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Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection

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Productivity of ruminant livestock depends on the rumen microbiota, which ferment indigestible plant polysaccharides into nutrients used for growth. Understanding the functions carried out by the rumen microbiota is important for reducing greenhouse gas production by ruminants and for developing biofuels from lignocellulose. We present 410 cultured bacteria and archaea, together with their reference genomes, representing every cultivated rumen-associated archaeal and bacterial family. We evaluate polysaccharide degradation, short-chain fatty acid production and methanogenesis pathways, and assign specific taxa to functions. A total of 336 organisms were present in available rumen metagenomic data sets, and 134 were present in human gut microbiome data sets. Comparison with the human microbiome revealed rumen-specific enrichment for genes encoding de novo synthesis of vitamin B12, ongoing evolution by gene loss and potential vertical inheritance of the rumen microbiome based on underrepresentation of markers of environmental stress. We estimate that our Hungate genome resource represents ~75% of the genus-level bacterial and archaeal taxa present in the rumen.

Climate change and feeding a growing global population are the two biggest challenges facing agriculture1. Ruminant livestock have an important role in food security2; they convert low-value lignocellulosic plant material into high-value animal products that include milk, meat and fiber products. Microorganisms present in the rumen3,4 ferment polysaccharides to yield short-chain fatty acids (SCFAs; acetate, butyrate and propionate) that are absorbed across the rumen epithelium and used by the ruminant for maintenance and growth. The rumen represents one of the most rapid and efficient lignocellulose depolymerization and utilization systems known, and is a promising source of enzymes for application in lignocellulose-based biofuel production5. Enteric fermentation in ruminants is also the single largest anthropogenic source of methane (CH4)6, and each year these animals release ~125 million tonnes of CH4 into the atmosphere. Targets to reduce agricultural carbon emissions have been proposed7, with >100 countries pledging to reduce agricultural greenhouse gas emissions in the 2015 Paris Agreement of the United Nations Framework Convention on Climate Change. Consequently, improved knowledge of the flow of carbon through the rumen by lignocellulose degradation and fermentation to SCFAs and CH4 is relevant to food security, sustainability and greenhouse gas emissions.

Understanding the functions of the rumen microbiome is crucial to the development of technologies and practices that support efficient global food production from ruminants while minimizing greenhouse gas emissions. The Rumen Microbial Genomics Network (http://www.rmgnetwork.org) was launched under the auspices of the Livestock Research Group of the Global Research Alliance (http://globalresearchalliance.org/research/livestock) to further this understanding, with the generation of a reference microbial genome catalog—the Hungate1000 project—as a primary collaborative objective. Although the microbial ecology of the rumen has long been the focus of research8,9, at the beginning of the project reference genomes were available for only 14 bacteria and one methanogen, so that genomic diversity was largely unexplored.

The Hungate1000 project was initiated as a community resource in 2012, and the collection assembled includes virtually all the bacterial

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and archaeal species that have been cultivated from the rumens of a diverse group of animals\textsuperscript{10}. We surveyed Members of the Rumen Microbial Genomics Network and requested they provide cultures of interest. We supplemented these with additional cultures purchased from culture collections to generate the most comprehensive collection possible. These cultures are available to researchers, and we envisage that additional organisms will have their genome sequences included as more rumen microbes are able to be cultivated.

Large-scale reference genome catalogs, including the Human Microbiome Project (HMP)\textsuperscript{11} and the Genomic Encyclopedia of Bacteria and Archaea (GEBA)\textsuperscript{12} have helped to improve our understanding of microbiome functions, diversity and interactions with the host. The success of these efforts has resulted in calls for continued development of high-quality reference genome catalogs\textsuperscript{13,14}, and led to a resurgence in efforts to cultivate microbial organisms\textsuperscript{15–17}. This high-quality reference genome catalog for rumen bacteria and archaea increases our understanding of rumen functions by revealing degradative and physiological capabilities, and identifying potential rumen-specific adaptations.

**RESULTS**

**Reference rumen genomes**

Members of nine phyla, 48 families and 82 genera (Supplementary Table 1 and Supplementary Note 1) are present in the Hungate Collection. The organisms were chosen to make the coverage of cultivated rumen microbes as comprehensive as possible\textsuperscript{10}. While multiple isolates were sequenced from some polysaccharide-degrading genera (Butyrivibrio, Prevotella and Ruminococcus), many species are represented by only one or a few isolates. 410 reference genomes were sequenced in this study, and were analyzed in combination with 91 publicly available genomes\textsuperscript{18}. All Hungate1000 genomes were sequenced using Illumina or PacBio technology, and were assembled and annotated as summarized in the Online Methods. All genomes were assessed as high quality using CheckM\textsuperscript{19} with >99% completeness on average, and in accordance with proposed standards\textsuperscript{20}. The genome statistics can be found in Supplementary Table 2.

The 501 sequenced organisms analyzed in this study are listed in Supplementary Table 1. We refer to these 501 genomes (480 bacteria and 21 archaea) as the Hungate genome catalog. Supplementary Table 3 provides a comprehensive chronological list of all publicly available completed rumen microbial genome sequencing projects, including anaerobic fungi and genomes that have been recovered from metagenomes but that were not included in our analyses.

Members of the Firmicutes and Bacteroidetes phyla predominate in the rumen\textsuperscript{21,22} and contribute most of the Hungate genome sequences (68% and 12.8%, respectively; Supplementary Fig. 1a), with the Lachnospiraceae family making up the largest single group (32.3%). Archaea are mainly from the Methanobrevibacter genus or are in the Methanomassiliicoccales order. The average genome size is ~3.3 Mb (Supplementary Fig. 1b), and the average G+C content is 44%. Most organisms were isolated directly from the rumen (86.6%), with the remainder isolated from feces or saliva. Most cultured organisms were from bovine (70.9%) or ovine (17.6%) hosts, but other ruminant or camelid species are also represented (Table 1).

The Global Rumen Census project\textsuperscript{23} profiled the microbial communities of 742 rumen samples present in diverse ruminant species, and found that rumen communities largely comprised similar bacteria and archaea in the 684 samples that met the criteria for inclusion in the analysis. A core microbiome of seven abundant genus-level groups was defined for 67% of the Global Rumen Census sequences\textsuperscript{22}. We overlaid 16S rRNA gene sequences from the 501 Hungate genomes onto the 16S rRNA gene amplicon data set from the Global Rumen Census project (Fig. 1). This revealed that our Hungate genomes represent ~75% of the genus-level taxa reported from the rumen.

Previous studies of the rumen microbiome have highlighted uncultivated bacteria as being among the most abundant rumen microorganisms\textsuperscript{10,21}, and we also report 73 genome sequences from strains that have yet to be taxonomically assigned to genera or phenotypically characterized (Supplementary Table 1). Most abundant among these uncharacterized strains are members of the order Bacteroidales (RC-9 gut group) and Clostridiales (R-7 group), and this abundance points to a key role for these strains in rumen fermentation\textsuperscript{22}. The RC-9 gut group bacteria have small genomes (~2.3 Mb), and the closest named relatives (84% identity of the 16S rRNA gene) are members of the genus Alistipes, family Rikenellaceae. The R-7 group are most closely related to Christensenellaceae (86% identity of the 16S rRNA gene), family Christensenellaceae.

**Table 1** Hungate1000 Collection

<table>
<thead>
<tr>
<th>Phylum</th>
<th>No. of cultures</th>
<th>Livestock source</th>
<th>No. of cultures</th>
<th>Country of origin</th>
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<td>Calf</td>
<td>20</td>
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<td>3</td>
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<tr>
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<td>Camel</td>
<td>8</td>
<td>China</td>
<td>5</td>
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<tr>
<td>Firmicutes</td>
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<tr>
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<td>2</td>
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<tr>
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Table 1 is expanded in Supplementary Table 1 and Supplementary Note 1.
Ruminants need efficient lignocellulose breakdown to satisfy their energy requirements, but ruminant genomes, in common with the human genome, encode very limited degradative enzyme capacity. Cattle have a single pancreatic amylase, and several lysozymes which function as lytic digestive enzymes that can kill Gram-positive bacteria. We searched the CAZy database for each Hungate genome (http://www.cazy.org) in order to characterize the spectrum of carbohydrate-active enzymes and binding proteins present (Supplementary Fig. 2 and Supplementary Table 4). In total, the Hungate genomes encode 32,755 degradative CAZymes (31,569 glycoside hydrolases and 1,186 polysaccharide lyases), representing 2.2% of the combined ORFeome. The largest and most diverse CAZyme repertoires (Fig. 2a) were found in isolates with large genomes including *Bacteroides ovatus* (over 320 glycoside hydrolases (GH) and polysaccharide lyases (PL) from ~60 distinct families), *Lachnospiraceae* bacterium NLAE-zl-G231 (296 GHs and PLs), *Ruminoclostridium cellubiovarum* ATCC 15832 (184 GHs and PLs) and *Cellvibrio* sp. BR (158 GHs and PLs). The most prevalent CAZyme families are shown in Supplementary Figure 3. Bacteria that initiate the breakdown of plant fiber are predicted to be important in rumen microbial fermentation (Fig. 2b), including representatives of bacterial groups capable of degrading cellulose, hemicellulose (xylan/xyloglucan) and pectin (Fig. 2c).

Examination of the CAZyme profiles (Supplementary Fig. 3) highlights the degradation strategies used by different taxa present in our collection. Members of the phylum Bacteroidetes have evolved polysaccharide utilization loci (PULs), genomic regions that encode all required components for the binding, transport and depolymerization of specific glycan structures. Predictions of PUL organization in all 64 Bacteroidetes genomes from the Hungate catalog have been integrated into the dedicated PULDB database (Fig. 2d). The pectin component rhamnogalacturonan II (RG-II) is the most structurally complex plant polysaccharide, and all the CAZymes required for its degradation occur in a single large PUL recently identified in *Bacteroides thetaiotaomicron*. Similar PULs encoding all necessary enzymes were also found in rumen isolates belonging to three different families within the phylum Bacteroidetes (Supplementary Fig. 2 and Supplementary Fig. 4). Another feature of the Bacteroidetes genomes and PULs is the prevalence of GH families dedicated to the breakdown of animal glycans (Supplementary Figure 2). Host glycans are not thought to be used as a carbohydrate source for rumen bacteria, and most of the genomes with extensive repertoires of these enzymes (*Bacteroides* spp.) were from species that were isolated from feces. However, ruminants secrete copious saliva and the presence of animal glycan-degrading enzymes in rumen *Prevotella* spp. may enable them to utilize salivary N-linked glycoproteins, and help explain their abundance in the rumen microbiome.

The multisubunit cellulosome is an alternative strategy for complex glycan breakdown in which a small module (dockerin) appended to glycans serves as a carbohydrate source for rumen bacteria, and most of the genomes with extensive repertoires of these enzymes were also found in rumen isolates belonging to three different families within the phylum Bacteroidetes (Supplementary Fig. 2 and Supplementary Fig. 4). Another feature of the Bacteroidetes genomes and PULs is the prevalence of GH families dedicated to the breakdown of animal glycans (Supplementary Figure 2). Host glycans are not thought to be used as a carbohydrate source for rumen bacteria, and most of the genomes with extensive repertoires of these enzymes (*Bacteroides* spp.) were from species that were isolated from feces. However, ruminants secrete copious saliva and the presence of animal glycan-degrading enzymes in rumen *Prevotella* spp. may enable them to utilize salivary N-linked glycoproteins, and help explain their abundance in the rumen microbiome.

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**Figure 2** Functions of the rumen microbiome. (a) Number of degradative CAZymes (GH, glycoside hydrolases and PL, polysaccharide lyases) in distinct families in each of the 501 Hugenholtz catalog genomes. Genomes are colored by phylum. (b) Simplified illustration showing the degradation and metabolism of plant structural carbohydrates by the dominant bacterial and archaeal groups identified in the Global Rumen Census project using information from metabolic studies and analysis of the reference genomes. The abundance and prevalence data shown in the table are taken from the Global Rumen Census project. Abundance represents the mean relative abundance (%) for that genus-level group in samples that contain that group, while prevalence represents the prevalence of that genus-level group in all samples (n = 684). The conversion of choline to trimethylamine, and propionaldehyde to propionate generate toxic intermediates that are contained within bacterial microcompartments (BMC). Cultures from the reference genome set that encode the genes required to produce the structural proteins required for BMC formation are shown in Supplementary Table 5. (c) Number of polysaccharide-degrading CAZymes encoded in the genomes of representatives from the eight most abundant bacterial groups. Cellulose: GH5, GH9, GH44, GH45, GH48; pectin: GH28, PL1, PL9, PL10, PL11, CE8, CE12; xylan: GH8, GH10, GH11, GH43, GH51, GH67, GH115, GH120, GH127, CE1, CE2.

**Fermentation pathways.** Most of what is known about microbial fermentation pathways in the rumen has been derived from measurements of end product fluxes or inferred from pure or mixed cultures of microorganisms *in vitro*, and based on reference metabolic pathways present in non-rumen microbes. The relative participation of particular species in each pathway, or their contribution to end product formation *in vivo*, is poorly characterized. To determine the functional potential of the sequenced species, we used genome information in combination with the published literature to assign bacteria to different metabolic strategies, on the basis of their substrate utilization and production of specific fermentation end products (Supplementary Table 5). The main metabolic pathways and strategies are present in at least one of, or combinations of, the most abundant bacterial and archaeal groups found in the rumen (Fig. 2b); as a result, we now have a better understanding of which pathways are encoded by these groups. The analysis also provides the first information on the contribution made by the abundant but uncharacterized members of the orders Bacteroidales and Clostridiales to the rumen fermentation. This metabolomic scheme provides a framework for the investigation of gene function in these organisms, and the design of strategies that may enable manipulation of rumen fermentation.

**Gene loss.** One curious feature of several rumen bacteria is the absence of an identifiable enolase, the penultimate enzymatic step in glycolysis, which is conserved in all domains of life. Examination of >30,000 isolates from the Integrated Microbial Genomes with Microbiomes (IMG/M) database revealed that enolase-negative strains were rare (<0.5% of total), and that a high proportion of such strains were rumen isolates belonging to the genera *Butyrivibrio* and *Prevotella* and uncharacterized members of the family *Lachnospiraceae* (Supplementary Table 5). In the genus *Butyrivibrio* approximately half the sequenced strains lack enolase, while some show a truncated form. The distribution of this enzyme in relation to the phylogeny of this genus is shown in Figure 3. This analysis suggests that enolase is in the process of being lost by some rumen *Butyrivibrio* isolates and that we may be observing an example of environment-specific evolution by gene loss. Although the adaptive advantage conferred by loss of enolase is not clear, there is a possible link with pyruvate metabolism and lactate production. Several enolase-negative *Butyrivibrio*
strains do not produce lactate and 12 also lack the gene for \(\ell\)-lactate dehydrogenase. Conversely the enolase and \(\ell\)-lactate dehydrogenase genes are co-located in seven strains. An attempt to identify additional functions exhibiting a similar pattern of gene loss (or a complementing gain of function) by comparing enolase-positive versus enolase-negative *Butyrivibrio* spp. strains yielded no substantial additional insights (Supplementary Table 6)

Another example of gene loss is seen in bacteria that have lost their complete glycozen synthesis and utilization pathway, as shown by the concomitant loss of families GH13, GH77, GT3 or GT5, and GT35 (Supplementary Fig. 2). These bacteria include nutritionally fastidious members of the Firmicutes (*Allisonella histaminiformans*, *Demitobacterium detoxificans*, *Oxobacter pfennigii*) and Proteobacteria (*Wolinella succinogenes*), and have also lost most of their degradative CAZymes, suggesting that they have evolved toward a downstream position as secondary fermenters where they feed on fermentation products (acetate, pyruvate, amino acids) from primary degraders.

**Biosynthetic gene clusters.** We searched the Hungate genomes for biosynthetic gene clusters (Supplementary Fig. 5 and Supplementary Table 7) to identify evidence of secondary metabolites that might be used as rumen modifiers to reduce methane production through their antimicrobial activity\(^{34}\). A total of 6,906 biosynthetic clusters were predicted from the Hungate genomes (Supplementary Note 2).

**CRISPRs.** Identification of CRISPR–Cas systems and their homologous protospacers from viral, plasmid and microbial genomes could shed light on past encounters with foreign mobile genetic elements\(^{35}\) and somewhat indirectly, habitat distribution and ecological interactions\(^{36}\). A total of 6,344 CRISPR spacer sequences were predicted from 241 Hungate genomes and searched against various databases (Supplementary Table 8). Searching spacers against a database of cultured and uncultured DNA viruses and retroviruses (IMG/VR) revealed novel associations between 83 viral operational taxonomic units (OTUs) and 31 Hungate hosts. The vast majority of these viruses were derived from human intestinal and ruminal samples. Details and additional results are furnished in Supplementary Note 3.

**Metagenomic sequence recruitment**

We evaluated whether the Hungate catalog can contribute to metagenomic analyses by using a total of 1,468,357 coding sequences (CDSs) from the 501 reference genomes to search against \(\approx 1.9\) billion CDS predicted from more than 8,200 metagenomic data sets from diverse habitats. A total of 892,995 Hungate CDSs (\(\approx 60\%\)) were hits to 13,364,644 metagenome proteins at \(\geq 90\%\) amino acid identity. 466 out of 501 Hungate isolates recruited sequences from 2,219 metagenomic data sets derived from host-associated, environmental or engineered sources (Fig. 4 and Supplementary Table 9). The large number of human samples recruited (1,699) can be attributed to the greater availability of human samples compared to metagenomes from other mammals, including ruminants. Considering the number of isolate CDSs with hits to metagenome sequences (\% coverage), most Hungate genomes (413/501) are represented in rumen metagenome samples, as well as in human or other vertebrate samples (Fig. 4). The average \% coverage for 466 recruited genomes was 26.5% of total CDS, with *Sharpia azabuensis* DSM 18934 showing the highest capture (95.6\%) in a sheep rumen metagenome (Supplementary Fig. 6).

Examining recruitment against available rumen metagenomes, a majority of 336 isolates were captured in 24 rumen samples (27\% average coverage) (Supplementary Fig. 7 and Supplementary Table 9). A further 52 rumen isolates may be included if the hit count recruitment parameter is relaxed from 200 to 50. These isolates are predicted to occur in relatively low abundance in these rumen metagenomes, and somewhat indirectly, habitat distribution and ecological interactions\(^{36}\). A total of 6,906 biosynthetic clusters were predicted from more than 8,200 metagenomic data sets from diverse habitats. A total of 892,995 Hungate CDSs (~60\%) were hits to 13,364,644 metagenome proteins at ≥ 90% amino acid identity. 466 out of 501 Hungate isolates recruited sequences from 2,219 metagenomic data sets derived from host-associated, environmental or engineered sources (Fig. 4 and Supplementary Table 9). The large number of human samples recruited (1,699) can be attributed to the greater availability of human samples compared to metagenomes from other mammals, including ruminants. Considering the number of isolate CDSs with hits to metagenome sequences (\% coverage), most Hungate genomes (413/501) are represented in rumen metagenome samples, as well as in human or other vertebrate samples (Fig. 4). The average \% coverage for 466 recruited genomes was 26.5% of total CDS, with *Sharpia azabuensis* DSM 18934 showing the highest capture (95.6\%) in a sheep rumen metagenome (Supplementary Fig. 6).

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A total of 68 isolates were recruited by both rumen and human intestinal samples and represent shared species between the rumen and human microbiomes (Fig. 4), possibly fulfilling similar roles. A further 66 Hungate isolates were recruited by human samples but were not detected in rumen samples, giving a total of 134 Hungate catalog genomes that recruited various human samples, making them valuable reference sequences for the analysis of human microbiome samples. This observation is also indirectly recapitulated by the CRISPR–CAS systems-based analysis, which showed links to spacers from human intestinal samples, particularly for Hungate isolates of fecal origin (Supplementary Table 8). Additional metagenome recruitment analysis details are provided in Supplementary Note 4.

**Comparison with human gut microbiota**

Many Hungate strains (134/501) were shared between rumen and human intestinal microbiome samples. This is unsurprising, as both habitats are high-density, complex anaerobic microbial communities, producing similar fermentation products, and with extensive interspecies cross-feeding and interaction 41. We performed a comparative analysis against available human intestinal isolates (largely from the HMP), to identify differences that can be attributed to distinct lifestyles and adaptive capacity of rumen microorganisms. The Hungate and human intestine isolate collections were curated to remove redundancy, low-quality genomes and known human pathogens. This resulted in a set of 458 rumen and 387 human intestinal genomes (Supplementary Table 10), which was used to identify protein families in the Pfam database that were differentially abundant in isolates from each environment. Out of 7,718 Pfam domains found in 458 non-redundant Hungate isolate genomes, we determined 367 were over-represented in the ruminal genomes and 423 were under-represented on the basis of the false-discovery rate (FDR), q-value < 0.001 (Supplementary Table 11). Over-represented Pfams (Fig. 5) included enzymes involved in plant cell wall degradation (GH11, GH16, GH26, GH43, GH53, GH67, GH115), carbohydrate-binding modules (CBM2, CBM3, and cohesin and dockerin modules associated with cellulose assembly) and GT41 family glycosyl transferases, which occur predominantly in the genera Anaerovibrio and Selenomonas. Notably, Pfams for the biosynthesis of cobalamin (vitamin B₁₂), an essential micronutrient for the host, were over-represented. Vitamin B₁₂ biosynthesis is one of the most complex pathways in nature, involving more than 30 enzymatic steps, and given its high metabolic cost, is only encoded by a small set of bacteria and archaea. We examined this biosynthetic pathway in more detail using other functional annotation types (KO and Tigrfam) across the 501 Hungate isolates, and discovered that 12 or more enzymatic steps were over-represented in the ruminal genomes, and at least 47 isolates might be capable of de novo B₁₂ synthesis (Supplementary Table 12). Many of these were members of the Class Negativicutes within the Firmicutes (Anaerovibrio, Mitsuokella, and Selenomonas). A further 140 (including 21 archaean) genomes encode enzymes for the salvage of B₁₂ from an intermediate, and may even work cooperatively (based on potential complementarity of lesions in the pathway in different members) to share and synthesize corrinoids for community and/or host benefit. These observations reflect the high burden of a requirement for vitamin B₁₂, which is needed as a cofactor for enzymes involved in gluconeogenesis from propionate in the liver. This process is essential for lactose biosynthesis and milk production in dairy animals 42, and dairy and meat products of ruminant origin are important dietary sources of B₁₂ (ref. 43). By contrast, it has been speculated that human gut microbes were unlikely to contribute significant amounts of B₁₂ for their host and were likely competitors for dietary B₁₂ (ref. 44).

Of the Pfams (Fig. 5) under-represented in Hungate genomes, the occurrence of all steps for the oxidative branch of the pentose phosphate pathway (OPPP) was striking. The role of the OPPP is primarily the irreversible production of reducing equivalents (NADPH), although other enzymes may serve as alternate sources of reducing equivalents. As discussed above, the Pfam for enolase appeared in the list of under-represented families. The list also contained several Pfams associated with bacteriophage functions and sporulation. The differential abundance of sporulation genes is interesting as the observation that sporulation genes are abundant in human gut bacteria has been made recently 16,31 and is potentially linked with resistance to oxygen exposure. This observation is particularly striking given the preponderance of Firmicutes, an archetypically spore-forming phylum 45, in the rumen set. Large and small subunits of an oxygen-dependent Class I type ribonucleotide reductase were also under-represented together with several other Pfams implicated in oxygen tolerance, suggesting that human intestinal isolates may encounter higher oxygen tension compared to the strictly anaerobic ruminal ecosystem. These observations indirectly suggest that...
host genetics and physiology influence rumen microbiome composition and that rumen microbes are likely to be vertically inherited as indicated in recent studies.46,47 Conversely, human intestinal (more specifically, fecal) isolates are transmitted from other sources in the environment31,48. We were able to recapitulate these findings in a metagenome-based comparison of these two environments (sheep rumen samples against normal human fecal samples; Supplementary Table 13), suggesting that these differences cannot be explained by cultivation or abundance biases in the isolate data sets.

### DISCUSSION

The Hungate genome catalog that we report here includes genomic analysis of 501 bacterial and archaeal cultures that represent almost all of the cultured rumen species that have been taxonomically characterized, as well as representatives of several novel species and genera. This high-quality reference collection will guide interpretation of metagenomics data sets, including genomes recovered from metagenomes (MAGs). The Hungate genome catalog also allows robust comparative genomic analyses that are not feasible using incomplete sequence data from metagenomes. Researchers have access to Hungate Collection strains, which will enable a better understanding of carbon flow in the rumen, including the breakdown of lignocellulose, through the metabolism of substrates to SCFAs and fermentation end products, to the final step of CH₄ formation.

The Hungate genome collection is by no means complete. Some important taxa are missing, especially members of the order Bacteroidales30,32. At the start of this project genome sequences were available for strains belonging to 11 (12.5%) of the 88 genera described for the rumen. Currently, genome sequences are available for 73 (83%) of those 88 genera, as well as for 73 strains that are only identified to the family or order taxonomic level. Of the rumen ‘most wanted list’ which comprises 70 rumen bacteria40, the Hungate Collection has now contributed 30 members. In addition to missing bacteria and archaea, the sequencing of rumen eukaryotes presents considerable technical challenges and although some progress has been made in sequencing of anaerobic fungi49, there are no genome data for rumen ciliate protozoa, and only preliminary data on the rumen virome50.

Microbiome research is moving from descriptive to mechanistic, and to translation of those mechanisms into interventions51. Using rumen microbiome data to engineer rumen to reduce CH₄ emissions52 and improve productivity and sustainability outcomes is now in sight53. The Hungate Collection provides a starting point for this, shedding light on what has been described as ‘the world’s largest commercial fermentation process’54. Future studies can use the Hungate resources to improve the resolution of rumen meta-omics analyses, to identify antimicrobials, to source carbohydrate-degrading enzymes from the rumen for use as animal feed additives and in lignocellulose-based biofuel generation, and as the basis for synthetic microbial consortia.

### METHODS

Methods, including statements of data availability and any associated accession codes and references, are available in the online version of the paper.

Note: Any Supplementary Information and Source Data files are available in the online version of the paper.

### ACKNOWLEDGMENTS

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### AUTHOR CONTRIBUTIONS


### COMPETING INTERESTS

The authors declare no competing interests.

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Cultures used in this study. The full list of cultures used in the project and their provenance is shown in **Supplementary Table 1** with additional information available in **Supplementary Note 1**. New Zealand bacterial cultures from the Hungate Collection are available from the AgResearch culture collection while other cultures should be obtained from the relevant culture collections or requested from the sources shown in **Supplementary Table 1**.

Genomic DNA isolation. Genomic DNA was extracted using the Qiagen Genomic-tip kit following the manufacturer's instructions for the 500/G size extraction. Purified DNA was subject to partial 16S rRNA gene sequencing to confirm strain identity, before being shipped to the DOE Joint Genome Institute (JGI), USA for sequencing.

Sequence, assembly and annotation. All Hungate genomes were sequenced at the DOE Joint Genome Institute (JGI) using Illumina technology or Pacific Biosciences (PacBio) RS technology. For all genomes, we either constructed and sequenced an Illumina short-insert paired-end library with an average insert size of 270 bp, or a PacBio SMRTbell library. Genomes were assembled using Velvet, ALLPATHS-LG or Hierarchical Genome Assembly Process (HGAP) assembly methods (specifics provided in **Supplementary Table 2**). Genomes were annotated by the DOE–JGI genome annotation pipeline. Briefly, protein-coding genes (CDSs) were identified using Prodigal followed by a round of automated and manual curation using the JGI GenePrimp pipeline. Functional annotation and additional analyses were performed within the Integrated Microbial Genomes (IMG-ER) platform. All data as well as detailed sequencing and assembly reports can be downloaded from [https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=HungateCollection](https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=HungateCollection).

Hungate Collection and the Global Rumen Censuses analysis. We used the 16S rRNA gene sequences generated from the Global Rumen Censuses (GRC) to map the phylogenetic positions of the Hungate Collection genomes onto the known global distribution of Bacteria and Archaea from the rumen. Ten-thousand predicted OTUs were randomly chosen from the total 673,507 OTUs identified from that study in order to construct a phylogenetic tree. The 16S rRNA gene sequences for Hungate Collection genomes were added to the GRC subsample, and all Bacteria and Archaea were checked for chimeras and to ensure they represented separate OTUs using Cdhit-OTU with a 0.97% identity Ribosomal Database Project (RDP) followed by visual inspection with JalView. Taxonomic classifications were taken from those predicted by the GRC study. A maximum likelihood tree was then separately constructed for the Bacteria and Archaea using two rounds of Fasttree (version 2.1.7). These were compared to the GTR model of evolution and options: -gt r -nt; the second round optimized the branch lengths for the resulting topology (options: -gt -nt -nome -mln). The resulting phylogenetic trees were visualized using iTOL with the mapped positions of the Hungate genomes.

Carbohydrate-active enzymes (CAZymes). For each of the 501 genomes, the protein sequences were subjected to parallel (i) BLAST queries against CAZy libraries, of both complete sequences and individual modules; and (ii) HMMER searches using CAZy libraries of module family and subfamilies. Family assignments and overall CAZyme modularity were further validated through a human curation step, when proteins were not fully aligned (without gaps) with >50% identity to CAZy records.

Conserved single-copy gene phylogeny. A set of 56 universally conserved single-copy proteins in bacteria and archaea was used for construction of the *Butyrivibrio* phylogenetic tree. Marker genes were detected and aligned using hmmsearch and hmmpfai included in HMMER3. Alignments were concatenated and filtered. A phylogenetic tree was inferred using the maximum likelihood methods with RAxML (version 7.6.3). Tree topologies were tested for robustness by using 100 bootstrap replicates and the standard LG model. Trees were visualized using FastTree followed by iTOL.

Prediction of biosynthetic clusters. Putative biosynthetic clusters (BCs) were predicted and annotated using AntiSMASH version 3.0.4 (ref. 72) with the “inclusive” and the “borderpredict” options. All other options were left as default.

CRISP-CAS system analysis. A modified version of the Crisp Recognition Tool (CRT) algorithm, with annotations from the Integrated Microbial Genomes with Metagenomes (IMG/M) system was used to validate the functionality of the CRISP–Cas types (only complete gene arrangements were used plus those cas ‘orphan’ arrays with the same repeat from a complete array within the same genome). This Hungate spacer collection was queried against the viral database from the Integrated Microbial Genome system (IMG/VR database), a custom global “spacerome” (predicted from all IMG isolate and metagenome data sets) and the NBCI refseq plasmid database. All spacer searches were performed using the BLASTn-short function from the BLAST+ package with parameters: e-value threshold of $1.0 \times 10^{-6}$, percentage identity of >94% and coverage of >95%. These cutoffs were recommended by a recent study benchmarking the accuracy of spacer hits across a range of % identities and coverage.

Recruitment of metagenomic sequences. 1,468,357 protein coding sequences or CDS from 501 Hungate isolate genomes were searched using LAST against ~1.9 billion CDS predicted from 8,200 metagenomic samples stored in the IMG database. Hungate genomes were designated as “recruiters” if the following criteria were met: a minimum of 200 CDS with hits at ≥90% amino acid identity over 70% alignment length to an individual metagenomic CDS or ≥10% capture of total CDS in each genome. The rationale for choosing the minimum 200 hit count was to ensure that the evidence included more than merely housekeeping genes (which tend to be more highly conserved). In a few instances, the 200 CDS hit count requirement was relaxed if at least 10% of the total CDS in the genomes was captured. The ≥90% amino acid identity cutoff was chosen based on Luo et al., who assert that organisms grouped at the ‘species’ level typically show >85% AAI among themselves. We ascertained that ≥90% identity was sufficiently discriminatory for species in the Hungate genome set by observing differences in the recruitment pattern (hit count or % CDS coverage) of different species of the same genus (e.g., *Prevotella spp.*, *Butyrivibrio spp.*, *Bifidobacterium spp.*, *Treponema spp.*) from every phylum against the same metagenomic sample.

For nucleotide read recruitment, total reads from an individual metagenome were aligned against scaffolds from each of the 501 isolates using the BWA aligner. The effective minimum nucleotide % identity was ~75% with a minimum alignment length of 50 bp. Alignment results were examined in terms of total number of reads recruited to an isolate (at different % identity cutoffs with ≥97% identity proposed as a species-level recruitment), average read depth of total reads recruited to a given isolate genome, as well as % coverage of total nucleotide length of the genome.

Genome comparisons. For rumen versus human isolates comparisons, human intestinal isolate genomes were carefully selected from the IMG database using available GOLD metadata fields pertaining to isolation source (and taking care to remove known pathogens). Genome redundancies within either the human set or the rumen set were eliminated after assessing the average nucleotide identity (ANI) of total best bidirectional hits and removing genomes sharing >99% ANI (alignment fraction of total CDS ≥ 60%) to another genome within that set. Furthermore, low-quality genomes within the human set were flagged and removed based on the absence of the “high-quality” filter assigned by the IMG quality control pipeline owing to lack of phylum-level taxonomic assignment or if the coding density was <70% or >100% or the number of genes per million base pairs was <300 or >1,200 (ref. 61). This approach resulted in 388 genomes delineated in the human set and 458 genomes in the rumen set (lists provided in **Supplementary Table 10**). Both collections of genomes had similar average genome sizes (3.3–3.5 Mbp) and completeness (evaluated by CheckM). Pairwise comparisons of gene counts for individual Pfams between members of each set were performed using Metastats, which employs a non-parametric two-sided t-test test (or a Fischer’s exact test for sparse counts) with false-discovery rate (FDR) error correction to identify differentially abundant features between the two genome sets. Most significant
features were delineated using a q-value cutoff of <0.001, and less populous or sparsely recruited Pfams were also eliminated (where the sum of gene counts in each genome set was <100) (Supplementary Table 11, worksheet designated “Q-val<0.001 editable”). A second worksheet labeled “Q-val<0.005” shows a larger subset of differentially abundant Pfams applying the less stringent threshold of Q-value < 0.005, and including results for Pfams with sparse counts. Pfam was chosen for this primary analysis because it is the largest and most widely used source of manually curated protein families, with nearly 80% coverage (on average) of total CDS in these microbial genomes. KO terms or TIGRFAMS were also assessed to validate and complement Pfam-based findings or to examine specific pathways more closely. For comparisons of enolase-positive versus enolase-negative Butyryrivibrio spp. strains, Metastats was employed in conjunction with contrasting upper and lower quartile or percentile gene counts, in order to identify additional functions with a similar pattern of preservation/loss as the glycolytic enolase gene.

For metagenomes-based comparisons, previously published sheep rumen (IMG IDs: 33000021254, 3300021255, 33000021256, 3300021387, 3300021399, 3300021400, 3300021426, 3300021431) and human intestinal (IMG IDs: 3300008260, 3300008496, 3300007299, 3300007296, 3300007361, 3300007305, 3300007717) metagenomes were reassembled using metaSPAdes, annotated and loaded into IMG. Estimated gene copy numbers (calculated by multiplying gene count with read depth for the scaffold the gene resides on) were compared using Metastats (as described above).  

**Statistical analysis.** Refer to the Life Sciences Reporting Summary.  

**Life Sciences Reporting Summary.** Further information on experimental design is available in the Life Sciences Reporting Summary.  

**Data availability.** All available genomic data and annotations are available through the IMG portal (https://img.jgi.doe.gov/). Additionally, a dedicated portal to download all 410 genomes sequenced in this study is provided: https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=HungateCollection.

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### Experimental design

1. **Sample size**
   
   Describe how sample size was determined.

   Sample size was determined by availability of cultured micro-organisms relevant to the ruminant gut environment.

2. **Data exclusions**
   
   Describe any data exclusions.

   N/A

3. **Replication**
   
   Describe whether the experimental findings were reliably reproduced.

   N/A

4. **Randomization**
   
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   N/A

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   - The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
   - A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
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For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). Nature Methods guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

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Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

Genome sequences are publicly available from JGI’s Integrated Microbial Genomes and Microbiome Samples (IMG/M) and GenBank. Additionally, a dedicated portal to download all 410 genomes sequenced in this study is provided: Cultures are available from the relevant culture collections or from individuals, full details are given in the manuscript.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

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a. State the source of each eukaryotic cell line used.

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11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

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12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

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