Novel insights into the genetic architecture and mechanisms of host/microbiome interactions from a multi-cohort analysis of outbred laboratory rats

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Abstract

The intestinal microbiome influences health and disease. Its composition is affected by host genetics and environmental exposures. Understanding host genetic effects is critical but extremely challenging in humans, due to the difficulty of detecting and mapping these effects. To address this issue, we analysed host genetic effects in four cohorts of outbred laboratory rats exposed to diverse environments. We found that polygenic host genetic effects were consistent across environments and we identified three replicated microbiome-associated loci. One of these loci involved a sialyltransferase gene and *Paraprevotella*, a bacteria that improves gut immunity, and we found a similar association in a human cohort. Moreover, we demonstrated that some bacteria are affected by host genetic effects and are also horizontally transmitted to cage mates, and that this coupling greatly increases the genetic variance of microbiome phenotypes. Our findings provide new insights into the genetic architecture and mechanisms of host/microbiome interactions.

Introduction

The mammalian intestinal tract is home to trillions of metabolically active, immuno-modulating microorganisms. In humans, the composition of the gut microbiome is correlated with many diseases and, in some cases, manipulations of the microbiome have suggested that these relationships are causal[1]. The composition of the gut microbiome is affected by a variety of factors, including maternal seeding at birth[2-5], diet[6], medication[6,7], host genetics effects[8-15] and acquisition of microbes from family members and unrelated social partners[16-18]. A better understanding of how these factors act could open new avenues for medicine.

Host genetic effects have been detected in humans[8-15] but questions remain as to the proportion of bacteria affected, how much variation in these bacteria is due to host genetic effects, whether host genetic effects are consistent across environments, and what the

underlying genetic loci are. Indeed, only two microbiome-associated loci have been replicated so far: the *LCT* lactase persistence locus and the *ABO* blood group locus, which interacts with the *FUT2* secretor status locus.

Furthermore, recent evidence indicates that many gut bacteria can be transmitted vertically (from parent to offspring) and/or horizontally (e.g. between unrelated individuals)[16-18], but these findings have not yet been integrated with findings on host genetic effects. In particular, whether some bacteria are affected by host genetic effects and are also transmissible, is unknown.

Many reasons contribute to the difficulty to detect, quantify and map host genetic effects in humans. Environmental factors such as diet, medication and social contacts affect the composition of the microbiome, and few human datasets have sufficient information on these variables. In addition, technical variation in the protocols and methods used to profile the microbiome complicate efforts to meta-analyse the data[11]. Given the difficulties of studying host genetic effects in humans, studies in other species are needed.

Due to the shared anatomy and physiology of mammals, laboratory rodents are a model of choice to study host-microbiome interactions[19]. Populations of laboratory rodents exist that are derived from multiple founders through many generations of outbreeding, resulting in high levels of genetic diversity, fewer rare variants and higher levels of linkage disequilibrium (**LD**) compared to humans. Higher levels of LD mean that fewer independent tests are performed in genome-wide association studies (**GWAS**) and smaller sample sizes can be used. The levels of LD observed in outbred laboratory rodent populations remain compatible with the identification of causal genes at associated loci[20,21]. Crucially, laboratory rodents live in a controlled environment, greatly reducing noise and confounding effects from non-genetic factors influencing the gut microbiome.

In this study we conducted a comprehensive analysis of host genetic effects in four cohorts of outbred “Heterogeneous Stock” (**HS**) rats, a population established from eight inbred strains[22] and thereafter maintained using an outbreeding scheme (Fig. 1A). The 4,154 male and female rats included in this study were part of a multisite project examining the genetic basis of physiological and behavioural traits[23-25], so we had access to genotype information at about 5 million single nucleotide polymorphisms (**SNPs**)[26]. The majority of the SNPs (>75%) were common (MAF > 0.01) (Suppl. Fig. 1A) because they are derived from one or more of the 8 founders (hence MAF $\geq$ 1/8), and LD between neighbouring variants extended slightly further than in humans (Suppl. Fig. 1B, average distance between SNPs with LD R^2 > 0.9 was 111$\pm$788Kb in HS rats, compared to 39$\pm$33Kb in humans).

The rats included in this microbiome study belonged to four distinct cohorts, referred to as **NY**, **MI**, **TN1** and **TN2** (the acronyms refer to the U.S.A. states where the rats were reared). The four cohorts differed in terms of rearing facilities, age and fasting state when the cecal (gut) microbiome was sampled, among other known and presumably unknown differences (Fig. 1B and Suppl. Table 1). In contrast, cross-cohort genetic differences were minimised by distributing the litters across the NY, MI and TN1 cohorts. Finally, all microbiome samples were profiled in a single laboratory using the same protocol. This experimental design was ideal to evaluate the consistency of host genetic effects across environments.

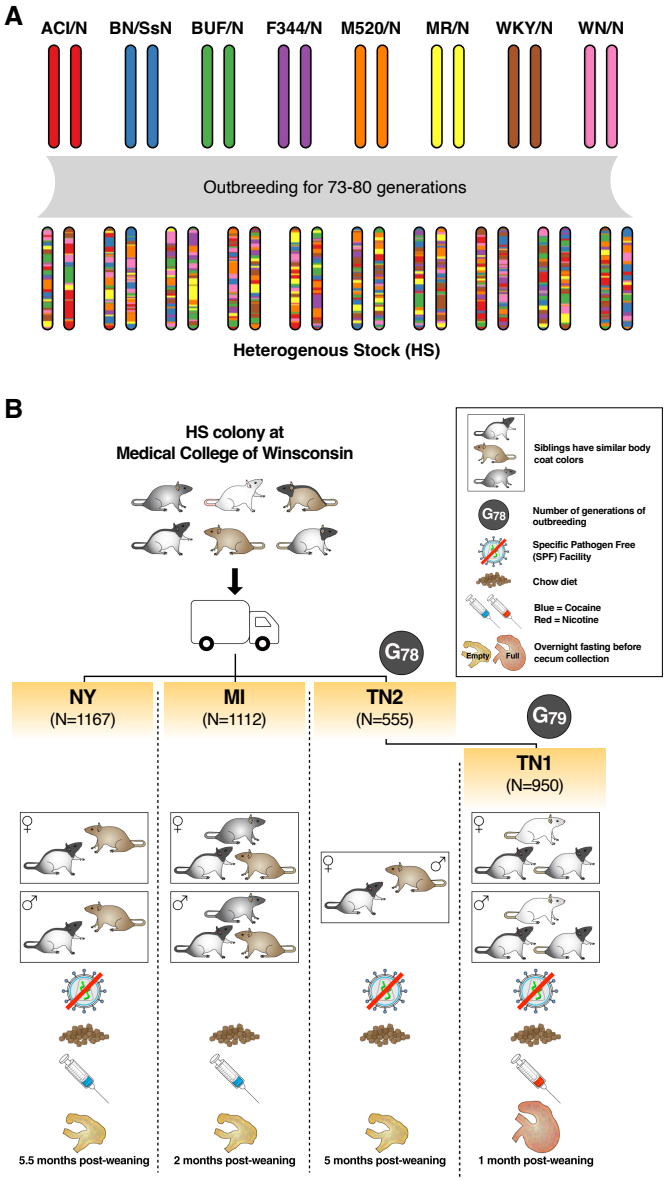

Figure 1 Experimental design with HS rats. (A) Provenance of the HS rats used in this study. (B). Overview of the four cohorts of HS rats included in this study. Detailed information is provided in Suppl. Table 1 and Methods.

Results

1. Between-environment variation in the cecal microbiome

This study focused on the rat cecal microbiome, which is a model for the human colonic microbiome since the cecum and colon are the main sites of fermentation of plant-based foods in the two species[19]. The cecal microbiome of the rats was profiled by amplicon sequencing targeting the 16S gene of gut bacteria and archaea. The microbiome phenotypes we considered were amplicon sequence variants (**ASVs**), which are error-corrected sequences providing the greatest taxonomic resolution possible with 16S data, as well as the higher-level bacterial taxa these ASVs were assigned to.

In all four cohorts, the *Lachnospiraceae* family was the most abundant bacterial family. Other abundant families (>10% relative abundance in at least one of the cohorts) were *Oscillospiraceae_88309*, *Muribaculaceae* and *Bacteroidaceae* (Fig. 2A). As expected, the composition of the gut microbiome was more similar among rats from the same cohort ("adonis" analysis of variance *p*-value < 0.001, Fig. 2B). The variation explained by cohort (R^2 = 0.31) was much greater than the variation explained by sex (R^2 = 0.0092). 130 out of 364 families were differentially abundant between the cohorts (Bonferroni adjusted analysis of variance *p*-value < 0.05), including the four most abundant families. In addition, within-sample (alpha) diversity was also significantly different between cohorts (analysis of variance *p*-value = 3.65×10^{-103}, Suppl. Fig. 2).

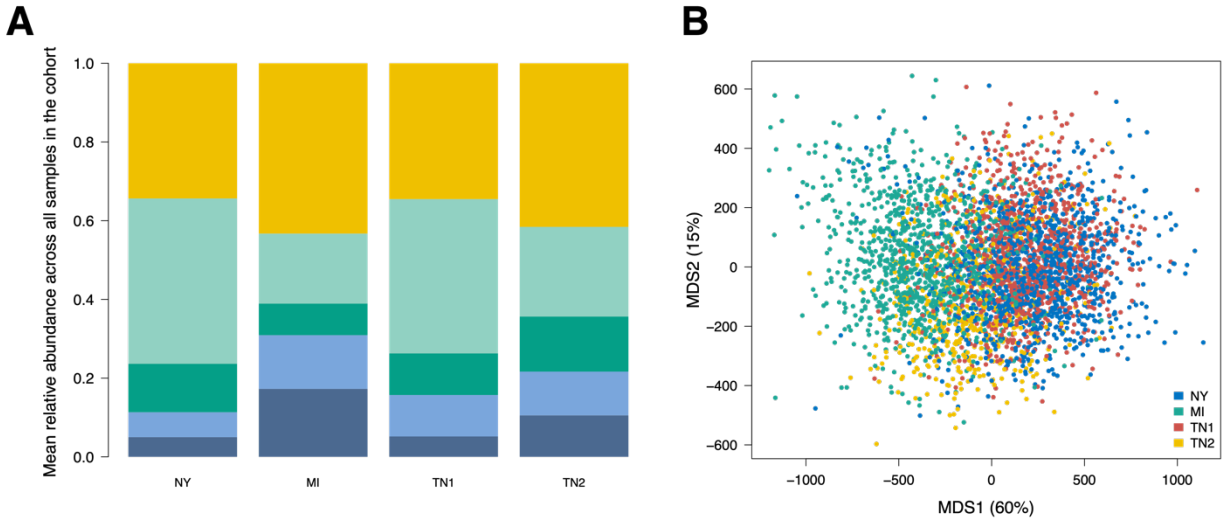

Figure 2 Variation in the HS rat gut microbiome. (A) Average family-level microbiome

profiles in the different cohorts. From top to bottom, yellow is for the sum of abundances of lower abundance families, light green is for *Lachnospiraceae* family, dark green is for *Oscillospiraceae_88309* family, light blue is for *Muribaculaceae* family and dark blue is for *Bacteroidaceae* family. (B) Between-sample ("beta") diversity across all four cohorts.

2. Polygenic host genetic effects and their consistency across environments

As a first step, we characterised polygenic host genetic effects using variance components models. In all our analyses, the compositional nature of microbiome data[27] was accounted for. Even though confounding between host genetic effects and cage (i.e. shared micro-environmental) effects was avoided by design in the NY, MI and TN1 cohorts (see Methods), we accounted for any potential confounding from maternal and cage effects in all our analyses, by fitting jointly random effects for host genetic effects, cage and maternal effects. We analysed the different cohorts separately to evaluate the consistency of host genetic effects across environments, and limited our analyses to ASVs and taxa present in at least 50% of the rats in a cohort, to get precise estimates of the variance components. Thus, hereafter a microbiome phenotype refers to a given ASV or taxon in a given cohort, and we considered 569, 589, 523 and 613 microbiome phenotypes in the NY, MI, TN1 and TN2 cohorts, respectively.

Heritability is a population-specific measure. Hence, the heritability of microbiome phenotypes is best understood when it is compared to the heritability of other phenotypes measured in the same population, or compared to the magnitude of other (non-genetic) effects. The SNP heritability of microbiome phenotypes was generally lower than the SNP heritability of behavioural and physiological phenotypes measured in the same rats (Fig. 3A). ASVs tended to have higher heritability than species and genera, suggesting that host genetic effects may be heterogeneous within bacterial species (Suppl. Fig. 3). Notably, the most heritable microbiome phenotypes were not the most abundant ones (Fig. 3B). Host genetic effects were comparable in magnitude to maternal effects on the microbiome and much lower than cage effects (Fig. 3C and Suppl. Fig. 4).

We next tested whether the heritability of an ASV or a taxon in one cohort was predictive of the heritability of the same ASV or taxon in another cohort. The heritability of ASVs and taxa measured in the largest cohort (NY) was significantly correlated with the heritability of the same ASVs and taxa in two other cohorts (MI and TN2, cor = 0.31 and cor = 0.13 respectively, p-value < 0.05 after Bonferroni correction accounting for the six correlations tested, Fig. 3D). These correlations reflect the extent to which the proportion of phenotypic variance explained by host genetic effects is conserved across cohorts, but they do not indicate whether the effects of individual variants are consistent across cohorts.

To address the latter question, we estimated the genetic correlation between the abundance of an ASV or a taxon measured in one cohort and the abundance of the same ASV or taxon measured in another cohort. We did so only for those ASVs and taxa that had a substantial heritability (> 5%) in both cohorts. The cross-cohort genetic correlations were rather high (median 0.5, median standard errors 0.3, Fig. 3E) and 60% of them were significant (FDR < 0.1), demonstrating substantial consistency of polygenic host genetic effects across cohort-associated environments. One ASV, in the genus *Anaerotruncus*, was particularly consistent across the different environments, with all between-cohort genetic correlations close to 1.

Motivated by the largely shared genetic basis of ASVs and taxa across cohorts, we analysed all samples jointly (fitting cohort as a fixed effect covariate) to identify significantly heritable ASVs and taxa. Using the joint sample (N = 3,784), we found that 214 out of 546 microbiome phenotypes (39.2%) were significantly heritable (FDR < 0.1). Host genetic effects explained an average of 3% of phenotypic variation for these 214 phenotypes, with a maximum heritability of 9.3% and a minimum heritability of 0.5%.

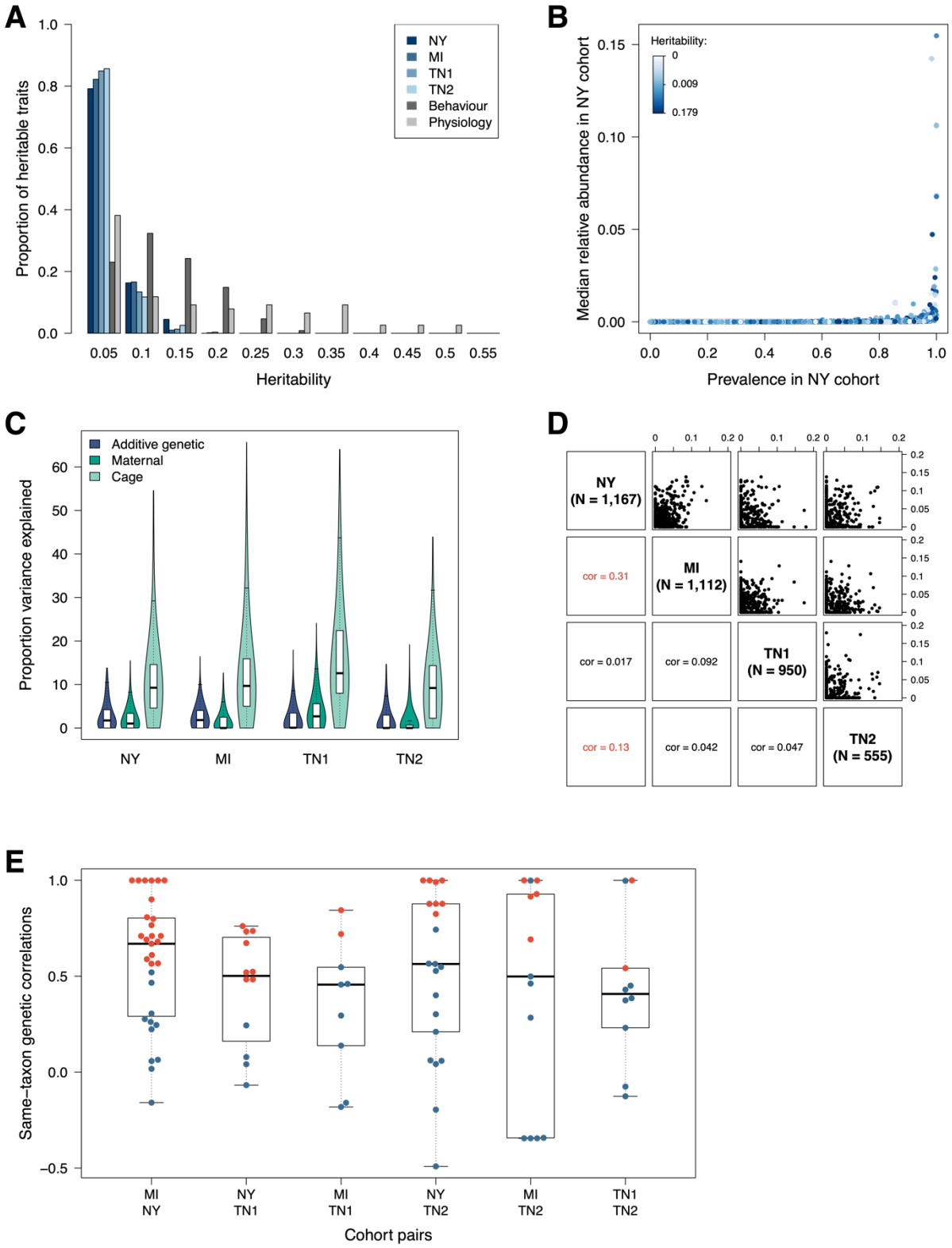

Figure 3 Characteristics of polygenic host genetic effects. (A) Comparison of the heritability of microbiome and physiological phenotypes. (B) Relationship between

prevalence, relative abundance and heritability for the microbiome phenotypes measured in the NY cohort (similar results are observed in the other cohorts, see Suppl. Fig. 5). (C) Relative magnitude of polygenic host genetic effects (SNP heritability), maternal effects and (shared micro-environmental) cage effects on microbiome phenotypes. (D) Correlation between heritability of one ASV/taxon in one cohort and heritability of the same ASV/taxon in another cohort. Only ASVs and taxa that are common (prevalence > 50%) in both cohorts were used. (E) Genetic correlation between the abundance of an ASV/taxon in one cohort and the abundance of the same ASV/taxon measured in another cohort. Only ASVs and taxa that are common in both cohorts and with a heritability greater than 5% were used. Correlations significantly different from 0 (p-value < 0.05) are shown as red dots.

3. Microbiome-associated loci and their replication across environments

We next mapped the genomic loci affecting the microbiome phenotypes measured in each cohort, considering only those ASVs and taxa present in at least 50% of the rats in each cohort. The genome-wide significance threshold (-logP >= 5.8), which corrects for the number of independent SNPs tested, was determined using permutations[28,29] and later adjusted to account for the number of independent microbiome phenotypes analysed in each cohort, yielding a similar threshold (-logP >= 8.4) in all four cohorts. 6 associations were significant in the NY cohort, 5 in the MI cohort, 2 in the TN1 cohort, and 0 in the TN2 cohort (Fig. 4). Seven of these associations were with the same locus on chromosome 1 (associated variants all in strong LD), including associations with *CAG-793* and *UMGS1994* detected in multiple cohorts (Suppl. Table 2). The seven associations involved different genera in the *Firmicutes_A* phylum, providing strong evidence of pleiotropy at this locus. One of the significant associations was on chromosome 4, for the genus *CAG-485* measured in the NY cohort. Although not significant at the stringent threshold we used (-logP >= 8.4), associations were also detected in the MI and TN1 cohorts for this locus and this genus at the less stringent threshold for genome-wide significance (-logP >= 5.8, Suppl. Table 3). Finally, five of the significant associations were with the same locus on chromosome 10 (associated variants all in strong LD), all of them with either the genus *Paraprevotella* or an ASV in the genus *Paraprevotella*, and in three different cohorts (NY, MI and TN1, Suppl. Table 4).

Given the observed consistency of polygenic host genetic effects across cohorts, we mapped host genetic effects in the full sample (N = 4,154), fitting cohort as a fixed effect to account for differences in mean abundances between cohorts and adjusting the genome-wide significance threshold to account for the effective number of common microbiome phenotypes considered in the full sample (-logP = 8.4). This analysis did not uncover any new associations compared to the analysis of the individual cohorts. Indeed,

the 11 significant associations detected with the full sample were between the three replicated loci on chromosomes 1, 4 and 10 and the previously described genera.

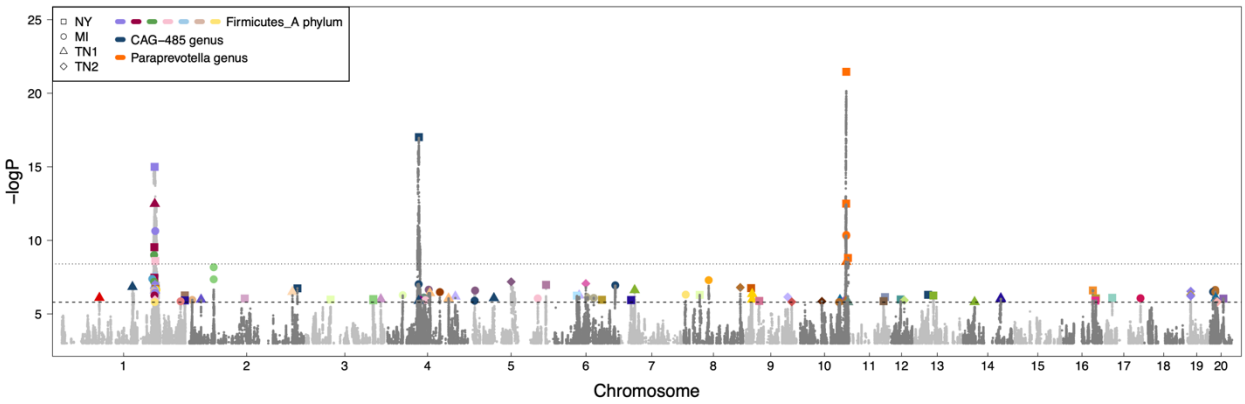

Figure 4 Microbiome-associated loci. This porcupine plot shows the association values for all microbiome phenotypes (n = 2,294 phenotypes from 4 cohorts). The lower line reflects the genome-wide significance threshold for an individual trait, which accounts for the number of independent SNPs tested; the higher line is the adjusted significance threshold, which in addition accounts for the number of independent microbiome phenotypes examined in each cohort. The larger, coloured dots highlight genome-wide significant associations for microbiome phenotypes that have an annotation at the genus level. The colour of the dot refers to the genus affected. The shape of the dot refers to the cohort in which the association was identified.

4. Mechanisms of host genetic effects on the gut microbiome

We next adopted a systems genetics approach to gain insights into the genetic variants and genes underlying the replicated associations at the chromosome 1, 4 and 10 loci, leveraging a wealth of genomic data, including an exhaustive catalogue of SNPs and small insertions/deletions segregating in the HS population[26], PacBio HiFi long-read genome sequencing data from the HS founders and a subset of HS rats, RNA isoform sequencing data from related laboratory rat strains, and publicly available genotype and short-read genome sequencing data from wild rats[30,31].

At the replicated locus on chromosome 1 (associated with various bacteria in the *Firmicutes_A* phylum), the variants in strong LD (defined as $R^2 > 0.9$) with the lead variant formed a large LD block extending over 3.2Mb (Suppl. Fig. 6). Such a large LD block is highly unusual in the HS population. Indeed, this was the largest LD block observed for any of the genome-wide significant microbiome-associated loci (median size was 0.57Mb). Since the associations at this locus were highly significant, we looked for variants that might affect protein structure and function. Among the variants in strong LD

with the lead variant, three were predicted to be probably or possibly damaging by Polyphen, all in the olfactory receptor gene *Or13a18c*, which has no obvious connection to the microbiome. On the other hand, four genes within this locus encode gel-forming mucins. In particular, *Muc2*, which encodes the most abundant mucin present in the gut and is known to play a key role in host/microbiome interactions, is contained within this locus.

At the replicated locus on chromosome 4 (associated with a single ASV in the *Muribaculaceae* family), the variants in strong LD with the lead variant also fell in a larger than usual block of LD, extending over 1.3Mb (Suppl. Fig. 7). Since the associations at this locus were also very significant, we again sought to identify variants affecting protein structure and function. One deleterious variant was present in each of four genes within this locus: *Pip*, *Prss58*, *Kel* and *Tas2r139*. An effect of PIP (prolactin induced protein) on the oral microbiome and various cultured bacterial strains was previously reported[32,33]. However, the effect of *Pip* on *Muribaculaceae*, which are mostly present in the lower gut, is novel.

The replicated locus on chromosome 10 (associated with *Paraprevotella*) harboured the most significant association of all (-logP = 21.5, Fig. 5A). The variants in strong LD with the lead variant were all specific to the WN/N founder and within a small 105Kb region harbouring only three genes: *St6galnac2, St6galnac1 and Mxra7*. Thirteen variants were annotated by Polyphen as possibly or probably damaging, all of them in *St6galnac1*, a gene responsible for the α2,6-sialylation of gut mucin O-linked glycans and also, potentially indirectly, N-linked glycans[34]. Increases in the depth of sequencing of a 9kb region for the WN/N HS founder, some outbred HS rats that carried the WN/N haplotype, and wild rats suggested a partial duplication, partial triplication of *St6galnac1* (Fig. 5B and Suppl. Fig. 8). Since this region of WN/N is identical by descent to the SHRSP/A3N inbred rat strain (Suppl. Fig. 9; SHRSP is not a founder of the HS population) and a *de novo* assembly of the genome of SHRSP/BbbUtx is available[35], we confirmed that the *St6galnac1* duplication/triplication was present in the SHRSP/BbbUtx genome assembly (Fig. 5C). Furthermore, using IsoSeq RNA sequencing reads from lymphoid tissue of an F1 rat that was a cross between SHRSP/BbbUtx (strain with three copies of *St6galnac1*) and WKY/Utx (single copy of *St6galnac1*), we found that one of the two extra copies encoded a full-length transcript, contradicting the current gene annotation of the SHRSP/BbbUtx assembly and suggesting that the copy number variant observed in the WN/N haplotype could result in increased expression of *St6galnac1.*

The causal role of *St6galnac1* was supported by an independent line of evidence: in HS rats *Akkermansia muciniphila* and *Muribaculum intestinale* were also associated with the *St6galnac1* locus (MI cohort, not genome-wide significant, see Suppl. Table 4 and Fig.

5D-F). Since these bacteria have been shown to be strongly affected by *St6galnac1* in a gene knock-out experiment by Yao et al.[34], the associations between *St6galnac1* and *A. muciniphila* and *M. intestinale* detected in HS rats further support a causal role of *St6galnac1*. The study by Yao et al. supports the α2,6-sialylation of gut mucin O-linked and N-linked glycans as most likely mechanism[34].

In a human cohort[9], the second most significant association for *Paraprevotella* abundance was with a locus harbouring *ST6GAL1* (*p*-value = 1.37×10^{-7}, not genome-wide significant; note that *Paraprevotella* was detected in only 451 out of 984 study participants, decreasing the power to detect a genome-wide significant association). ST6GAL1 catalyses the α2,6-sialylation of mucin N-glycans[34,36], a function shared with ST6GALNAC1, suggesting shared modalities of host-microbiome interactions in humans and rats.

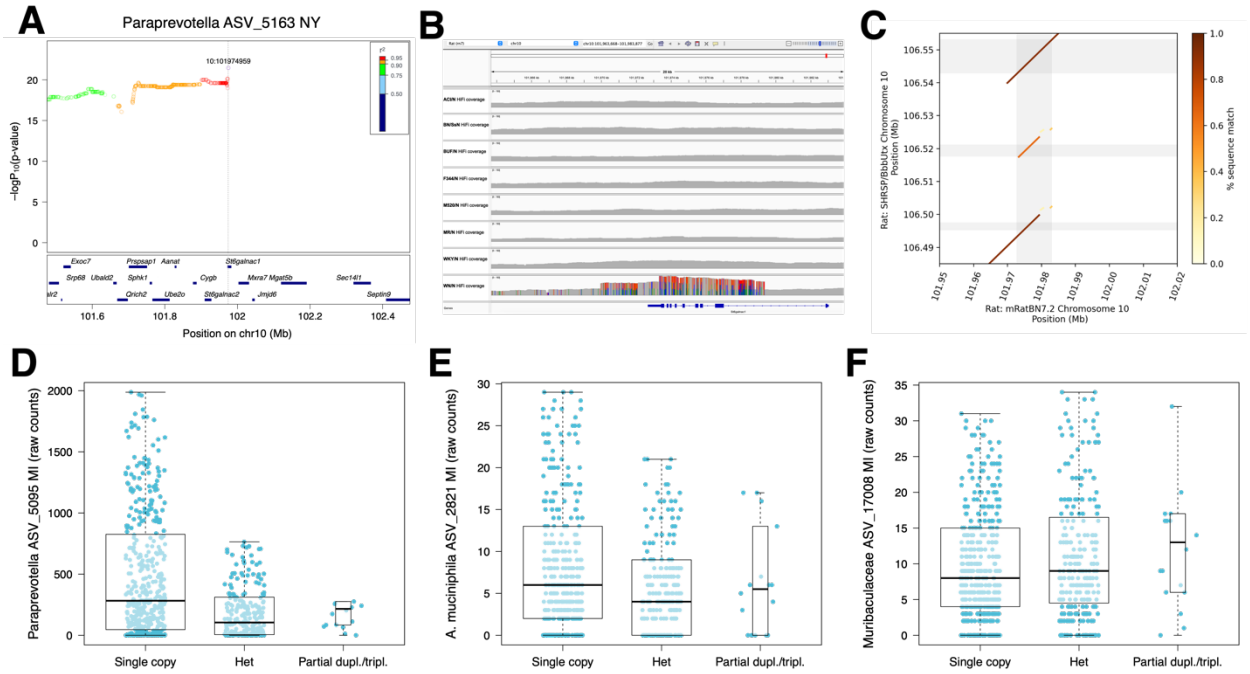

Figure 5 Dissection of the mechanisms underlying the replicated association between *Paraprevotella* and the *St6galnac1* locus on chromosome 10. (A) Local association (LocusZoom) plot for ASV_5163 (genus *Paraprevotella*) measured in the NY cohort and the *St6galnac1* locus. 8 genes were omitted for graphical purposes. A wider plot is shown in Suppl. Fig. 10. (B) Alignment of PacBio HiFi long reads from the eight founders of the HS population to the rat reference genome assembly (rn7). (C) Comparison of the rat reference genome assembly (rn7, from strain BN/NHsdMcwi) and the *de novo* genome assembly of the strain SHRSP/BbbUtx, which is identical by descent to WN/N at the locus. (D-F) Genotypic effects on *Paraprevotella*, *A. muciniphila* and

Muribaculum ASVs that map to the *St6galnac1* locus (see Suppl. Table 4). A few outliers were omitted for better visualisation of the quartiles.

5. Coupling of host genetic effects and horizontal microbial transmission

Recent studies in humans that tracked microbial strains across pairs of socially interacting individuals provided strong evidence that gut microbes can be horizontally transmitted[16-18]. However, whether some bacteria are affected by host genetic effects and are also horizontally transmissible is unknown. In addition, the quantitative impact of these two processes on microbiome variation has not been estimated. We developed an approach to address these questions, based on a large body of work on "indirect genetic effects"[37-39] (**IGE**, genetic effects on the phenotype of an individual that arise from genotypes of other individuals through social interactions). This approach does not require strain-level microbiome data. As illustrated in Fig. 6A, when the abundance of a microbe is influenced by host genetic effects (hereafter "direct genetic effects" on the microbe, **Mic-DGE**) and that same microbe is transmitted between socially interacting individuals, IGE are expected to affect the abundance of the microbe (**Mic-IGE**). In that situation, Mic-DGE and Mic-IGE will arise from the same variants, hence, be positively correlated.

We fitted jointly random effects for Mic-DGE, Mic-IGE, cage effects, maternal effects and other environmental effects (See Methods). The modelling of Mic-DGE and Mic-IGE focused solely on polygenic effects. As we expected Mic-IGE to be generally weaker than Mic-DGE[40,41], we analysed all four cohorts jointly (N = 3,767 rats) to maximise statistical power to detect Mic-IGE and to obtain precise estimates of the correlation between Mic-DGE and Mic-IGE. We used a bootstrap approach to obtain the distribution of *p*-values expected under the null hypothesis of no Mic-IGE, and verified that these *p*-values followed a uniform distribution, i.e. were calibrated (Suppl. Fig. 13). We then calculated a Mic-IGE *p*-value for each microbiome phenotype and applied a conservative Bonferroni correction to account for the total number of microbiome phenotypes considered ($-\log_{10}(0.05 / 546) = 4$). Three ASV phenotypes were significantly affected by Mic-IGE at this threshold. These ASVs were in different genera of the *Muribaculaceae* family, which is abundant in rodents but also found in humans[42]. At a less stringent false discovery rate (**FDR**) threshold of 10%, 26 microbiome phenotypes were significantly affected by Mic-IGE. Furthermore, a comparison of observed Mic-IGE *p*-values against the *p*-values expected under the null hypothesis of no Mic-IGE (Fig. 6B) suggested that many more bacteria are affected by Mic-IGE.

For the three phenotypes significantly affected by Mic-IGE (Bonferroni corrected threshold), the correlation between Mic-DGE and Mic-IGE was very close to 1 (1.0 ± 0.16, 0.91 ± 0.091, 1.0 ± 0.19), providing strong evidence that horizontal microbial transmission

mediates Mic-IGE. Similarly, the correlation between Mic-DGE and Mic-IGE was above 0.9 for 20 of the 26 phenotypes affected by Mic-IGE at the 10% FDR threshold.

For the same three phenotypes we calculated the total genetic variance[43] explained by Mic-DGE, Mic-IGE and their covariance. This total genetic variance reflects the impact of host genetic effects on the individual's own microbiome phenotype and on the microbiome phenotypes of its cage mates. Therefore, it captures not only the genetic variance for *acquiring* microbes but also for *transmitting* microbes[44]. The total genetic variance was 4.4, 7.7 and 4.8 times greater than the variance explained by host genetic effects in a model without Mic-IGE (Fig. 6C), highlighting the quantitative impact of Mic-IGE on inter-individual variation in microbiome composition.

Finally, we hypothesized that because related individuals were included in the joint sample but rats sharing a cage were unrelated (Suppl. Table 1 and Methods), and because Mic-DGE and Mic-IGE are positively correlated, Mic-DGE might be underestimated by a model not accounting for Mic-IGE. We tested this hypothesis with simulations (see Methods) and confirmed that ignoring Mic-IGE results in underestimated Mic-DGE (Fig. 6D and Suppl. Fig. 14).

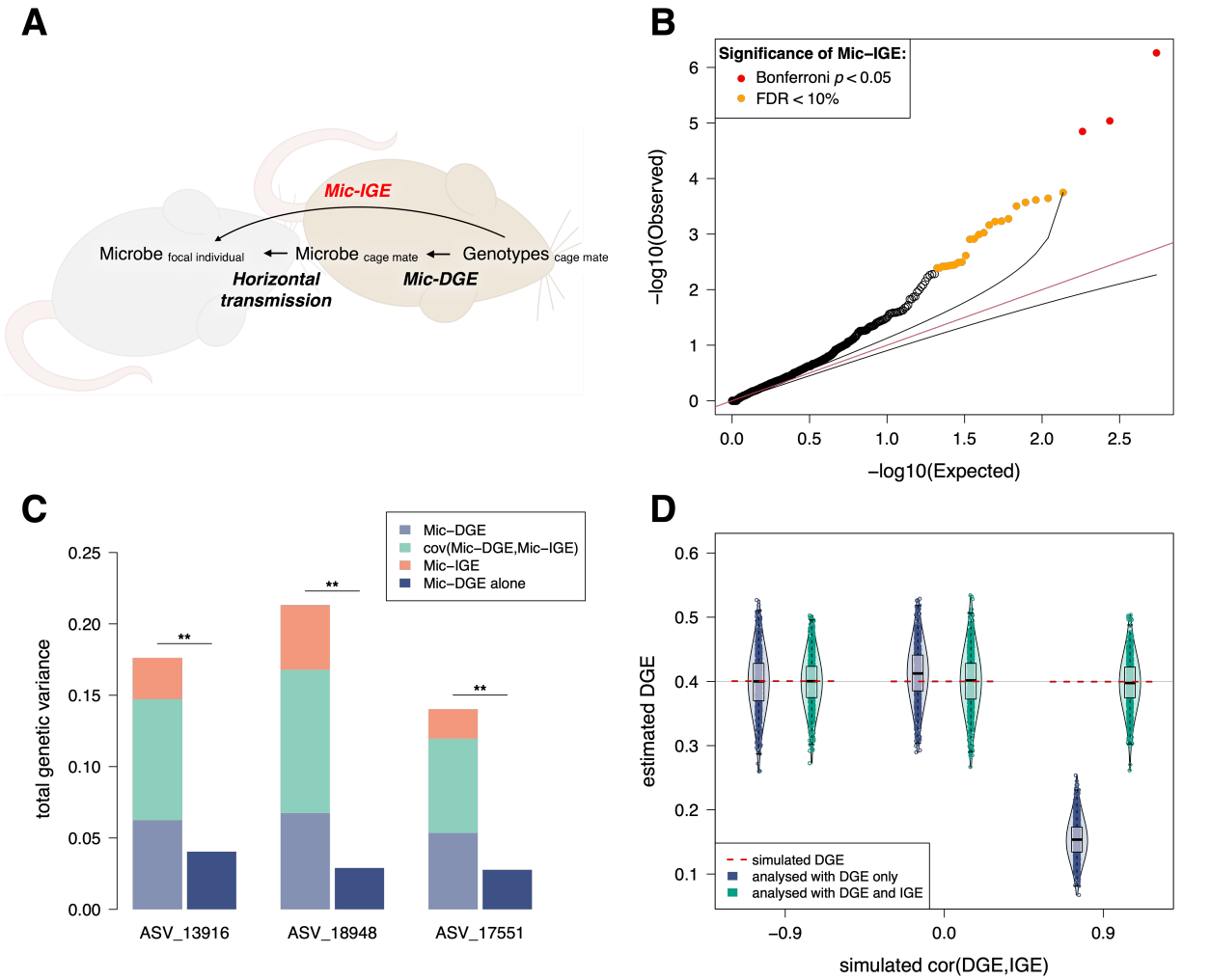

Figure 6 Indirect (social) genetic effects on microbiome phenotypes (Mic-IGE). (A) Schematic illustrating how Mic-IGE arise, from the coupling of host genetic effects (Mic-DGE) and horizontal transmission. (B) QQ plot comparing the observed Mic-IGE -logP values to the Mic-IGE -logP values expected under the null hypothesis of no Mic-IGE. We show in Suppl. Fig. 13 that Mic-IGE *p*-values are calibrated, i.e. follow the expected uniform distribution. (C) Bar plot comparing the total genetic variance explained by Mic-DGE, Mic-IGE and their covariance to the genetic variance explained by Mic-DGE in a model not including Mic-IGE. (D) DGE (e.g. Mic-DGE) estimates from 1,000 phenotypes simulated with DGE, IGE and cage effects and analysed either with a model including IGE or not.

Discussion

We carried out an in-depth analysis of host genetic effects affecting the gut microbiome in four cohorts of HS rats. We demonstrated that host genetic effects are consistent across the environments experienced by the different cohorts of rats and identified three

significant microbiome-associated loci that replicated in three or four cohorts. At one of these loci we identified the causal variant and gene, and we found a similar association in a human cohort. In addition, we presented a novel approach to study the coupling between host genetic effects and horizontal transmission, and showed that horizontal transmission greatly increases the total genetic variance of microbiome phenotypes and that failing to account for it can lead to underestimating host genetic effects.

This is the largest ever characterisation of the rat cecal microbiome. In the human colon, *Lachnospiraceae* is the most abundant bacterial family, followed by *Bacteroidaceae*, *Oscillospiraceae* (formerly *Ruminococcaceae*) and *Bifidobacteriaceae*[45]. In the rat cecum, *Lachnospiraceae* was also the most abundant family, followed by *Bacteroidaceae*, *Oscillospiraceae* and *Muribaculaceae* (formerly *S24-7*). Thus, human and rat microbiomes are similar in terms of the most abundant bacterial families.

We uncovered 214 significantly heritable microbiome phenotypes (39.2%, FDR < 0.1). Host genetic effects for these 214 phenotypes explained an average of 3% of phenotypic variation. This value is slightly smaller than the values (6%, 8% and 10%) reported in three pig studies that had sample sizes three times smaller than ours[15,46], and consistent with greater statistical power in our study to detect microbes with significant but very small heritabilities. It appears inconsistent, however, with values (30% and 20%) reported in two human studies with sample sizes similar to ours[6,8,15]. One explanation is that the heritability estimates in the two human studies are inflated[6,47]. However, it is possible that host genetic effects are truly larger in humans, if they are mediated by lifestyle choices, because laboratory and farm animals do not have such choices.

We found consistent host genetic effects across cohorts. While our study is the first to examine the degree of consistency of polygenic host genetic effects across cohorts, our results are consistent with a previous cross-cohort analysis of microbiome GWAS in humans[11]. Indeed, that study reported that most significant microbiome-associated loci had consistent effect sizes across cohorts, despite substantial heterogeneity in microbiome composition across cohorts. These results suggest that statistical power is the main limitation for replicating microbiome-associated loci.

Remarkably, we detected three microbiome-associated loci replicated in three or four cohorts of HS rats. At one locus, associated with *Paraprevotella* in all four cohorts of HS rats, we identified the causal variant, a 9kb copy number variant segregating in HS rats and wild rats, and affecting the gene *St6galnac1*. Evidence from both our study and a published study[34] indicated that this effect was likely mediated by the sialylation of mucin O- and/or N-linked glycans by *St6galnac1* and their desialylation by *Paraprevotella*, which gives to the bacteria a competitive advantage. In humans, we found evidence suggesting

that *Paraprevotella* abundance is associated with *ST6GAL1*, a gene involved in the sialylation of mucin N-glycans. Hence, these findings suggest shared modalities of host genetic effects on the microbiome in rats and humans and they add to the evidence showing that host glycans play an important role in host/microbiome interactions[48-50]. They are also important for the following reasons.

First, they suggest a causal mechanism behind the increase in *Paraprevotella* in patients with immunoglobulin A nephropathy (**IgAN**)[51,52] and the association between *ST6GAL1* and IgAN[53]. IgAN is an autoimmune disease in which desialylated IgA molecules cross the intestinal epithelium into circulation, where they are recognized by IgG autoantibodies, forming immune complexes that deposit in the kidneys. Our findings revealed that *Paraprevotella* and *A. muciniphila* have a similar sialidase activity, which mediates their association with *St6galnac1* in HS rats. Together with evidence that *A. muciniphila* desialylates IgA and induces IgAN in mice[54], our results suggest that *Paraprevotella* can also desialylate IgA and contribute to IgAN. This effect will be magnified by the coating of *Paraprevotella* with IgA, which results from *Paraprevotella*'s ability to induce trypsin autodegradation and protect gut IgA from degradation by trypsin[55].

Secondly, our results suggest that *Paraprevotella* mediates the association between *ST6GAL1* and breakthrough SARS-CoV-2 infection[56], through two distinct mechanisms. First, *Paraprevotella*'s trypsin-degrading activity reduces the entry of coronaviruses into the host's gut epithelial cells[55] and, secondly, *Paraprevotella*'s IgA-protective effect potentiates vaccine efficiency, as demonstrated, in mice, for a gut pathogen[55]. If *Paraprevotella*, an anaerobic gut bacterium, indeed influences breakthrough SARS-CoV-2 infection, it would suggest that these breakthrough infections originate from the gut. Thus, our results support a role for fecal-oral transmission of SARS-CoV-2[57].

Given the evidence discussed above and elsewhere that host genetic effects are involved in selecting beneficial commensals from the pool of microbes able to colonize the gut in and fighting off pathogens[58], it is clear that modelling approaches that fully account for microbial transmission in the population are necessary to understand evolution and how it affects disease in current-day populations. This is most obvious for infectious diseases, an area where IGE models are under active development[43], but also for the broad range of diseases influenced by the microbiome[16,59,60]. Our modelling of Mic-IGE has already demonstrated that some bacteria are affected by host genetic effects and are also horizontally transmitted, leading to a total genetic variance that is greater than suggested by classical estimates of host genetic effects. To the extent that the microbiome influences disease, these results will extend to disease phenotypes.

Finally, using simulations we showed that ignoring Mic-IGE, *and more generally IGE on any phenotype*, can result in underestimating DGE (i.e. heritability). So far, only a risk of overestimating DGE had been reported[40,61,62]. DGE will be underestimated when (distantly) related individuals are included in the sample, IGE occur only between unrelated individuals, and DGE and IGE are positively correlated. Because the UK biobank includes distantly related individuals[63], this issue could affect, for example, phenotypes measured in the UK biobank that are affected by spousal IGE and for which DGE and spousal IGE are positively correlated[64].

Our study has limitations. First, 16S data do not allow for precise characterisation of the functional profile of the microbiome. A comparison of hundreds of mouse and human microbiomes has revealed that microbial functions rather than microbial species are conserved between the two host species[65]. Hence, to fully exploit HS rats as a model for humans, it will be important to characterise the microbiomes of HS rats at the functional level. Secondly, our results (QQ plot Fig. 5B) suggest we had limited power to detect polygenic Mic-IGE, and we were clearly underpowered to map Mic-IGE. In the future additional HS rat cohorts can be profiled, as this population is actively used by the research community and cecal samples are easy to collect and share.

Online methods

Animals

All procedures were approved by the University at Buffalo, the University of Michigan and the University of Tennessee Institutional Animal Care and Use Committees. The rat Heterogeneous Stock (HS) colony was established at the NIH in 1984 from eight inbred strains: ACI/N, BN/SsN, BUF/N, F344/N, M520/N, MR/N, WKY/N, and WN/N population founded at the NIH[22] and thereafter maintained using an outbreeding scheme. The rats included in this study all originate from the HS colony maintained at the Medical College of Wisconsin (official nomenclature: MCW: NMcwi:HS, Rat Genome Database ID: 2314009) and are from generations 73 to 80. At weaning, the rats were shipped to one of three facilities, in the states of Michigan (MI), New York (NY) and Tennessee (TN). The rats that arrived in MI and NY (MI and NY cohorts) had their behaviour profiled. The rats that arrived in TN (TN2 cohort) were bred for a single generation to produce offspring (TN1), whose behaviour was profiled. All protocols were approved by the Institutional Animal Care and Use Committees for each of the relevant institutions.

Experimental design and confounding

Typically, one male and one female from each litter born at the Medical College of Wisconsin were selected for shipment to MI, NY and TN, limiting the number of siblings included in each of the MI, NY and TN2 cohorts and avoiding siblings being co-housed after weaning. Since siblings were not co-housed in the MI, NY and TN2 cohorts, there is no confounding of genetic effects (relatedness) with cage (shared micro-environmental) effects in these cohorts. In contrast, in the TN1 cohort, same-sex siblings were co-housed. To avoid confounding in the TN1 cohort, we accounted for cage effects in our genetic analyses. To use the same model for all cohorts, we accounted for cage effects in all cohorts. The use of multiple offspring from each mother permits distinguishing between genetic effects and maternal effects, and we accounted for maternal effects in all our genetic analyses. The models are described in more details below.

Housing conditions

The type of cages used and pathogen status of the various facilities varied: at the Medical College of Wisconsin, the rats were housed in ventilated cages in an SPF facility; in MI, the rats were housed in conventional cages in a non-SPF facility; in NY, they were housed in conventional cages in an SPF facility; finally, in TN, the rats were housed in conventional cages for those rats studied before March 2016 and in ventilated cages after March 2016, always in SPF facilities. The number of rats co-housed in a cage also varied between the cohorts: in the NY and TN2 cohorts, the rats were housed in groups of 2; in MI, in groups of 3, and in the TN1 cohort, in groups of 2 or 3. All rats were on a chow diet but the food vendors varied across the different facilities: at the Medical College of Wisconsin, the rats were fed with Teklad 5010 diet ad libitum (Envigo, Madison, Wisconsin); at the University of Michigan, they were fed irradiated Picolab Laboratory Rodent Diet (LabDiet, St. Louis, Missouri); at the University at Buffalo, Teklad 18% Protein Rodent Diet (Envigo); at the University of Tennessee Health Science Center, Teklad Irradiated LM-485 Mouse/Rat Diet (Envigo).

Phenotyping

The behaviour of the rats in the NY, MI, and TN1 cohorts was profiled using different assays that focused on traits relevant to substance (cocaine and nicotine) use disorder in humans[66,67]. In addition, physiological measures were collected in all four cohorts, in particular from tissues collected at sacrifice. The rats from the MI, NY and TN2 cohorts, but not the rats from the TN1 cohort, were fasted overnight before euthanasia and tissue collection. For euthanasia, in NY and TN the rats were anesthetized with isoflurane, before being quickly decapitated. In NY and MI, the rats were euthanised at 6.5 and 3 months of age, respectively. TN1 rats were on average 2 months old when their ceca were collected, and TN2 rats 6 months old.

Isolation of the cecal microbiome

The ceca were dissected from each rat within minutes of euthanasia. The cecum was removed by cutting immediately at the entrance of the small intestine (ileum) to the cecum and immediately below the exit of the cecum to the large intestine (colon). The cecum was placed into a sterile container and stored at -80C. The cecal content for microbiome analysis was taken from the apical part of the ceca. Ceca were thawed on ice to the extent that they could be cut, cut in half using a clean razor blade, and ~100 ul of content (without host tissue) was scooped and transferred into 1.5 ml and frozen on dry ice.

DNA extraction, library preparation and sequencing of the 16S amplicon

DNA was extracted from the cecal content within a few hours of the cecal dissection, using the MoBio (now Qiagen) PowerSoil DNA high-throughput isolation kit as per the manufacturer's recommendations.
The V4 region of the 16S SSU rRNA gene was amplified using the current, barcoded primers used in the Earth Microbiome Project (https://earthmicrobiome.org/protocols-and-standards/16s/). 5–10% PhiX was added to each library. The libraries were run in eleven batches on a MiSeq (Illumina) machine to obtain 150bp paired-end reads (average library depth 20,842 pairs, minimum: 6,624, maximum: 34,495).

Sample filtering

Negative controls and rats with unreliable metadata or no genotypes were excluded from subsequent analyses. In addition, we excluded samples with too few or too many sequencing reads (mean +/- 2 x standard deviation), as extreme variation in library size could be problematic for compositional data analysis, even when statistical methods are used to account for it (see section on CLR transformation below). This left a total of 3,897 rats across the four cohorts.

16S data processing and identification of amplicon sequence variants (ASVs)

Raw sequencing data were first demultiplexed and quality control was carried out using split_libraries_fastq.py (qiime2 version 1.9.1). This resulted in a median number of reads per sample of 20.9K. Secondly, reads were trimmed to length 150bp and adapter sequences removed using Trimming.py (qiime2 version 1.9.1). ASVs were identified using Deblur (2021.09 workflow) and Greengenes 1 ("Greengenes 13.8") as reference. At this point the deblur reference hit tables were chosen. ASVs were filtered using filter_features.py (qiime2 version 2023.2.0) against the Greengenes 2 ("Greengenes

2022.10") reference. Subsequently, these data objects were merged to yield microbiome profiles with 93,090 ASVs for 4,422 samples, including 268 negative controls (30 samples with too few reads were dropped by the Deblur workflow).

ASV taxonomy assignment

We assigned taxonomy to each ASV using the latest Greengenes 2 taxonomy (downloaded from http://greengenes.microbio.me/greengenes_release/2022.10-rc1/2022.10.taxonomy.asv.nwk.qza), using the following qiime command line:
qiime greengenes2 taxonomy-from-table --i-reference-taxonomy 2022.10.taxonomy.asv.nwk.qza --i-table 175568_feature-table.qza --o-classification biom.taxonomy.qza.

Rarefaction of the counts table (for average microbiome profiles and alpha diversity)

For calculating average microbiome profiles (Fig. 2A) and alpha diversity (Suppl. Fig. 2) only, the count matrix (analysis ID 57950 in Qiita, artifact ID 175568) was rarefied to 10,000 reads in Qiita.

Calculation of average microbiome profiles

Average microbiome profiles were calculated for each cohort separately, after rarefying the count table and collapsing ASVs at the family level (summing up their relative abundances).

Alpha diversity calculation

Within-sample ("alpha") diversity was calculated after rarefying the count table and collapsing ASVs at the family and genus levels. Richness was calculated as the number of observed families or genera in a sample.

Centered log-ratio (CLR) transformation of raw ASV abundances (for beta-diversity and all genetic analyses)

To account for the compositional nature of the data[27], we transformed the raw abundance values of each ASV using the CLR transformation (null values were replaced by 0.00001). CLR transformed values are to be interpreted as relative abundances with respect to the geometric mean of the sample.

Beta-diversity calculation

Between-sample ("beta") diversity across all rats was calculated from the CLR-transformed ASV abundance values collapsed at the family level, as the Euclidian distance between samples. This distance is equivalent to the Aitchison distance [27]. Fig. 2B. shows the two first principal components of the CLR-transformed, family-level abundance table.

Across-samples normalisation of microbiome phenotypes and regression of the effects of the experimental covariates

For all genetic analyses and to satisfy the assumption of normality made by the linear mixed models we used for all the genetic analyses, each microbiome phenotype was quantile (i.e. rank) normalised, with ties were broken at random. We also regressed out any potential effect of sex, phenotyping batch, 16S library preparation batch, library size, and, for the TN1 and TN2 samples, weaning suite, using fixed effects in linear models. We used the residuals of these models for genetic analysis.

Genotyping

Genomic DNA was isolated from spleen samples using the Beckman Coulter DNAdvance Kit (Beckman Coulter Life Sciences, Indianapolis, IN, USA). Genomic library preparation, sequencing, and genotyping were all conducted using the pipeline described by Chen et al.[68]. Briefly, genomic samples were prepared using both double-digest genotyping by sequencing (ddGBS) and low-coverage whole genome sequencing (lcWGS) techniques. ddGBS libraries were produced following Gileta et al.[69] and sequenced on an Illumina HiSeq 4000 DNA sequencer (Illumina, San Diego, CA, USA) using 100-bp single-end reads. lcWGS libraries were produced following Chen et al.[68] and sequenced on an Illumina NovaSeq 4000 using 150-bp paired-end reads. All libraries were sequenced at the UC San Diego Institute for Genomic Medicine Genomics Center.
Sequenced libraries were demultiplexed using fastx_toolkit v0.0.14 (for ddGBS samples)[70] and fgbio v1.3.0 (lcWGS)[71], trimmed using cutadapt v4.4 (ddGBS, lcWGS)[72] and bbDuk v38.94 (lcWGS)[73], and aligned to the rat reference genome mRatBN7.2 (rn7) from the Rat Genome Sequencing Consortium (NCBI RefSeq assembly GCF_015227675.2)[74] using bwa-mem v0.7.17[75]. Mapped sequences were used to impute SNP genotypes using STITCH v1.6.6[76]. From this set, we removed all SNP loci with low imputation quality scores produced by STITCH v1.6.6 (INFO < 0.9). Genotypes for the 7,358,643 SNPs passing this filter are available at https://library.ucsd.edu/dc/object/bb29129987. This dataset includes many more rats

than the rats used in this study. The files downloaded from this URL were renamed as "P50_Rn7" (see below).
For all analyses in this study we focused on SNPs that were on the autosomes (chromosomes 1 to 20 in the rat). For constructing genetic relatedness matrices and for GWAS, but not for the LocusZoom plots, we additionally removed loci with high missing data (missing rate > 0.1) or low minor allele frequencies (MAF < 0.05), leaving 4,880,609 autosomal SNPs. For GWAS, missing genotypes at these 4,880,609 SNPs were mean imputed.

Construction of the SNP-based genetic relatedness matrices (GRMs)
For the heritability and genetic correlation analyses, a GRM was constructed from a subset of pruned SNPs on autosomes 1 to 20. For GWAS, 20 different GRMs were constructed for use in the leave-one-chromosome-out (LOCO) framework[77-79], using the same subset of pruned SNPs but excluding SNPs on one chromosome at a time.

We used PLINK v1.90b6.2[80] to prune SNPs and create the GRMs:

```
#prune:
plink --bfile ./P50_Rn7 --indep 50 5 2 --out ./P50_Rn7_pruned_50_5_2
```

We used the following command to create the GRM from all SNPs on chromosomes 1-20

```
#create GRM from SNPs on chromosomes 1-20:
plink --bfile ./P50_Rn7 --make-rel square --keep ./P50_Rn7_rats2include.txt --chr 1-20 --extract ./P50_Rn7_pruned_50_5_2.prune.in --maf 0.05 --geno 0.1 --out ./P50_Rn7_pruned
#create LOCO GRMs for chr in {1..20}:
plink --bfile ./P50_Rn7 --make-rel square --not-chr $chr 23 24 26 --keep ./P50_Rn7_rats2include.txt --extract ./P50_Rn7_pruned_50_5_2.prune.in --maf 0.05 --geno 0.1 --out ./P50_Rn7_pruned_LOCO_${chr};
```

Analyses of polygenic host genetic effects

We estimated the magnitude of polygenic host genetic effects (SNP heritability) using the following linear mixed model:

$$\mathrm{y} = Xb + \mathrm{a} + e + \mathrm{Wc} + \mathrm{W'm} \qquad (1)$$

where y is the vector of phenotypic residuals, X is a vector describing how many rats are in each cage and b the corresponding estimated fixed effect, a is a vector of random additive genetic effects, e is a vector of random non-genetic effects, W is the matrix of cage assignments and c the corresponding vector of random cage effects. $\mathrm{W'}$ is the matrix relating the phenotyped individuals to their mothers and m the corresponding vector of random maternal effects. a follows a multivariate normal distribution $\mathrm{N}(0, A)$, where A is

the GRM (see section above). e follows a multivariate normal distribution $\mathrm{N}(0, I)$, where I is the identity matrix.

Due to missing information for a few cages, the final sample sizes in all genetic analyses were 1,107 for the MI cohort, 1,166 for the NY cohort, 941 for the TN1 cohort, and 553 for the TN2 cohort (3,767 for the joint sample).

All models were fitted via restricted maximum likelihood using the LIMIX software[28,81] and a new covariance class implemented to fit bivariate models. The significance of heritability was assessed using a log likelihood ratio (LLR) test with 1 degree of freedom, comparing model (1) to a reduced model without additive genetic effects a. To estimate the genetic correlation between two microbiome phenotypes, a bivariate version of model (1) was used.

GWAS

Model (1) was modified to include a fixed effect for the variant being tested and a different GRM matrix (one of the leave-one-chromosome-out GRMs, see section above). The genome-wide significance threshold (-logP > 5.8), which accounts for the number of independent SNPs tested, was calculated by permuting the rows (rats) of the genotype matrix 1,000 times, running a GWAS on these permutations, recording the smallest *p*-value for each, and eventually calculating the 95th percentile of the distribution of these minima[28,29]. The adjusted significance threshold, which further accounts for the number of independent microbiome phenotypes considered in a cohort, was calculated by Bonferroni correction of the genome-wide significance threshold. This number was estimated from a principal component analysis of the microbiome phenotypes measured in the cohort, counting the number of eigenvalues necessary to explain 99% of the total variance. All models were fitted using the LIMIX software.

Analysis of indirect genetic effects on microbiome phenotypes (Mic-IGE)

The following model, which is similar to the model used in two of our previous studies on IGE[40,41], was used to quantify indirect genetic effects:

$$\mathrm{y} = Xb + \mathrm{a}_D + \mathrm{Za}_S + \mathrm{e}_D + \mathrm{Ze}_S + \mathrm{Wc} + \mathrm{W'm} \quad (2)$$

y, X, b, W, c, W' and m are defined as in the previous section. a_D is the vector of random additive direct genetic effects (Mic-DGE). a_S is the vector of random additive indirect genetic effects (Mic-IGE) and Z is the matrix indicating, for each rat, which are the cage mates (importantly $Z_{i,i} = 0$). e_D and e_S, also random effects, refer to the non-genetic component of direct and indirect effects.
The joint distribution of all random effects was defined as:

$$\begin{bmatrix} \sigma^2_{A_D}A & \sigma_{A_DA_S}A & 0 & 0 & 0 & 0 \\ \sigma_{A_DA_S}A & \sigma^2_{A_S}A & 0 & 0 & 0 & 0 \\ 0 & 0 & \sigma^2_{E_D}I & \sigma_{E_DE_S}I & 0 & 0 \\ 0 & 0 & \sigma_{E_DE_S}I & \sigma^2_{E_S}I & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma^2_{C}I & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma^2_{M}I \end{bmatrix}$$

All models were fitted using the LIMIX software. The significance of Mic-IGE was assessed using a LLR test, comparing model (2) to a reduced model without Mic-IGE (i.e. Za_S) but with indirect environmental effects (Ze_S). Because Mic-DGE and Mic-IGE are correlated ($\sigma_{A_DA_S}$), the LLR statistics follows a mixture of χ^2 distributions with degrees of freedom 1 and 2. To determine which mixture parameter was appropriate, we used a parametric bootstrap approach, simulating phenotypes under the null hypothesis of no Mic-IGE, calculating *p*-values for them using a LLR test with mixture parameter varying between 1 and 2, and choosing the mixture parameter (0.7) that yielded calibrated *p*-values (see Suppl. Fig. 13).

The total heritable variance[82] was calculated as:

$$\sigma^2_H = \sigma^2_{A_D} + 2(n-1)\sigma_{A_{DS}} + (n-1)^2\sigma^2_{A_S}$$

where n is the average number of rats in a cage.

Alignment of wild rat sequences

Raw sequences from wild rats caught in various locations in China were downloaded from SRA with accession number SRP078989[30]. Trimming of adapters was performed using TrimGalore[83]. The remaining reads were aligned to the rn7 reference genome using bwa mem 0.7.17 with default parameters[75]. BAM files were sorted and filtered, retaining only reads with a mapping quality (MQ) >= 30 using samtools 1.12[84]. Mate coordinates and sizes were fixed using samtools fixmate -m. Subsequently, duplicates were removed using samtools markdup -r -s. Variant calling was performed using GTAK 4.1.8[85]. Briefly, we called variants using HaplotypeCaller and used Base Quality Score Recalibration (BQSR) to recalibrate the base quality scores of BAM files. Germline calling was performed. Instead of using the VQSR step with polymorphisms from laboratory strains, we applied hard filtering of the final VCFs to avoid bias towards the variants present in the laboratory animals.
We lifted over the available public New York rat data, which used the rn5 rat genome assembly, to rn7 using USCS chain files[86] and Picard tools 2.25.5 LiftoverVcf[87].

VCF files from wild Chinese rats, wild rats from NYC, and inbred rat strains were then merged using bcftools isec[84].

Other bioinformatics tools

The Variant Visualizer tool from the Rat Genome Database[88,89] was used to identify variants segregating in the eight HS founders and SHRSP, and their functional consequences predicted by Polyphen[90].
Plink[91] was used to calculate LD (R^2).
The standalone version of LocusZoom (version 1.3) was used.
The R code used to generate Suppl. Fig. 4 was adapted from the code published by Grieneisen et al. [92].
IGV[93] was used to generate Suppl. Fig. 8.

Data and code availability

All 16S sequencing data and metadata are available from Qiita[94] study ID 11479 (https://qiita.ucsd.edu/study/description/11479). The genotype data are available from UCSD's Library Digital Collections at https://doi.org/10.6075/J0X63N54. Wild rat from China raw sequences were downloaded from SRA with accession number SRP078989[30]. NYC metro rats genotypes were downloaded from: https://datadryad.org/stash/dataset/doi:10.5061/dryad.08kprr4zn[31]. Rat inbred strains vcf files were obtained from the Rat Genome Database: https://download.rgd.mcw.edu/strain_specific_variants/Dwinell_MCW_HybridRatDiversityProgram/Jan2023/mRatBN7/.
The R scripts used to generate all the results and figures reported in the paper are available from https://github.com/Baud-lab/P50/tree/Master/16S.
The extended LIMIX code used for the genetic analyses is available from https://github.com/Baud-lab/CoreQuantGen.

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Conflict of interest statement

Rob Knight is a scientific advisory board member, and consultant for BiomeSense, Inc., has equity and receives income. He is a scientific advisory board member and has equity in GenCirq. He is a consultant for DayTwo and receives income. He has equity in and acts as a consultant for Cybele. He is a co-founder of Biota, Inc., and has equity. He is a cofounder of Micronoma and has equity and is a scientific advisory board member. The terms of these arrangements have been reviewed and approved by the University of California, San Diego in accordance with its conflict-of-interest policies.

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