFD, similar to the findings for \textit{A. muciniphila} (Fig. 4E). It has been reported that \textit{C. cocleatum} levels are decreased in patients with irritable bowel syndrome (IBD) (24). However, the association between \textit{C. cocleatum} and metabolic syndromes (such as obesity and T2D) has not been explored. \textit{Clostridium} spp. are
known to degrade some animal mucin (25). Recently, an increase in Clostridium spp. was reported during metformin treatment of mice on an HFD (11). Although the relative abundance of *C. coeleatum* was minor compared to that of *A. muciniphila*, *C. coeleatum* may be associated with metabolic improvement during metformin treatment.

The effects of metformin treatment on metabolic biomarker expression in both liver and fat pads differed by gender (Fig. 2). In addition, differences in the gut microbiota were observed between male and female mice (Fig. 5). In previous studies, metformin treatment differentially affected body weight according to gender, and metabolic hormones—such as leptin and adiponectin—were differentially affected by metformin treatment (26, 27). The effect of the gut microbiota on metabolic disease according to gender has not been reported to date. Recently, the vaginal microbiota was shown to differ significantly on the basis of menopausal status (14), which suggests that hormones in females were highly associated with the composition of the human vaginal microbiota. It may be suggested that human gut microbiota could likewise be impacted by human hormone levels. Moreover, female hormones are involved in glucose and lipid metabolism and are known to exert a protective effect against metabolic disorders (28, 29). Therefore, differences in the gut microbiota between male and female mice during metformin treatment might be caused by differences in hormone levels, which might be associated with metabolic phenotypes.

We further predicted that the significant metabolic pathways would show differences in expression during metformin treatment of mice on an HFD, based on the bacterial abundances determined using PICRUSt. The HFD, HFD-ND, and HFD-Met groups were clearly clustered by predicted KEGG pathways and bacterial diversity (Fig. 6A). Therefore, we expected that the significant metabolic phenotypes during metformin treatment might be caused by different metabolic functions of the gut mi-

**FIG 6** Comparison of KEGG pathways predicted using PICRUSt according to diet and metformin treatment. Groups categorized according to metformin treatment and diet were clearly clustered on the basis of the KEGG pathways predicted using PICRUSt, as well as the bacterial diversity. A total of 245 KEGG pathways were generated, and the KEGG pathways that were significantly increased during metformin treatment were further analyzed using PCoA and LEfSe. (A) Clustering of five groups by KEGG pathways using PCoA. (B) Predicted KEGG pathways during metformin treatment and a dietary change to an ND. A total of 30 KEGG pathways were increased during metformin treatment of mice on an HFD. Among them, 2 and 12 KEGG pathways that were increased overlapped those that were increased in the HFD-ND and ND-Met groups, respectively. Finally, 18 unique KEGG pathways were predicted to be increased during metformin treatment of mice on an HFD. (C) LEfSe results showed a statistically significant increase in the abundance of KEGG pathways in the HFD-ND, HFD-Met, and HFD groups. LEfSe results showed a sequentially significant ranking ($P < 0.05$) among classes (Kruskal-Wallis test) and between subclasses (Wilcoxon’s test). The threshold for the logarithmic LDA score was 3.0.
crobiota. In this study, 18 specific metabolic pathways of the gut microbiota were significantly increased by metformin alone, when other influences were controlled for (Fig. 6C). The increased metabolic activities of sphingolipid and fatty acid metabolism are closely associated with metabolic syndromes and may be important for the metabolic improvement induced by metformin treatment. This may be because specific sphingolipid signaling pathways influence the major biological processes, including insulin resistance, lipid metabolism, inflammation, and the immune response (30–32). In addition, Everard et al. have shown that the expression of lipogenic genes—such as fatty acid synthase (FASN) and acetyl coenzyme A carboxylase 1 (ACC1)—is upregulated by _A. muciniphila_ treatment of mice on an HFD (12). Thus, the abundance of _A. muciniphila_ may be associated with lipid metabolism by the gut microbiota.

The amelioration effect of metformin on the abundance of _A. muciniphila_ was demonstrated using in vitro growth assays in BHI medium supplemented with metformin. Metformin or phenformin administration increased the abundance of _A. muciniphila_ (Fig. 8). Interestingly, _A. muciniphila_ was not detected in ND mice, and its level was slightly increased in mice on an HFD. However, after metformin treatment in mice on an HFD, the abundance of _A. muciniphila_ increased by ~18-fold (12.44%) compared with that in mice in the HFD group (0.68%). Therefore, the effect of _A. muciniphila_ on metabolic disorders and improvement may be dose dependent.

In conclusion, the diversity and composition of the gut microbiota changed significantly during metformin treatment of mice on an HFD, and the changes were correlated with the levels of various metabolic biomarkers. Furthermore, specific pathways associated with lipid metabolism (including sphingolipid and fatty acid metabolism) may play a key role in the metabolic improvement induced by metformin treatment. We suggest that the specific composition of the gut microbiota during metformin treatment has therapeutic effects on metabolic diseases, including obesity and T2D.

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REFERENCES


