Changes in the gut mycobiome are associated with Type 2 diabetes mellitus and metformin treatment across populations

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ABSTRACT

The gut mycobiome may be involved in human health and disease. Previous studies evaluating the human gut mycobiome have small sample sizes, do not account for the use of oral pharmaceuticals, and report inconsistent findings regarding the relationship between Type 2 diabetes mellitus (T2D) and fungal species. Pharmaceuticals, including the antidiabetic drug metformin, interact with gut bacteria and can alter bacterial metabolism. The potential interactions of pharmaceuticals with the mycobiome remain unknown. These potentially confounding factors necessitate a critical re-evaluation of existing claims and validation in larger human cohorts. Thus, we reanalyzed shotgun metagenomics data from nine studies to quantify if and to what degree there is a conserved relationship between gut fungi and T2D. We used Bayesian multinomial logistic normal models to account for numerous sources of variation and confounding factors, including batch effects induced by differences in study design and sample processing (e.g., DNA extraction or sequencing platforms). Using these methods, we analyzed data from over 1,000 human metagenomic samples and performed a mouse study to demonstrate reproducibility. Metformin and T2D were consistently associated with differences in the relative abundance of some gut fungi that were predominantly members of the Saccharomycetes and Sordariomycetes classes, but generally accounted for less than 5% of total mycobiome variation. Gut eukaryotes may be involved in human health and disease, but this work takes a critical lens to previous claims and suggests that perturbations to the most abundant and prevalent fungi in T2D may be smaller than previously thought.

INTRODUCTION

The gut microbiome is a complex ecosystem of billions of micro-organisms, but research has traditionally focused on bacteria. Interest in non-bacterial intestinal communities such as the gut mycobiome, the fungal community of the gut microbiome, has increased in recent years. Intestinal fungi and yeasts comprise a small proportion of gut microbial biomass [1] and can be difficult to analyze with traditional next-generation sequencing approaches. Nevertheless, multiple reports in the last few years suggest that the gut mycobiome may contribute to gut homeostasis and can instigate inflammation when dysregulated [2–5]. Observations of differences in fungal diversity or community composition between disease states and healthy comparisons have suggested a state of fungal dysbiosis [6,7] analogous to bacterial dysbiosis that contributes to the development of metabolic diseases [8,9]. Indeed, a recent review described perturbed gut fungi in multiple disorders including irritable bowel syndrome, colorectal cancer, liver diseases, COVID-19 infection, obesity, Type 2 diabetes, and neurological disorders [6]. However, human cohort studies of the gut mycobiome have small sample sizes and individual reports yield conflicting evidence, particularly in Type 2 diabetes (T2D).

In 2022, 28.7 million Americans had diagnosed Type 1 or Type 2 diabetes [10]. In 2017, the direct healthcare costs of diagnosed diabetes in the United States was USD 237 billion, and are projected to reach USD 825 billion by 2030 [11,12]. Perturbations in the gut microbiome are reported in human and animal models of T2D, which may contribute to sub-clinical inflammation and insulin resistance [8,13,14]. Metformin is the most widely prescribed antidiabetic drug [15] and is known to modulate gut bacteria composition and

alter bacterial metabolism [16–19]. These impacts may have downstream effects on glucose metabolism, such as by inhibiting the growth of *Bacteroides* species which leads to a loss of bile acid hydrolase activity and subsequent inhibition of farnesoid nuclear X (FRX) signaling [16]. Metformin-induced changes in gut microbiota are associated with increased lactate production in the intestinal lumen [20], suggesting a role of metformin in modulating the intestinal metabolic environment. While the gut mycobiome has been implicated in T2D [6,7], individual reports are conflicting. For example, *Saccharomyces* was relatively increased in newly diagnosed T2D compared to healthy subjects in one study [21] but decreased in two others [22,23]. Increased *Candida* relative abundances in T2D was reported in two studies [22,24] while a third study did not report differences in *Candida*. Significant shifts in overall fungal community composition (beta diversity) compared to healthy subjects was also reported [22,23]. In these studies, most or all subjects with existing T2D diagnoses were using antidiabetic therapies, which may confound the relationship between T2D and the gut mycobiome. Furthermore, all studies had sample sizes of 14-30 people per group. Both small sample sizes and lack of stratification based on pharmaceutical use could contribute to the observed discrepancies between studies. Examining the relationship between T2D, metformin, and alterations in the gut mycobiome on a larger scale in heterogeneous populations is necessary to better understand this potentially clinically important question.

In recent years, there has been a call to explore the relationships between human disease and gut eukaryotes [6,25,26]. We identified an additional opportunity to untangle the effects of T2D from the oral antidiabetic medication metformin, as it is

plausible that given the interactions of metformin with bacterial communities [16–19,27], there may be direct or indirect impacts on the gut mycobiome. To examine the robustness and reproducibility of associations between the gut mycobiome with T2D and metformin treatment, we reanalyzed data from 3 randomized clinical trials and 6 cross-sectional cohorts, resulting in a combined dataset of over 1,000 human samples. Our analytic methods are specifically designed to address numerous complexities of such meta-analyses including count variation, sparsity, compositional constraints, and batch effects common these data. Moreover, we performed a novel mouse study to further validate the reproducibility of our conclusions. Overall, the work provides a critical and rigorous assessment of associations between gut fungi, metabolic disease, and oral pharmaceuticals.

RESULTS

Data Curation and Analysis

A literature search yielded nine studies with publicly available human stool metagenomic data and individualized T2D and treatment status. The aggregated dataset comprised 1,194 samples from 963 individuals, representing three randomized clinical trials (RCTs) and three cross-sectional cohort studies that included metformin-treated individuals, in addition to three cross-sectional studies from the MetaHIT cohort containing only normoglycemic individuals (Supplementary Table S1). The aggregated dataset included T2D individuals with metformin treatment (T2D-MET; n = 218), T2D individuals without metformin treatment (T2D-NOMET; n = 248), and normoglycemic individuals without metformin treatment (NORM; n = 611). Five countries were represented across Asia and Europe. A standardized bioinformatics pipeline was applied to each of the nine studies to obtain raw fastq files from sequence archives, perform quality control and host read removal, and obtain sequence count tables (see Methods). After filtering to remove very low abundant taxa, the composite dataset contained 67 fungal species comprising 43 genera that primarily represented the phylum Ascomycota, a few from Basidiomycota, and one genus from Microsporidia. Of the 43 total genera, 34 were detected in all nine studies. Analyses were conducted at the genus level to increase confidence in taxonomic assignment given the low abundance of fungal reads in shotgun metagenomics.

We developed an analytical approach specifically designed to assess the reproducibility and robustness of candidate associations between gut fungi and host factors. Specifically, we used Bayesian models that have been purposely designed to

address key complexities of sequence count data (e.g., sampling variation, sparsity, and compositional constraints) [28,29] and designed our analyses to address the challenges of combining datasets (e.g., batch effects) [30,31]. We address this later challenge in two ways. First, all models fit to the combined dataset included random intercepts to minimize inter-study variation. Second, candidate associations identified from analyses of the combined dataset were further interrogated to ensure that the inferred effect was consistent when analyses were performed independently on each dataset. This later step reduces the risk that our findings are due to batch effects or outliers. Unless otherwise specified, results are stated in terms of mean Centered Log Ratio coordinates that reflect proportional changes in fungal abundance with 95% credible intervals of the posterior distributions in brackets. Further methodological details are provided in the Methods.

Metformin associations with the gut mycobiome in T2D

We first compared the total dataset of T2D-MET (n=218) to T2D-NOMET (n=238) to determine if a relationship between metformin treatment and the human gut mycobiome emerged. An overall association of metformin was detected in *Fusarium* (0.147 [0.041, 0.255]; increased in T2D-MET), *Tetrapisispora* (0.230 [0.186, 0.371], increased in T2D-MET), and *Nakaseomyces* (-0.162 [-0.207, -0.036], decreased in T2D-MET) (Figure 1A). The partial r^2 of metformin treatment (e.g., the amount of variability in the mycobiome that could be attributed to metformin) was 0.66% in the aggregate dataset, ranging from 1-10% in within-study models. Despite the variability in dosage and treatment duration, metformin had a consistently similar effect size direction and magnitude in at least four of these six studies. However, we note that while

Nakaseomyces was found to be decreased in T2D-MET compared to T2D-NOMET in the aggregate comparison only, within-study analyses depicted higher between-study variability and conflicting directions of effect sizes for this genus, illustrated in Figure 1A.

Next, we probed the short-term effects of metformin treatment in newly-diagnosed, treatment-naïve T2D individuals in three RCTs (n=93). Short-term metformin treatment was associated with changes in *Zygotorulaspora* (0.298 [0.094, 0.504], increased in T2D-MET), *Tetrapisispora* (0.194 [0.013, 0.377], increased in T2D-MET), and *Botrytis* (-0.248 [-0.429, -0.074], decreased in T2D-MET) (Figure 1B). In this comparison, metformin treatment accounted for approximately 1.5% of variation (partial r^2) in the gut mycobiome, ranging from 2-8% in within-study models. The gut mycobiomes of individual subjects had varied responses to metformin, as visualized in Figure 1D. We observed greater mycobiome variation in participants from one study that were sampled before and after receiving 2,000 mg metformin/day for three days [16] compared to participants from two other clinical trials that received 500-2000 mg/day for 7 days [19] or 1,700 mg/day for 2 months [17] (Figure 1B & D). This variability in timing and dosage could contribute to study differences and inter-individual variation.

To further compare the effect of metformin treatment on fungal relative abundance in T2D, three cross-sectional studies including T2D-MET (n = 90) and T2D-NOMET (n = 101) were compared in a similar fashion. In these studies, participants could have long-term T2D and/or metformin treatment compared to participants in RCTs who were newly diagnosed with T2D and placed on metformin for the first time. Six fungal genera were different between T2D-MET and T2D-NOMET; *Aspergillus* (0.297 [0.037, 0.553]; increased in T2D-MET]), *Brettanomyces* (-0.269 [-0.488, -0.003];

decreased in T2D-MET), *Fusarium* (0.401 [0.148, 0.648]; increased in T2D-MET), *Scheffersomyces* (-0.260 [-0.478, -0.041]; decreased in T2D-MET), and two unassigned genera from the Saccharomycetales order and Saccharomycetaceae family (-0.385 [0.722, -0.056] and -0.467 [-0.738, -0.212] respectively; both decreased in T2D-MET) (Figure 1C). In this comparison, metformin accounted for 2.8% of mycobiome variability, ranging from 3-10% within each study (partial r^2). In these three studies, fasting blood glucose (FBG) and hemoglobin A1c (HbA1c) were similar in T2D-MET (FBG median ± inter-quartile range (IQR) 146 ± 30.6 mg/dL, HbA1c median ± IQR 6.82 ± 1.2%) compared to T2D-NOMET (FBG median ± IQR 135 ± 36.9 mg/dL, HbA1c median ± IQR 7.0 ± 3.4%) indicating that in the cross-sectional study sub-analysis, our comparison assessed the effects of pharmaceuticals and not controlled versus uncontrolled diabetes. Interestingly, the metformin-associated genera in the cross-sectional study sub-analysis differed from the genera identified in the RCT sub-analysis.

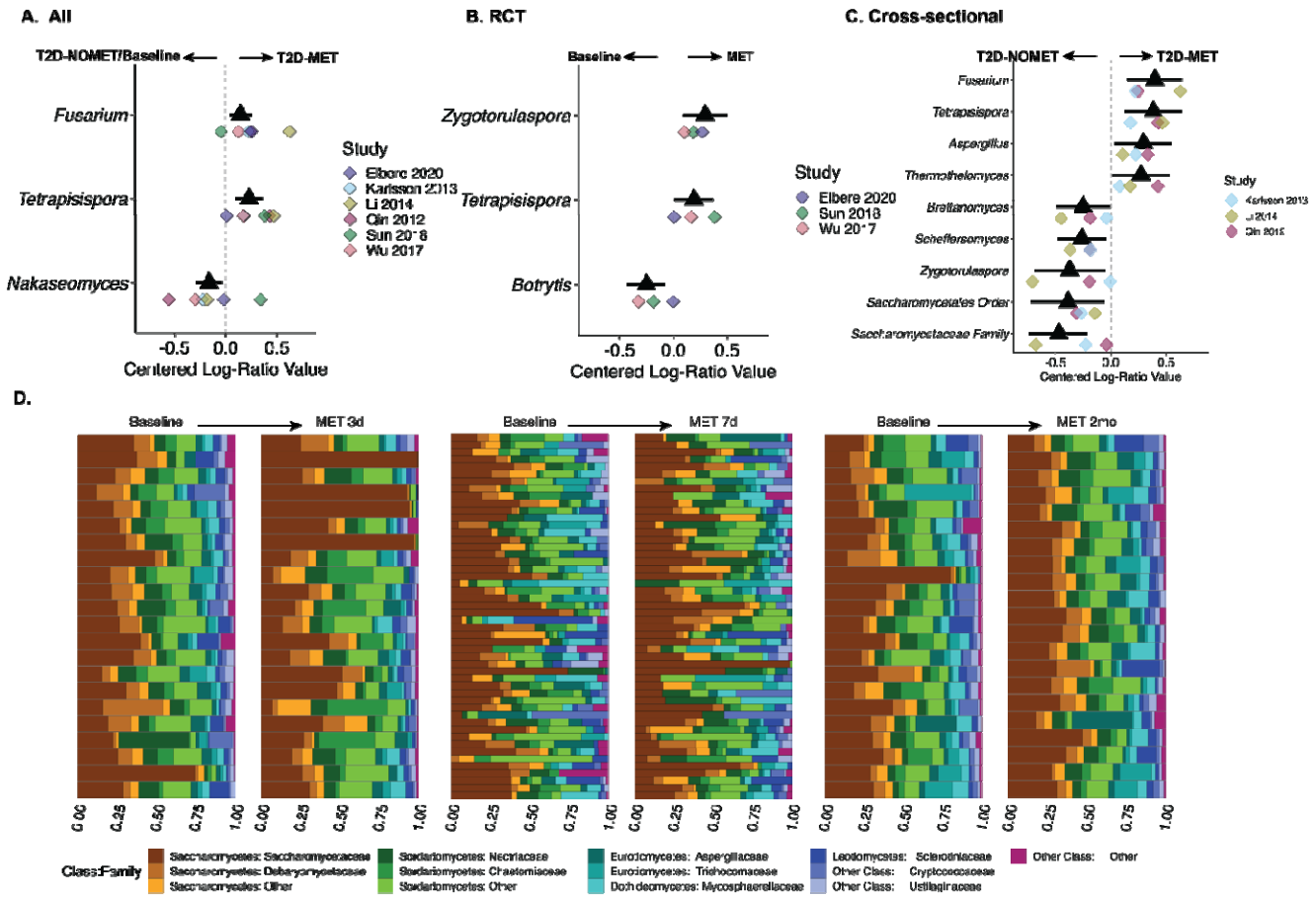

Figure 1: Metformin's associations with gut fungi in T2D in (A) the total dataset, (B) randomized clinical trials (RCTs), and (3) cross-sectional studies. The black triangle and pointrange shows posterior mean and posterior 95% credible intervals of the aggregate dataset. Colored diamond points show posterior means of individual studies. The arrows show increased abundance at baseline (left) or during metformin (MET) treatment (right). The dashed vertical line denotes zero association. (D) Paired samples from the same individual are shown as neighboring horizontal bars of proportional relative abundance at baseline and during metformin treatment. Taxa are colored as Class:Family, and less relatively abundant taxa are merged in the "other" category.

The mycobiome in metformin-treated T2D differs from normoglycemic individuals

To determine differences in the mycobiome of metformin-treated T2D compared to normoglycemic subjects (NORM), we compared data within three studies containing both T2D-MET (total n = 82) and NORM (total n = 262) individuals. Fungal genera that differed between T2D-MET and NORM included *Fusarium* (0.274 [0.044, 0.506],

increased in T2D-MET), *Thermothielavioides* (0.222 [0.039, 0.408], increased in T2D-MET), *Cryptococcus* (0.164 [0.028, 0.307], increased in T2D-MET), and an unassigned genus from the Saccharomycetales order (-0.421 [-0.792, -0.040], decreased in T2D-MET) (Figure 2). The combination of T2D and metformin accounted for 1.3% of mycobiome variation (partial r2, ranging from 0.9-9% within each study. To determine the reproducibility of these findings, these candidate fungal genera were assessed in mice treated with metformin or placebo for seven days. While the metformin-treated mice were healthy and normoglycemic, we were encouraged to note similar direction and magnitude of the effect size of metformin on the mouse and human mycobiomes (Figure 2). In this controlled environment on a standard diet, metformin explained a relatively high proportion of variability in the mouse cecal mycobiome (partial r^2 = 25.7%), suggesting that heterogeneity between experimental designs, diets, or geography may lead to an underestimation of the true treatment effect.

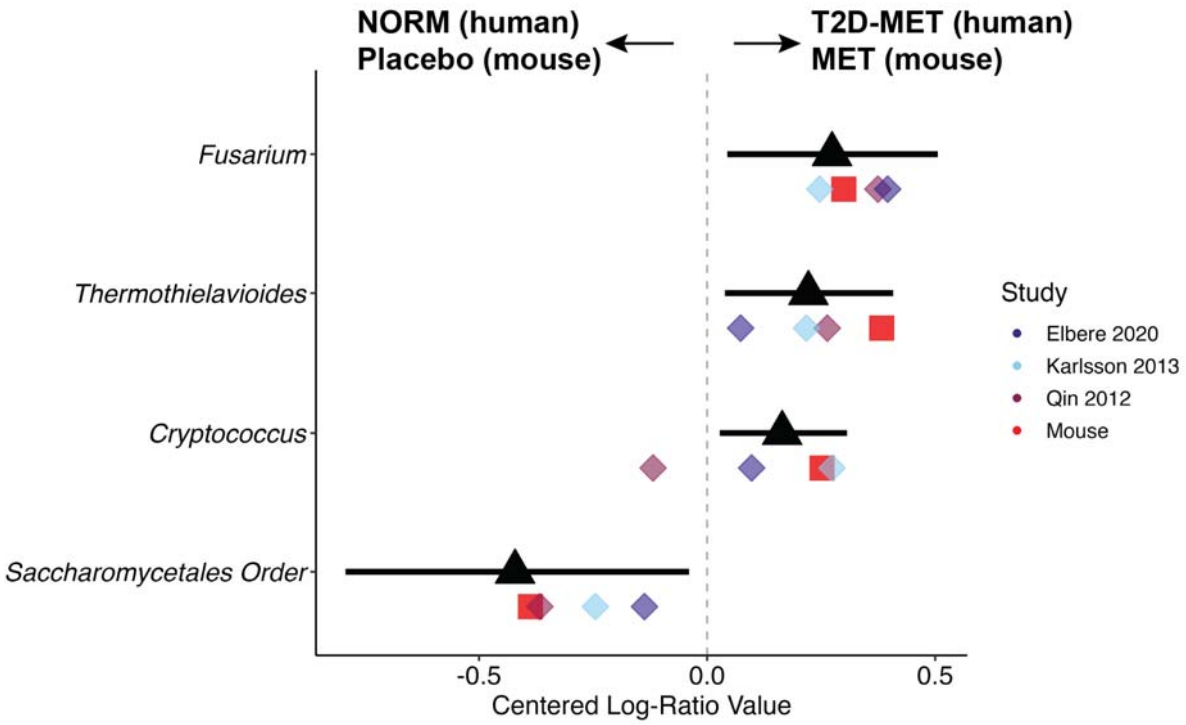

Figure 2: Metformin is associated with similar differences in the human and mouse mycobiomes. Black triangles and line ranges shows posterior mean and posterior 95% credible intervals of the aggregate dataset. Colored diamond points show posterior means of individual studies. Red squares show the posterior means of the mouse study. The arrows show increased abundance in NORM subjects or mice with placebo treatment (left) or T2D-MET subjects and metformin-treated mice (right). The dashed vertical line denotes zero association.

Fungal compositional shifts in metabolic disease without the confounding factor of drug treatment

Assessing the impact of metabolic disease on the gut mycobiome necessitated removing the confounding factor of metformin treatment. Therefore, we compared T2D without metformin treatment (T2D-NOMET; n = 134) to normoglycemic (NORM; n= 262) individuals, and additionally probed clinical indices of metabolic disease while adjusting for metformin treatment (see Methods). Shifts in fungal composition between T2D-NOMET and NORM were detected for *Saccharomyces* (0.580 [0.210, 0.959], increased in T2D-NOMET), *Nakaseomyces* (0.277 [0.085, 0.469], increased in T2D-NOMET), and

Zygosaccharomyces (-0.434 [-0.697, -0.172], decreased in T2D-NOMET) (Figure 3A). While T2D represented approximately 1.2% of mycobiome variation in the combined dataset, within-study partial r^2 ranged from 3-9%. To represent a wider range of metabolic phenotypes than dichotomous T2D status and increase the sample size, we leveraged individualized clinical data of fasting blood glucose (FBG; n = 784), fasting plasma insulin (FPI; n = 697), hemoglobin A1c (HbA1c; n = 815), and (body mass index, BMI; n = 766) while adjusting for metformin treatment. We found that *Saccharomyces* was positively associated and *Brettanomyces* was negatively associated with increased FBG (0.199 [0.060, 0.335] and -0.149 [-0.250, -0.045], respectively) despite variability between individual studies (Figure 3B). FPI was associated with decreased *Zygosaccharomyces* and *Tetrapisispora* (-0.098 [-0.177, -0.022] and -0.130 [-0.231, -0.030], respectively) (Figure 3C). *Ustilago* was increased with both increased BMI and FPI (0.132 [0.786, 0.184] and 0.137 [0.083, 0.193], respectively) and *Zygotorulaspora* was associated with decreased BMI and FPI (-0.257 [-0.364, -0.148] and -0.130 [-0.231, -0.030], respectively; Figure 3C & D). None of the clinical variables were statistically associated with *Nakaseomyces* or *Fusarium* which were previously associated with metformin treatment (Figures 1, 2). In contrast to FBG, HbA1c had very weak associations to gut fungi with high between-study variability, and no candidate genera had similar effect size direction and magnitude greater than |0.1| Centered Log-Ratio change across studies despite high within-study partial r^2. The aggregated comparisons suggested that FBG, FPI, HbA1c, and BMI had low contributions to overall mycobiome variability (partial r^2 = 0.55-0.59%), but within-study analyses demonstrated stronger relationships that ranged from 3-11%.

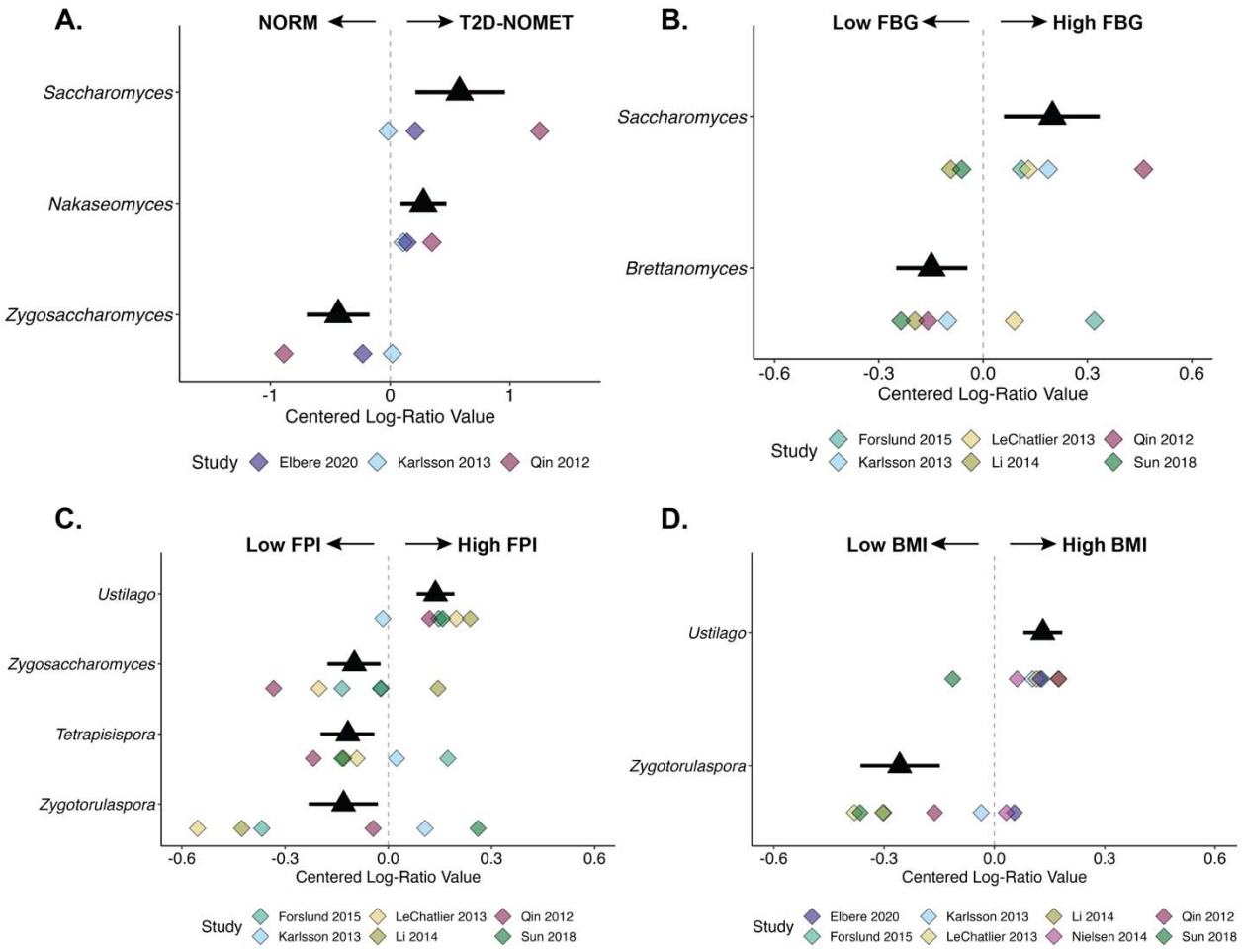

Figure 3: Metabolic disease is associated with a shift in genera belonging to the Saccharomycetes class. Subjects with T2D-NOMET were compared to NORM (A), and markers of metabolic disease were compared; (B) fasting blood glucose (FBG), (C) fasting plasma insulin (FPI), and (D) body mass index (BMI). In all panels, black triangles and line ranges shows posterior mean and posterior 95% credible intervals of the aggregate dataset. Colored diamond points show posterior means of individual studies. Arrows show increased fungal abundance. The dashed vertical line denotes zero association.

DISCUSSION

The gut mycobiome may be more involved in human health and disease than previously thought, but existing studies on the gut mycobiome in T2D are conflicting and did not account for use of antidiabetic pharmaceuticals. To critically evaluate existing

claims, we reanalyzed published human metagenomics to determine if and to what extent there are conserved associations with gut fungi, T2D, and metformin treatment. This analysis represents the largest to-date, multi-country cohort of gut mycobiome data. Given the established interactions of metformin and gut bacteria [16–19,27], we hypothesized that metformin would alter the abundance of fungal genera. To test this hypothesis, we compared baseline data from newly-diagnosed T2D subjects to samples collected after the start of metformin treatment in three RCTs. We found that metformin was consistently associated with increased *Fusarium* and *Tetrapisispora* across RCTs and cross-sectional studies. Beyond humans, the signature of metformin on certain gut fungi was reproducible in a mouse study.

This re-analysis provides, to our knowledge, the first assessment of the effects of antidiabetic drugs on the gut mycobiome. Antidiabetic drugs have not been examined in the context of the human gut mycobiome, but one *in vitro* experiment observed a direct interaction of metformin with the yeast *Ustilago* and postulated that metformin may extend the lifespan of microeukaryotes as it does in other eukaryotic model organisms [32]. However, the nature of this dataset precludes us from drawing any conclusions beyond associations, and the overall small contribution of metformin on gut mycobiome variability leads us to speculate that gut fungi may be indirectly affected by the metformin-induced shift in the intestinal metabolic environment [27].

The interactions of oral pharmaceuticals with the gut bacteriome [33] and potentially with the gut mycobiome, as suggested in this study, necessitate accounting for these factors when assessing gut microorganisms in the context of metabolic disease. Independent of metformin treatment, T2D was associated with an increase in

two genera of the Saccharomycetes class, *Saccharomyces* and *Nakaseomyces*, with a corresponding decrease of *Zygosaccharomyces*, also in the Saccharomycetes class. This was validated in the comparison of clinical markers of metabolic disease, which showed a positive correlation of *Saccharomyces* with fasting blood glucose and a negative correlation of *Zygosaccharomyces* with fasting plasma insulin. However, the effect sizes of the differences in fungal abundance between T2D-NOMET and NORM subjects were smaller than what has been previously reported. For example, Al Bataineh and colleagues reported that T2D explained 13% of variation compared to normoglycemic controls (diabetic treatment was unspecified) [23]. When comparing models fit to individual studies, we noticed that some studies had greater differences between T2D and NORM individuals while others had negligible differences across the board. Given the constraints of using publicly available data, we cannot exclude the possibility that these discrepancies are due to technical artifacts such as differing sequencing depths or DNA extraction techniques.

Our analysis represents the largest to-date gut mycobiome cohort. There is ongoing debate over what constitutes the healthy human mycobiome in addition to speculation of the true scope of intestinal fungal diversity [34–37]. We purposefully limited our analyses to the most abundant and prevalent fungal genera to exclude minor taxa that may be determined by environmental exposures or may even be spurious taxonomic assignments. For example, the two least prevalent fungi in our aggregated dataset, two unassigned genera from the families Chaetomiaceae and Mycosphaerellaceae, were detected in only a few individuals from one study and have not been previously associated with the human gut mycobiome. The most abundant

fungi across the dataset were prevalent in approximately 95% of subjects, suggesting a ubiquitous presence regardless of diet or geography, and were similar to previous reports that confirmed the presence of 34 fungal genera with culture-dependent approaches [37].

This analysis is limited by the constraints of using publicly available data, as laboratory controls such as DNA extraction blanks and clinical metadata such as dietary habits and additional pharmaceutical consumption are simply not available. Dietary recommendations are standard of care for newly diagnosed T2D, and thus it is possible that some differences attributed to T2D could be due to dietary changes [38]. As fungi comprise a low proportion of total gut microbial biomass [1], the detection of fungi in shotgun metagenomics reads can be difficult. We took a simplistic approach with short-read taxonomic assignment using similar methods to existing mycobiome surveys [26,39,40]. The pitfalls of this bioinformatics approach include a risk of false positives that inflate the dataset or detection of contaminants as true taxa. We minimized these risks by first removing human host reads and reads that aligned to a bacterial & archaeal database, and then comparing the unaligned reads to the fungal database, and further filtered out very low abundant taxa with the *a priori* assumption that they may be spurious assignments or contaminants. The Bayesian Multinomial Logistic-Normal modeling approach ensured that between-study variation was minimized, and our priors were conservatively chosen to assume there were no true differences between comparison groups. In addition to that approach, we further confirmed candidate taxa identified in the aggregated dataset were not driven by outliers by ensuring those taxa were consistently different across multiple independent studies and with similar

direction. Given the large amount of variability in populations, experimental design, and sample preparation methods between the included studies, the consistent reproducibility of our results suggests non-trivial associations of some gut fungi with T2D and metformin treatment.

In summary, we identified candidate taxa such as *Fusarium* that were consistently increased in metformin-treated humans and mice and showed shifts in Saccharomycetes genera in T2D. However, metformin and T2D generally accounted for less than 5% of total mycobiome variation in the aggregate comparisons, suggesting a minimal or indirect effect of metformin and T2D on the gut fungal environment. By applying carefully conservative analyses and providing multiple lines of independent evidence, we ensured reproducibility in our results. This analysis provides a framework by which to critically evaluate the claims that human diseases are associated with shifts in the human gut mycobiome. While we support the findings that some gut fungi are affected by oral pharmaceutical treatment and T2D, we speculate that the previous effect sizes may have been overstated. As such, analyses across larger sample sizes and heterogeneous populations provide validation of findings reported in smaller, isolated human studies. Future research should seek to integrate data across gut bacteria, fungi, and other microbial inhabitants of the human gastrointestinal tract to further understand the contributions of all microbial life to human gut homeostasis.

METHODS

Metagenomics acquisition and bioinformatics

To obtain whole-genome metagenomics data, a literature search was performed, and relevant articles were screened for the following criteria: human studies, collection of stool samples for shotgun metagenomics sequencing, and type 2 diabetes or metformin treatment. Three additional datasets from the MetaHIT cohort were included to increase the sample size of normoglycemic comparisons (accessions PRJEB5224, PRJEB4336, PRJEB1220). Duplicate participant IDs between the three accession numbers were removed, and the MetaHIT cohorts retain the label of the study they first appeared in. Thus, nine studies were included in the analysis comprising 1,194 samples (Supplementary Table S1).

Metagenomic data was accessed in fastq format and re-analyzed under one standard pipeline to minimize between-study variability. None of the studies provided sequences from technical controls. Metagenomic data was first downloaded from NCBI Sequence Read Archive or European Nucleotide Archive with Entrez Direct software [41]. Adapter contamination was removed with fastp v0.20.1 and human reads were removed with bowtie2 v2.4.2 aligning to the human genome version HG37v0.1 [42,43]. Quality and length trimming was performed in fastp to discard reads with a quality score in a 4-base sliding window under 20 and length under 2/3 of the average read length. Bacterial taxonomy was assigned by mapping to the standard kraken2 v2.1.1 database build [44]. The unassigned reads were then mapped to the standard fungal library build in kraken2, which comprises the complete RefSeq fungal genomes and proteins. Both databases were retrieved in November 2021. Kraken2 reports were converted to biom tables with

kraken-biom (https://github.com/smdabdoub/kraken-biom). Further analyses were conducted in R software v4.0.13 [45]. A filtering approach was undertaken to remove very low abundant taxa. Filtering was applied within each study to account for differences in sequencing depth. Taxa that were unassigned at the phylum level and taxa detected in fewer than 10% of samples within a study were removed, and taxa were further filtered to remove species with fewer than 0.001 of total assigned reads. Samples with zero fungal reads were removed (n = 7, all from Qin et al 2012).

Clinical and phenotypic metadata were collected from NCBI's Sequence Read Archive metadata tables, the study's supplementary materials, or data provided by the study authors through institutional Data Transfer Agreements. Metadata was only collected if individualized data was provided and if the data could be matched back to the archived sequencing sample through a provided sample name. Metformin and T2D status were assigned to each sample based on the categorization given in the study metadata.

Bayesian multinomial logistic-normal linear regression modeling

To model the effect of these covariates on fungal and bacterial composition, we used a Bayesian multinomial logistic-normal linear regression model [46]. We selected this model since it accounts for sampling variation in the observed counts and satisfies compositional constraints. This model is efficiently implemented via the pibble function in the R package *fido* [46]. This structure models the log ratio coordinates using a Bayesian linear regression model. The structure for each model was dependent on the scientific question; covariates used for each model in the main text are defined Table 1. In global comparisons that included time-series data from randomized clinical trials, a

random intercept was added for each individual. To avoid misattributing variability to study differences, global models contained only matched data from each study; that is, instead of comparing all T2D-MET individuals to all NORM individuals, we only used data from studies that included both T2D-MET and NORM.

Since we chose a Bayesian regression model, we set four specific hyperparameters — Γ, Θ, Ξ, and υ —for model fitting. We set Γ to be a Q dimensional identity matrix where Q is the number of covariates in a given model. This reflected a weak prior assumption that the covariates are uncorrelated. Additionally, we set Θ to be a $(D - 1) \times Q$ matrix of zeros where Q is defined as before and D denotes the number of taxa. This reflects a prior belief of a null relationship in the additive log-ratio space (ALR) between each covariate and taxa. Furthermore, we chose our values of Ξ and υ to reflect a weak prior belief that each taxon is uncorrelated in terms of absolute abundances. Thus, we chose $\upsilon = D + 3$ and selected Ξ such that it corresponded to a D-dimensional identity matrix in the space of log abundances scaled by a factor of $(\upsilon - D)$. This corresponds to a $(D - 1) \times (D - 1)$ matrix with $\xi_{ii} = (\upsilon - D)$ and $\xi_{ij} = (\upsilon - D)/2$. These specifications were checked using prior predictive checks available in *fido*. Missing values in each model were removed. We simulated 5,000 posterior draws for each model. The function in *pibble* natively fits these models in terms of ALR coordinates. After model fitting, we transformed the resultant parameters to centered log ratio (CLR) coordinates using the *fido* function to_clr. For each parameter of interest, we calculated posterior means and 95% credible intervals. The resulting intervals were assessed for whether or not they contain zero; parameters for which these intervals did not cover zero were investigated further. This model was fit to the aggregated dataset

for each comparison, and candidate genera identified as having 95% credible intervals outside of zero were subjected to further filtering. These candidate genera were assessed in models fit to each study and only retained if the majority of studies agreed in the effect size direction (positive or negative fold change) and non-trivial magnitude (Centered Log-Ratio change > |0.1|). This filtering approach ensured that the aggregate comparisons were robust to between-study differences or outliers. Due to the model structure, partial pooling of the estimates occurs and multiple hypothesis corrections are unnecessary [29,47].

Table 1: Bayesian MLN model covariates. All models except the mouse data (marked with *) were fit to the aggregate dataset and further validated with individual study models. Individual study models were identical to the global model without the $[x_j,(study)]$ covariate. $[x_k...,(individual)]$ represents a random intercept for each individual in time-series designs.

Comparison	*Figure*	*Covariates*
T2DMET - T2DNOMET; All	Figure 1A	$[1, x_j,(study), x_j,(metformin), x_k...,(individual)]$
T2DMET - T2DNOMET; RCT	Figure 1B	$[1, x_j,(study), x_j,(metformin), x_k...,(individual)]$
T2DMET - T2DNOMET; Cross-sectional	Figure 1C	$[1, x_j,(study), x_j,(metformin)]$
T2DMET - NORM; Humans	Figure 2	$[1, x_j,(study), x_j,(metformin)]$
T2DMET - NORM; Mouse*	Figure 2	$[1, x_j,(metformin), x_k...,(individual)]$
T2DNOMET - NORM	Figure 3A	$[1, x_j,(study), x_j,(T2D)]$
Fasting blood glucose (FBG)	Figure 3B	$[1, x_j,(study), x_j,(metformin), x_j,(FBG)]$
Fasting plasma insulin (FPI)	Figure 3C	$[1, x_j,(study), x_j,(metformin), x_j,(FPI)]$
Hemoglobin A1c (HBA1C)	-	$[1, x_j,(study), x_j,(metformin), x_j,(HBA1C)]$
Body mass index (BMI)	Figure 3D	$[1, x_j,(study), x_j,(metformin), x$

		$j,(BMI)]$

Animal Study

Eight-week-old C57Bl/6N mice on a standard diet were treated with normal water (placebo, n=6) or 2 mg/mL metformin in drinking water (n=6) for seven days. Mice were maintained in a specific pathogen-free (SPF) environment, and all animal protocols for mouse experimentation were reviewed and approved by the National Cancer Institute (NCI) Animal Care and Use Committees of National Institutes of Health (NIH). On day 7, the mice were fasted for 3 hours prior to euthanasia and cecal contents were collected. Genomic DNA was extracted from cecal contents with MagMax reagents (ThermoFisher Scientific) in an automated Kingfisher instrument following manufacturer instructions. One extraction blank and one mock community (ZymoBiomics Microbial Community Standard) were included in DNA extraction and carried through sequencing. Extracted DNA quantity was quantified on a Qubit and genomic DNA was shipped overnight on dry ice to Novogene Corporation (Sacramento, California, USA) for shotgun metagenomics sequencing on the Illumina NovaSeq platform, resulting in 150x150 bp paired-end reads. The shotgun metagenomics data was subjected to an identical bioinformatics pipeline as described above. Taxa not assigned at the phylum level were removed, and putative contaminants based on the blank control were detected with the decontam R package. A brief report of the control samples is presented in Supplementary Figure 1.

Data Availability

The metagenomic data generated from the mouse study is available at the NCBI Sequence Read Archive under accession PRJNA940065. The accession codes of archived data obtained in this study are PRJNA486795, PRJEB1786, PRJEB39500, PRJEB2054, PRJEB4336, PRJEB5224, PRJEB1220, PRJNA422434, and PRJNA361402. Individualized phenotypic data is available in each study's supplementary material or the corresponding SRA repository. Individualized clinical data from two studies (Elbere 2020 and Sun 2018) were obtained from study authors or through an institutional Data Transfer Agreement. Source code that generated all analyses and figures are available at https://github.com/gandalab/metformin-mycobiome.

Acknowledgements

We would like to thank Dr. Istvan Albert for his guidance in modifying bash scripts originally provided in the Biostar Handbook. Computations for this research were performed on the Pennsylvania State University's Institute for Computational and Data Sciences' Roar supercomputer. We are also grateful to the participants of these studies and the study investigators who made the data publicly available.

Funding Statements

E.V.S. was supported on the PSU/NIDDK funded "Integrative Analysis of Metabolic Phenotypes (IAMP) Predoctoral Training Program (T32DK120509). This work is supported by AFRI Predoctoral Fellowship [grant no. 2022-67011-36461] from the USDA National Institute of Food and Agriculture. This research was supported, [in part], by the Intramural Research Program of the National Cancer Institute, Center for Cancer Research. JDS and MPN were supported in part through NIH 1R01GM148972-01. This

work was supported [in part] by the USDA National Institute of Food and Agriculture and Hatch Appropriation under Project #PEN04752 Accession #1023328.

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