Relationships of Personality Traits With the Taxonomic Composition of the Gut Microbiome Among Psychiatric Inpatients

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Objective: Through the brain-gut-microbiome axis, myriad psychological functions that affect behavior share a dynamic, bidirectional relationship with the intestinal microbiome. Little is known about the relationship between personality—a stable construct that influences social- and health-related behaviors—and the bacterial ecosystem. The authors of this exploratory study examined the relationship between general and maladaptive personality traits and the composition of the gut microbiome.

Methods: In total, 105 psychiatric inpatients provided clinical data and fecal samples. Personality traits were measured with the five-factor model of personality, the Structured Clinical Interview for DSM-IV Axis II Personality Disorders, and the Personality Inventory for DSM-5; 16S ribosomal DNA sequencing and whole-genome shotgun sequencing methods were used on fecal samples. Machine learning (ML) was used to identify personality traits associated with bacterial variability and specific taxa.

Results: Supervised ML techniques were used to classify traits of social detachment (maximum area under the receiver operating characteristic curve [AUROC]=0.944, $R^2>0.20$), perceptual disturbance (maximum AUROC=0.763, $R^2=0.301$), and hoarding behaviors (maximum AUROC=0.722) by using limited sets of discriminant bacterial species or genera. Established bacterial genera associated with psychosis (e.g., *Peptococcus* and *Coprococcus*) were associated with traits of perceptual disturbance. Hoarding behaviors were associated with a defined gut microbial composition that included *Streptococcus*, a known contributor to the development of pediatric autoimmune neuropsychiatric disorders.

Conclusions: Observations from this study are consistent with recent findings demonstrating person-to-person interactions as a mode of gut microbiome transmission. This study adds to the emerging literature on the intricate connections between brain and gut function, expanding the interdisciplinary field of psychiatric microbiology.

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The gut microbiome and associated by-products influence various physiological systems, including immune function, metabolism, and organ development (1), and extend to interactions with the central nervous system, influencing functioning in a dynamic, bidirectional exchange referred to as the microbiome-gut-brain axis (2). Through this axis, the human intestinal microbiome influences psychological functioning and behavior, including mood, stress responses, anxiety, cognition, perception, and pain experience (3). Given the relevance of these factors to mental health, researchers have shown a link between gut microbiome composition and severity of psychiatric symptoms (4).

The composition of the gut microbiome is largely derived from maternal seeding of microbial taxa in utero and at birth (5). By the age of 2 years, an infant's expanded microbial communities in the gut achieve stability and extend into adulthood (1, 6). However, despite this core stability, microbiome composition varies on the basis of several factors, especially diet, lifestyle (e.g., physical activity, smoking status, and work habits), hygiene, sex (assigned at birth), and medication use (7). The microbiome also varies according to the social environment. Recent studies have demonstrated that microbial strains in the gut are transmitted interpersonally, with substantial strain sharing among household members and within populations (6, 8).

Recent efforts have begun to explore personality traits that influence social engagement and interactions, as well as other health-related behaviors, and that have been found to influence the structure of the gut microbiome. In a pilot study of 60 healthy Korean adults, personality traits were found to be associated with different stable gut microbiome clusters, referred to as enterotypes (9), with the traits of novelty seeking and reward dependence being higher in an enterotype characterized by abundances of *Bacteroidaceae.* (10). In a larger study (N=672) of healthy Korean adults (11), high neuroticism was linked to increased abundances of *Gammaproteobacteria*, high conscientiousness was associated with higher prevalence of *Lachnospiraceae*, and low conscientiousness was connected to increased levels of *Proteobacteria*. Those with high trait openness had greater microbial genus richness than those with low openness, and higher agreeableness was related to increased microbiome diversity, but the effect size was small. In a study from an international sample of adults (12), higher abundances of *Akkermansia*, *Lactococcus*, and *Oscillospira* were noted among individuals with higher sociability, whereas individuals with lower sociability had increased *Desulfovibrio* and *Sutterella*. Individuals with higher neuroticism had lower abundances of *Streptococcus* and *Corynebacterium*. In support of the social transmission hypothesis (6), people with larger social networks had more gut microbiome diversity.

Preliminary studies have established connections between the gut microbiome composition and personality traits; however, these studies are few, and findings are discrepant, underscoring the need for more research. This study builds on seminal literature to explore the relationship between the gut microbiome and personality traits in a psychiatric inpatient sample. We hypothesized that personality traits affecting social- and health-related behaviors would differentially affect gut microbiome composition. Specifically, we posited that participants with greater extraversion and lower detachment would exhibit differential genus or species signatures in the microbiome given that they are more likely to interact with others, including novel others, and potentially have more diverse dietary choices. Additionally, we hypothesized that people with significant personality pathology (namely cluster B traits, such as poor impulse control) would also have notable differences in gut microbiome composition related to adverse health behaviors and outcomes.

METHODS

Participants and Setting

Data for this study were collected over 2 years, drawn from individuals (N=105) who were admitted to a psychiatric inpatient hospital with longer than typical lengths of stays, with a mean±SD length of 49.7±14.5 days for stabilization and treatment. During this time, the participants received several personalized psychiatric and psychological interventions, as well as medical intervention as indicated. The treatment setting offered a multimodal approach to addressing symptomatology, which included individual and group psychotherapy, family work, milieu engagement, and 24-hour nursing support.

Procedures

After hospital admission procedures were completed, psychological measures were administered within 72 hours. Self-collected fecal swabs were gathered on average 20.1±12.8 days after admission and were stored in a −80°C freezer until analysis. Data were collected as part of a larger study aimed at gathering treatment outcome data and as part of a separate study designed to identify the potential role of biomarkers in mental illness and treatment outcomes (13). Information about current medications that may affect the gut microbiome was drawn from the hospital's pharmacy database, with particular classes of medications selected a priori, namely, opioids, antipsychotic medications, antidepressants, probiotics, and antibiotics. We previously demonstrated that these medication classes did not influence the structure or function of the gut microbiome in this study sample (4). Thus, we chose not to include medications in the subsequent analyses.

Measures

A standardized survey was used to gather information about patients' demographic characteristics, history of psychiatric illness, and pertinent health data. To identify personality disorders, master's-level research assistants administered the Structured Clinical Interview for DSM-IV Axis II Personality Disorders (SCID-II) (14). The SCID-II provided data on item-level endorsements of criteria for personality disorders, dimensional raw scores for each personality disorder, and categorical information about whether participants met criteria for a personality disorder. Information was included for six of the 10 traditional personality disorder categories: avoidant, obsessive-compulsive, schizotypal, narcissistic, borderline, and antisocial. Because of low base rates of <1% over the 2 years of data collection, other personality disorders were not included. The personality traits in the five-factor model (i.e., openness, extraversion, conscientiousness, agreeableness, and neuroticism) were measured with the Big Five Inventory (BFI) (15). The BFI has strong reliability, converges with the NEO (Neuroticism, Extraversion, and Openness) Five-Factor Inventory, and has demonstrated good internal consistency in other studies using this patient sample (Cronbach's $\alpha=0.81$) (16). To measure personality pathology, the Personality Inventory for DSM-5 (PID-5) (17) was used. The PID-5 comprises 220 items that load onto discrete personality trait facets. The 25 facets form the subscales for five overarching personality domains, namely, detachment, disinhibition, negative affect, psychoticism, and antagonism. The PID-5 has shown good psychometrics and has provided incremental validity over and above the five-factor model (16).

Sample Collection and Genetic Analyses

The MO BIO PowerSoil DNA Isolation Kit (MO BIO, Carlsbad, Calif.) was used to isolate bacterial genomic DNA (gDNA) from fecal samples. The Illumina MiSeq System (Illumina, San Diego) was used to polymerase chain reaction (PCR) amplify and sequence the 16S ribosomal DNA (rDNA) V4 region of microbes with the 515F-806R amplification primer pair, which includes single-end barcodes and MiSeq adapters for sequencing of PCR products and sample pooling. DNA alignment–based phylogenetic methods were used to analyze 16S rDNA sequences. The identifying molecular barcodes were demultiplexed and merged with USEARCH, version 7.0.1090, software. Demultiplexed read pairs underwent an initial quality filtering to remove Illumina adapters, PhiX reads, and reads with a Phred quality score <15 and length <100 bp after trimming. Quality-controlled reads were merged and then further filtered to remove reads exceeding a maximum expected error rate and not matching the expected length. To cluster the 16S rDNA into observed operational taxonomic units (OTUs), the UPARSE algorithm was used. The minimum rarefaction depth of sequencing reads was set at 4,815 and selected automatically via a bootstrapping method by using the R software Agile Toolkit for Incisive Microbial Analyses. The cutoff was set at 97% sequence similarity. In addition, the SILVA database, version 138.1, of only the 16S V4 region was also employed to annotate OTUs. Abundance values were calculated by mapping demultiplexed reads to OTUs. No samples had to be excluded because of insufficient reads. The result was an OTU table suitable for phylogenetic analysis, as well as diversity (alpha and beta) analysis.

A whole-genome shotgun-sequencing (WGS) approach was used for bacterial gDNA in order to minimize background amplification and increase the yield of gDNA (18, 19). Data were scanned to identify any Illumina PhiX or low-quality sequences in the paired-end sequencing reads. The software bbduk was then used to remove the Illumina adapters (BBMAP, version 37.58) (20). Following the corrections, Bowtie 2 (version 2.3.4.3e) (21) software was used to map the final sequences to the human hg38 reference database. To prevent host contamination at the sequence level, the mapping process was performed with high stringency. Taxonomic profiles of microbial DNA were created with MetaPhlAn2 (22). HUMAnN2 (23) was used for functional profiling of the microbial community. The data were put into a final format according to the Biological Observation Matrix (24).

For supervised machine-learning (ML) analyses, relative abundance of microbial 16S rDNA sequences at the genus level was used. For WGS, relative abundance at the species level, computed with MetaPhlAn2, and metabolic pathway abundance, computed with HUMAnN2, were used. ML models were built by using random forest approaches (25), support vector machines (SVMs) (26), and k-nearest neighbor, either for classification (yes-no personality traits) or for regression (numerical personality traits). Data were split into 80% used for training while models were computed, and testing was then used with the remaining 20%; the R package caret was used to implement the cross-validation iterations (27). Classification performance was measured with the area under the receiver operating characteristic curve (AUROC), and regression performance was measured by using the goodness-of-fit R^2. The training-testing split was repeated over 100 cross-validation iterations, and the median and distribution of the performance metrics were collected. Feature importance was assessed with the Interpretable Machine Learning R package (28). Furthermore, only features determined as important in at least 70% of the cross-validation iterations were reported. For the best-performing model for each ML problem, the top 10 increased and top 10 decreased informative features were reported. Preliminary ML analyses of potential confounding associations of age and sex with the gut microbiome (16S rDNA and WGS) revealed weak associations and were therefore excluded from subsequent analyses.

TABLE 1. Baseline demographic and burden-of-illness characteristics of the study sample comprising psychiatric inpatients (N=105)

Characteristic	N	%
Demographic		
Female sex	57	54
White race	94	90
Single and never married	46	44
Some college or greater	91	87
Unemployed in past 30 days	56	53
Clinical		
Alcohol use disorder	40	38
Substance use disorder	38	36
Major depressive disorder	59	56
Bipolar disorder	6	6
Generalized anxiety disorder	23	22
Any personality disorder	38	36
≥1 year of psychotherapy	57	54
≥2 outpatient psychotherapists (lifetime)	84	80
≥2 psychopharmacologists (lifetime)	71	68
Hospitalization for acute psychiatric care (lifetime)	53	50
Hospitalization for extended psychiatric care (lifetime)	40	38

Ethics Statement

We followed guidelines and ethical principles as outlined in the Declaration of Helsinki. After having been given a full explanation of all procedures, each participant provided written informed consent. Study participants attested to the voluntary nature of their participation and were allowed to withdraw from the study at any time without consequence to the clinical care they were receiving at the study hospital. The institutional review board at Baylor College of Medicine approved this study.

RESULTS

Sample Characteristics

The study sample (N=105) consisted primarily of young White adults with a relatively even split between sexes; the mean age was 36.4±13.8 years. The demographic and clinical characteristics of the sample are presented in Table 1.

TABLE 2. Machine-learning classification and regression analysis results of the relationships between personality traits and microbiome diversity among psychiatric inpatients[a]

Trait	16S rDNA	WGS
SCID-II item (N=105)	Median AUROC	Median AUROC
Lack of close friends or confidants other than first-degree relatives	0.789	0.944
Ideas of reference (excluding delusions of reference)	0.763	0.588
Is unable to discard worn-out or worthless objects even when they have no sentimental value	0.722	0.471
Shows arrogant, haughty behaviors or attitudes	0.684	0.500
Impulsivity	0.679	0.579
Chronic emptiness	0.635	0.610
Has a sense of entitlement (i.e., unreasonable expectations of especially favorable treatment or automatic compliance with his or her expectations)	0.605	0.611
Is preoccupied with details, rules, lists, order, organization, or schedules to the extent that the major point of the activity is lost	0.592	0.522
Is unwilling to get involved with people unless certain of being liked	0.583	0.412
Is inhibited in new interpersonal situations because of feelings of inadequacy	0.578	0.575
PID-5 item or facet (N=83)	Median R^2	Median R^2
I have seen things that weren't really there.	0.301	0.052
Detachment domain average score	0.060	0.232
I'm better than almost everyone else.	0.228	0.078
I don't hesitate to cheat if it gets me ahead.	0.220	0.126
I prefer to keep romance out of my life.	0.043	0.197
I avoid social events.	0.030	0.163
Values artistic, aesthetic experiences	0.162	0.029
Detachment domain total score	0.058	0.155
I just skip appointments or meetings if I'm not in the mood.	0.056	0.151
Withdrawal raw score	0.032	0.145

[a] Results for top-performing machine-learning models are shown. AUROC=area under the receiver operating characteristic curve; PID-5=Personality Inventory for DSM-5; rDNA=ribosomal DNA; SCID-II=Structured Clinical Interview for DSM-IV Axis II Personality Disorders; WGS=whole-genome shotgun sequencing.

Most participants had completed some college, and slightly over one-half were unemployed. Many of the participants had multiple axis I disorders and had high levels of functional impairment and service utilization. More than one-third of the sample met formal diagnostic criteria for a personality disorder. Participants had engaged in significant outpatient and inpatient psychiatric treatment before the index hospitalization. The 16S rDNA microbiome analysis was performed for 105 participants, and WGS analysis was performed for 100 participants. SCID-II traits were available for 105 participants, and PID-5 traits were available for 83 participants.

ML Analysis

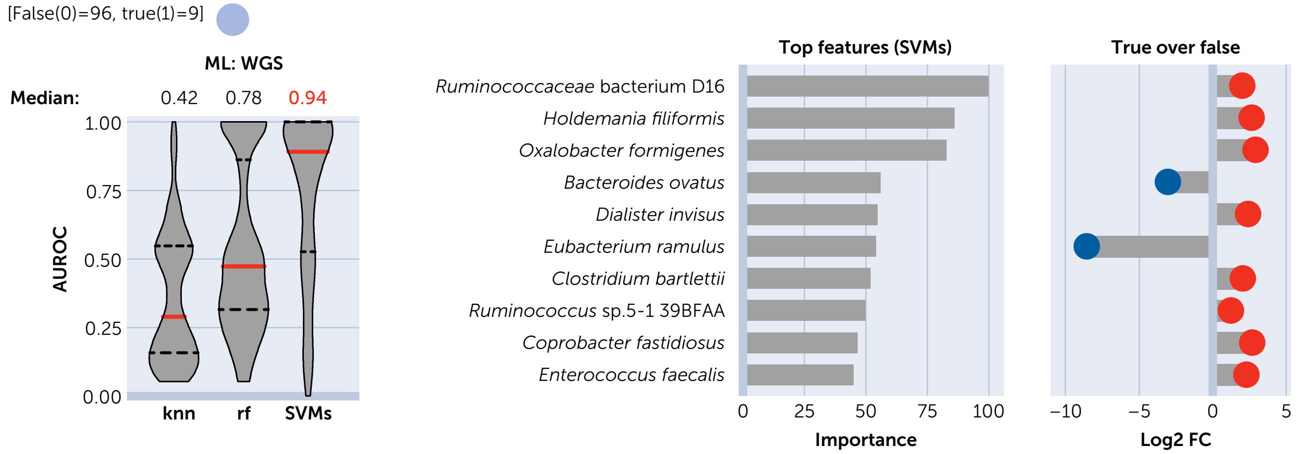
Supervised ML results for the relationships between SCID-II items and the 16S and WGS data revealed three items with acceptable classification performance (median AUROC >0.70). Each of the top 10 PID-5 items and facets evidenced a meaningful percentage of variance explained (median R^2 range 0.145–0.301), although the performance of the ML models varied on the basis of whether they were obtained with 16S rDNA or WGS data (Table 2).

We noted two notable overlapping patterns of items and domains between the SCID-II and PID-5 data: social detachment and perceptual disturbance. For participants who endorsed on the SCID-II that they lacked close friends or confidants other than first-degree relatives, the best-performing classification model was derived with SVMs on the WGS data (median AUROC=0.94, interquartile range [IQR]= 0.83–1.00, with 17 informative microbial species); conversely, for the detachment domain score from the PID-5, the best-performing regression model was obtained with the random forest method using the WGS data (R^2= 0.23, IQR=0.11–0.35, with 35 informative species). An examination of the informative features for the previous two ML problems revealed one species in common (i.e., *Clostridium bartlettii*, as shown in Figure 1). For participants who endorsed ideas of reference on the SCID-II, the best-performing classification model was derived by using SVMs on the 16S rDNA data (median AUROC=0.76, IQR=0.41–0.95, with 10 informative microbial genera); for a single item from the PID-5 related to perceptual disturbance, the best regressor was the random forest method (median R^2=0.30, IQR=0.06–0.49, with 14 informative genera). An examination of the top informative genera associated with the abovementioned SCID-II and PID-5 traits revealed that these traits had two genera (i.e., *Desulfovibrio* and *Eubacterium*) in common (Figure 2).

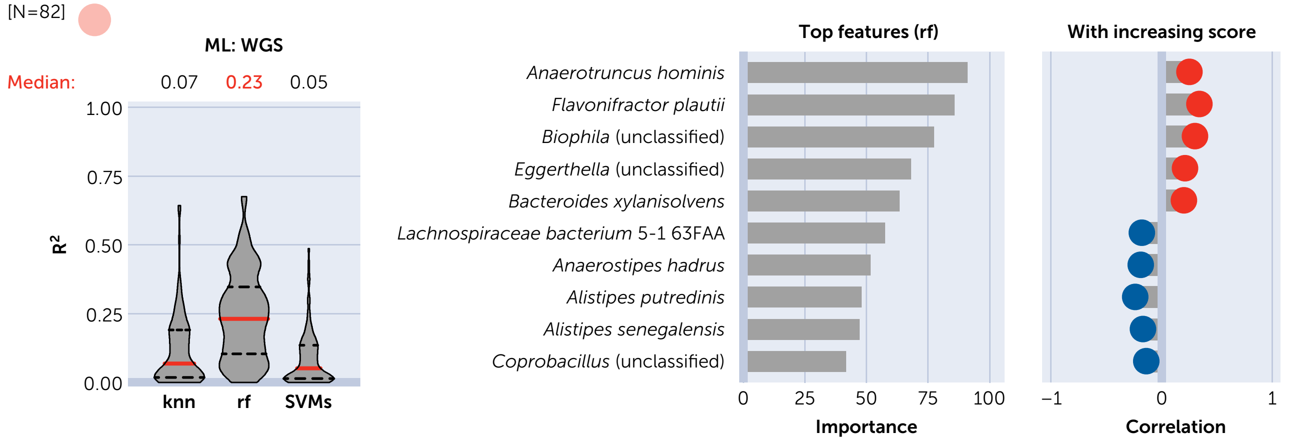
The remaining top-performing items and their distinguishing features are presented in Figure 3. Notable among these items and features was the observation that participants who endorsed an item from the SCID-II associated with hoarding behaviors differed from those who did not endorse the item in a unique bacterial pattern that included *Streptococcus* as the top feature; the best-performing model was the SVMs method on 16S rDNA data (median AUROC=0.72, IQR=0.52–0.83, with 76 informative genera). For the PID-5 item "I'm better than almost everyone else," the best model was obtained with the random forest method using 16S rDNA data (median R^2=0.23, IQR=0.11–0.34, with

FIGURE 1. Microbiome features predicting social detachment among psychiatric inpatients (N=105)[a]

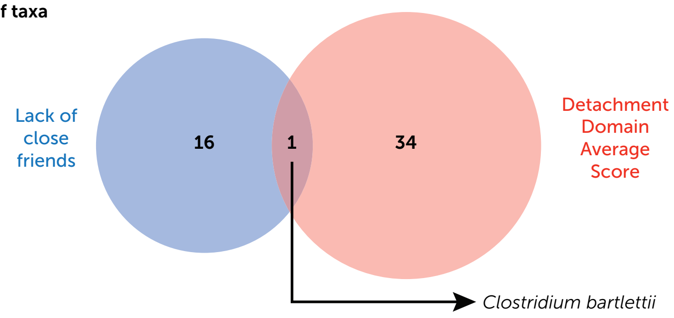
A. Lack of close friends or confidants other than first-degree relatives



B. Detachment Domain Average Score



C. Overlap of taxa



[a] Panel A shows a violin plot of machine-learning (ML) classifications, obtained with ML analyses that included random forest (rf), support vector machines (SVMs), and k-nearest neighbor (knn) methods using microbial whole-genome shotgun-sequencing (WGS) sample data and true-or-false responses to the item "lack of close friends or confidants other than first-degree relative"; the median area under the receiver operating characteristic curve (AUROC) is indicated. Top informative species identified with the SVMs method are shown, along with the log2 fold change (FC) between true and false samples (the horizontal axis in the charts in this and the other panels shows a relative measure of importance, with higher values indicating greater importance). Panel B shows a violin plot of classifications obtained with ML regression analyses by using data from WGS samples and detachment domain average scores, with median R^2 indicated. Top informative microbial species identified with the rf method are shown, along with the correlation of average score with species expression. Panel C illustrates overlap of the species that were identified as being informative in at least 70% of the ML iterations from panels A and B. For panels A and B, values shown in red font indicate the best-performing model.

21 informative genera). Finally, for the PID-5 item "I don't hesitate to cheat if it gets me ahead," the best model was achieved with the random forest method using 16S rDNA data (median R^2=0.22, IQR=0.06–0.33, with 22 informative genera).

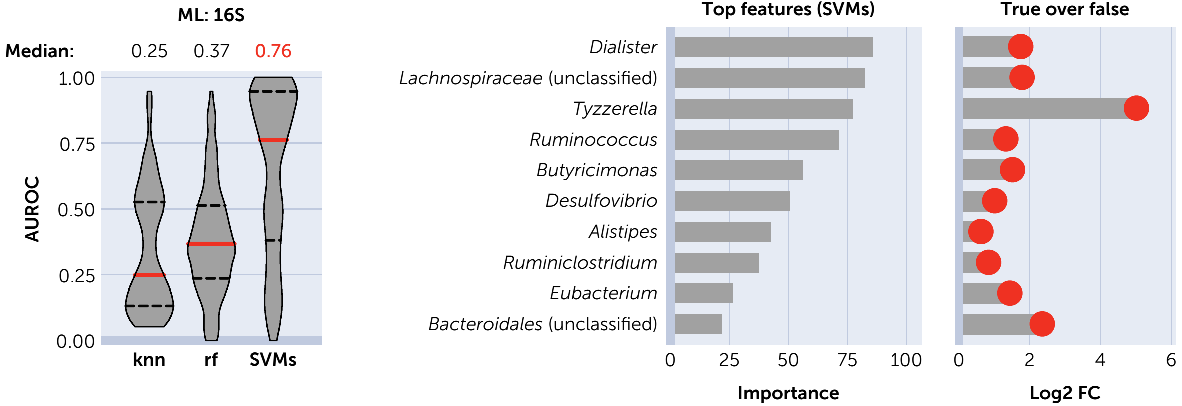
DISCUSSION

We hypothesized that levels of extraversion or detachment would differentially affect the composition of the gut microbiome at either the genus or species level. In support

FIGURE 2. Microbiome features predicting ideas of reference or perceptual disturbance among psychiatric inpatients (N=105)[a]

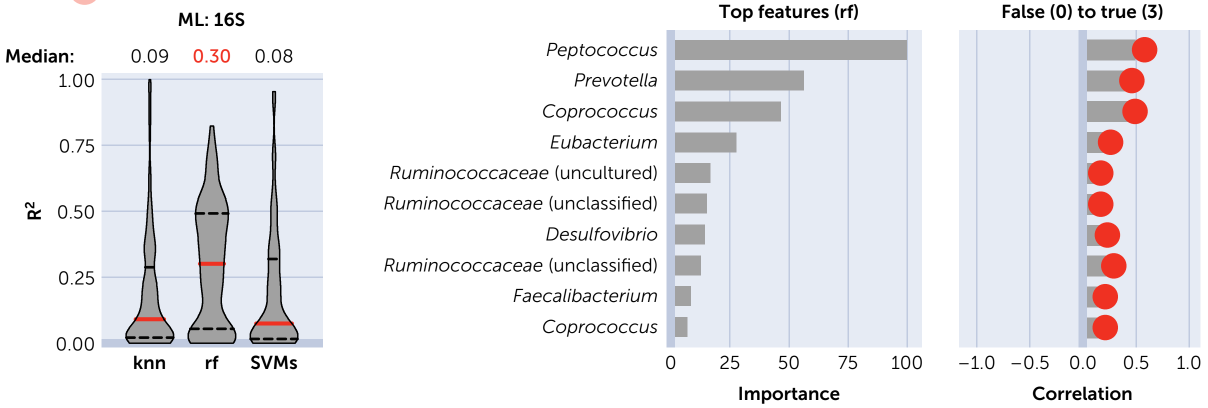
A. Ideas of reference (excluding delusions of reference)

[False(0)=96, true(1)=9] ●

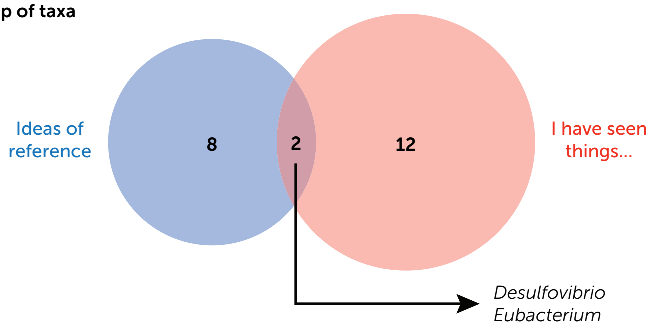


B. "I have seen things that weren't really there"

[N=82] ●



C. Overlap of taxa

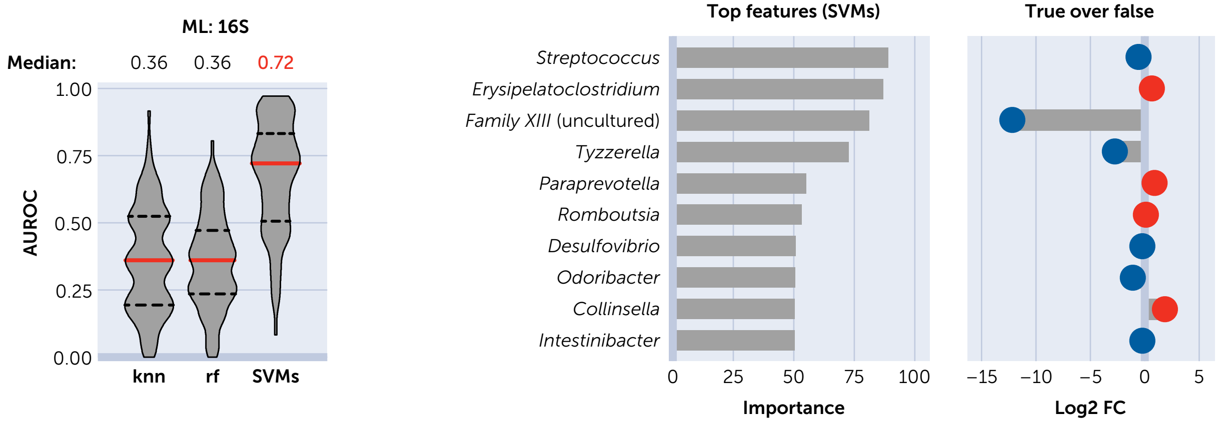


[a] Panel A shows a violin plot of machine-learning (ML) classifications, obtained with ML analyses that included random forest (rf), support vector machines (SVMs), and k-nearest neighbor (knn) methods using microbial 16S ribosomal DNA samples and true-or-false responses to the ideas of reference item; the median area under the receiver operating characteristic curve (AUROC) is indicated. Top informative genera identified with the SVMs method are shown, along with the log2 fold change (FC) between true and false samples (the horizontal axis in the charts in this and the other panels shows a relative measure of importance, with higher values indicating greater importance). Panel B shows a violin plot of classifications obtained with ML regression analyses by using 16S rDNA samples and Personality Inventory for DSM-5 scores, with median R^2 indicated. Top informative genera identified with the rf method are shown, along with the correlation of average score with genera expression. Panel C illustrates overlap of the genera that were identified as being important in at least 70% of the ML iterations from panels A and B. For panels A and B, values shown in red font indicate the best-performing model.

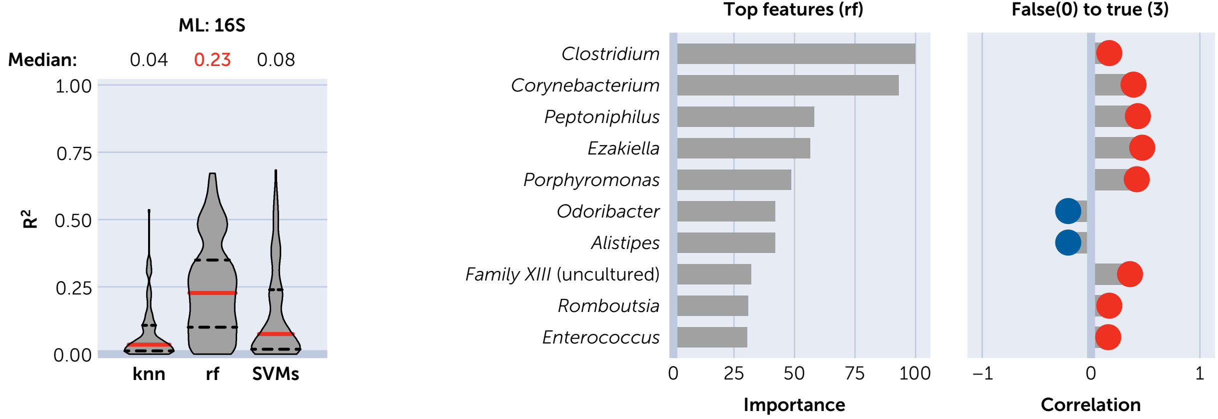
of this hypothesis, findings from this nascent effort to examine personality traits and taxonomic composition of the gut microbiome suggest that individuals with higher social detachment have a microbiome composition that is distinguishable from the microbiome compositions of those with higher social integration. Individuals high in detachment are known to avoid social engagement, likely reducing microbial input from social exchanges, with implications for gut microbiome composition. These results are consistent with recent findings indicating that transmission of gut microbiome organisms occurs through person-to-person interactions within a shared environment (6, 8) and that gut microbiome diversity is associated with social network size (12). It is compelling to hypothesize that this decreased

FIGURE 3. Microbiome features predicting other top-performing behaviors and traits among psychiatric inpatients (N=105)[a]

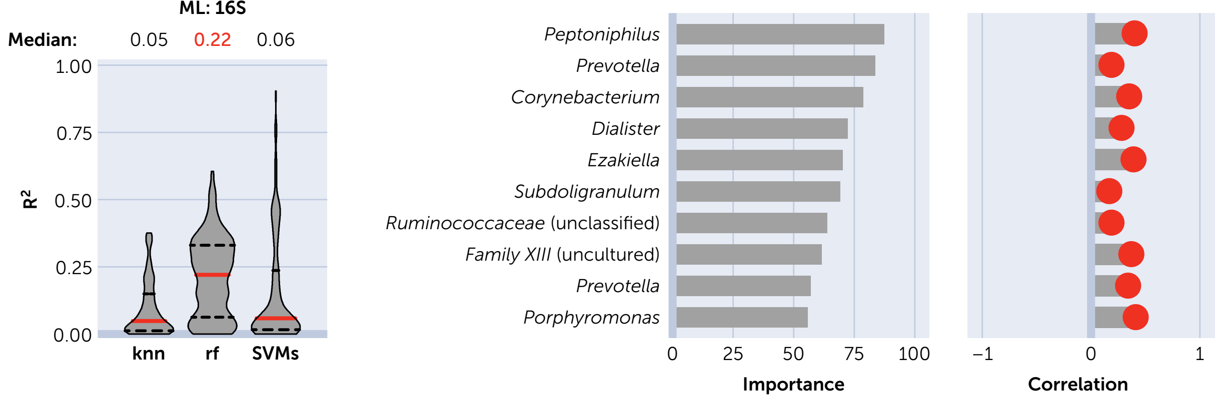
A. Is unable to discard worn-out or worthless objects even when they have no sentimental value
[False(0)=91, true(1)=14]



B. "I'm better than almost everyone else"
[N=82]



C. "I don't hesitate to cheat if it gets me ahead"
[N=82]



[a] Panel A shows a violin plot of machine-learning (ML) classifications, obtained with ML analyses that included random forest (rf), support vector machines (SVMs), and k-nearest neighbor (knn) methods using 16S ribosomal rDNA samples and true-or-false responses to personality trait items, with the median area under the receiver operating characteristic curve (AUROC) indicated. Top informative microbial genera identified with the SVMs method are shown, along with the log2 fold change (FC) between true and false samples (the horizontal axis in the charts in this and the other panels shows a relative measure of importance, with higher values indicating greater importance). Panels B and C show violin plots of ML classifications, obtained with ML analyses that used microbial 16S rDNA samples and Personality Inventory for DSM-5 scores, with the median R^2 value indicated. Top informative microbial genera identified with the rf method are shown, as is the correlation of average score with genera expression. For panels A–C, values shown in red font indicate the best-performing model.

microbial input may render the gut microbiome vulnerable to compositional or functional imbalances known to play a role in gut dysbiosis; the gut microbiome may partially mediate the link between social isolation and loneliness and adverse health effects (12). Of note, proinflammatory immune responses and chronically activated hypothalamic pituitary adrenocortical axis activity are known to drive the relationship between social isolation and poor health (29). These mechanisms appear to converge with our growing understanding that gut dysbiosis, possibly worsened by social detachment, plays a role in activating inflammatory responses with far-reaching physiological and psychological consequences mediated through the gut-brain axis (30).

Additionally, those who endorsed items associated with visual hallucinations and ideas of reference were found to have distinct gut microbial compositions. Although these findings were based on item-level analysis and cannot be assumed to reflect personality trait domains, these items are often associated with perceptual dysregulation, psychosis, and schizotypal personality disorder. Individuals who endorsed visual hallucinations had microbiomes defined by *Peptococcus*, *Prevotella,* and *Coprococcus*. Although *Peptococcus* is not typically associated with psychosis or schizophrenia, some evidence suggests that this genus shows distinct differences in prevalence between people with schizophrenia and healthy individuals (31). *Peptococcus* has also been found to be present among individuals with treatment-resistant depression (32) and in mice showing obsessive-compulsive disorder (OCD)–like behaviors (33). A clearer picture emerges regarding *Prevotella* and *Coprococcus* species, with increased relative abundances of *Prevotella* and decreased relative abundances of *Coprococcus* having been consistently linked to psychosis (34). *Prevotella* has also been associated with childhood sexual trauma (35), as well as with anxiety and depression (36). *Coprococcus* appears to be consistently underrepresented among depressed individuals and to be associated with greater levels of psychiatric disorder severity (4). We found that individuals who endorsed ideas of reference had a microbiome most notably characterized by *Dialister*, unclassified *Lachnospiraceae*, *Tyzzerella,* and *Ruminococcus*. All of these genera, aside from *Tyzzerella*, have been previously linked to psychosis (34). Although *Tyzzerella* has not previously been connected with psychosis, it has been implicated in arthritis, suggesting that this genus has a role in immune-mediated inflammatory disease (37).

These findings did not support the hypothesis that cluster B personality pathology significantly affects the composition of the gut microbiome. However, a notable finding from this study was that individuals who endorsed a criterion of OCD (i.e., unable to discard worn-out or worthless objects) had a defined gut microbial composition, including the genera *Streptococcus*, *Erysipelatoclostridium*, uncultured *Clostridiales Family XIII bacterium*, and *Tyzzerella.* This finding is consistent with those of previous research linking abundances of *Streptococcus* to reduced neuroticism (12). Reduced abundances of *Streptococcus* have also been linked to brain development, with depletions in this genus being evident among infants who could pass a joint attention task (38). Interestingly, *Streptococcus* is associated with PANDAS (pediatric autoimmune neuropsychiatric disorders associated with streptococcal infections), a condition in which OCD or tic disorders emerge directly after a *Streptococcus* infection in childhood (39). The onset of symptoms is thought to be driven by antibodies arising from immune responses to *Streptococcus* that interact with neurons in the basal ganglia. We are not aware of other research linking the remaining bacteria with obsessive or obsessive-compulsive features, although the bacterial order *Clostridiales* has been associated with OCD (40).

The role of these taxa individually and interactively in the context of interpersonal functioning should be explored in greater detail in future studies. Dysbiosis is causally linked to atypical immune responses, which are often accompanied by an upregulated production of inflammatory cytokines that are related to the pathophysiology of depression and anxiety (30).

Strengths of this study included the comparatively large number of fecal donors and the systematic assessment of personality traits and pathology in a controlled physical setting. However, several limitations must be recognized and should be addressed in follow-up initiatives. A number of key findings revealed correlations at both the item and personality trait domain levels. Although item-level endorsements were derived from measures of personality functioning, it is possible that some endorsements may have reflected clinical syndromes not typically associated with personality pathology, such as schizophrenia or OCD. The study population consisted of psychiatric inpatients with a wide range of comorbid conditions, including somatic distress with both organic and psychological etiologies. Discordant results may be observed in a patient population with greater diagnostic homogeneity (e.g., exclusively participants with borderline personality disorder). Fecal samples were collected early during the hospitalization but not systematically. The variability in the number of days between admission and fecal sample collection may have affected the findings. Participants were variably exposed to a controlled environment with scheduled and prepared meals as well as observed abstinence from alcohol and drugs, which also may have affected findings. Additionally, the study participants had a limited number of nutritional options in the hospital, but they were free to select meals from a menu of options. This variation in dietary consumption was not consistently monitored and could have influenced our findings. Future studies should take nutritional intake into account. Such studies should also measure and quantify adverse health behaviors, especially substance use, to control for possible cofounding effects. For certain personality traits, the prevalence was 8%–14%; we used a stringent cross-validation approach in this study, but future studies should be conducted to validate our findings in larger participant samples.

CONCLUSIONS

Our knowledge of the gut microbiome's mechanistic significance in the onset and maintenance of interpersonal functioning, as well as psychiatric illness, must be further developed. This study contributes to the emerging body of research on the intricate connections between gut and brain functions, expanding the interdisciplinary field of psychiatric microbiology. As the relationships between gut and brain functions are elucidated, these data form the foundation for interventional studies. In the future, it may be possible to directly and indirectly manipulate bacterial structure and function to address the psychological and physiological consequences of psychiatric symptomatology and illness.

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