



# High-Quality Whole-Genome Sequences of the Oligo-Mouse-Microbiota Bacterial Community

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**ABSTRACT** The Oligo-Mouse-Microbiota (Oligo-MM<sup>12</sup>) is a community of 12 mouse intestinal bacteria to be used for microbiome research in gnotobiotic mice. We present here the high-quality whole genome sequences of the Oligo-MM<sup>12</sup> strains, which were obtained by combining the accuracy of the Illumina platforms with the long reads of the PacBio technology.

In a recent study, we described a defined intestinal community of 12 murine strains, termed Oligo-Mouse-Microbiota (Oligo-MM<sup>12</sup>), which permanently colonize gnotobiotic mice over several generations and provide colonization resistance against *Salmonella enterica* serovar Typhimurium (1). This bacterial consortium has been thoroughly characterized by biochemical and molecular methods, and the individual strains have been deposited at the German Culture Collection of Microorganisms and Cell Cultures (DSMZ) (Table 1). The genomes of the 12 bacteria were previously sequenced and assembled via different techniques and algorithms (1–3). Since the Oligo-MM<sup>12</sup> strains are being used by an increasing number of research groups (1, 3–5), the multitude of genome sequences precludes the possibility of a meaningful exchange of data within the scientific community. Thus, there is a strong need for availability and constant update of the Oligo-MM<sup>12</sup> reference genomes.

It is well recognized that sequences from the Illumina platforms have low error rates, with systematic errors being mainly situated at the end of the reads, but are too short for an efficient complete genome assembly (6). On the contrary, the long reads generated by PacBio sequencing are less accurate and contain random errors (6). Aiming to create a set of reference genomes, in this study we present the high-quality genome sequences of the Oligo-MM<sup>12</sup> bacteria, which were assembled by a hybrid approach combining Illumina and PacBio sequences (Table 1).

As previously described (1), the complete genome sequence of *Acutalibacter muris* KB18 was obtained on the PacBio RSII platform and assembled using the RS\_HGAP\_Assembly.3 protocol (default parameters). Error correction was then performed by mapping Illumina reads onto the finished genome with the Burrows–Wheeler Alignment tool (7), with subsequent variant calling using CLC Genomics Workbench version 7.0.4. Here, Illumina MiSeq reads (1) of the remaining 11 bacterial genomes were assembled onto their respective PacBio complete genomes (2) by applying a reference-guided approach using SPAdes (8), with a minimum contig length of 500 bp. Assemblies were evaluated with QUAST (Quality Assessment Tool for genome assemblies) (9), and the final genomes were automatically annotated using RAST (Rapid Annotations using Subsystems Technology) (10). In future studies, genetic variation, genome evo-

Received 20 June 2017 Accepted 11 August 2017 Published 19 October 2017

**Citation** Garzetti D, Brugiroux S, Bunk B, Pukall R, McCoy KD, Macpherson AJ, Stecher B. 2017. High-quality whole-genome sequences of the Oligo-Mouse-Microbiota bacterial community. *Genome Announc* 5:e00758-17. <https://doi.org/10.1128/genomeA.00758-17>.

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**TABLE 1** Assembly information and accession numbers of the Oligo-MM<sup>12</sup> genomes

Oligo-MM strain	Total length (bp)	No. of contigs	No. of genes	DSM no.	Accession no.
[ <i>Clostridium</i> ] <i>innocuum</i> I46	4,468,984	1	4,629	26113	<a href="#">CP022722</a>
<i>Bacteroides caecimuris</i> I48	4,800,416	19	4,225	26085	<a href="#">NHMU00000000</a>
<i>Lactobacillus reuteri</i> I49	2,063,604	3	2,006	32035	<a href="#">NHMT00000000</a>
<i>Enterococcus faecalis</i> KB1	3,025,555	1	2,942	32036	<a href="#">CP022712</a>
<i>Acutalibacter muris</i> KB18	3,802,813	1	3,990	26090	<a href="#">CP021422</a>
<i>Bifidobacterium animalis</i> subsp. <i>animalis</i> YL2	2,021,926	2	1,732	26074	<a href="#">NHMR00000000</a>
<i>Muribaculum intestinale</i> YL27	3,306,969	1	2,786	28989	<a href="#">CP021421</a>
<i>Flavonifractor plautii</i> YL31	3,813,655	5	3,924	26117	<a href="#">NHMQ00000000</a>
[ <i>Clostridium</i> ] <i>clostridioforme</i> YL32	7,157,460	16	7,735	26114	<a href="#">NHTR00000000</a>
<i>Akkermansia muciniphila</i> YL44	2,737,167	1	2,731	26127	<a href="#">CP021420</a>
<i>Turicimonas muris</i> YL45	2,887,709	20	2,754	26109	<a href="#">NHMP00000000</a>
<i>Blautia coccooides</i> YL58	5,128,482	1	5,230	26115	<a href="#">CP022713</a>

lution, and functional genomics, among other research applications, of the Oligo-MM<sup>12</sup> community can be assessed by high-quality analyses.

**Accession number(s).** The assembled whole-genome sequences of the Oligo-MM<sup>12</sup> strains have been deposited in DDBJ/ENA/GenBank under the accession numbers given in Table 1.

#### ACKNOWLEDGMENTS

We thank Cathrin Spröer, Nicole Heyer, and Simone Severitt for sequencing of the KB18 PacBio genome.

This work was supported by the German Center for Infection Research (DZIF), the Center for Gastrointestinal Microbiome Research (CEGIMIR), and the German Research Foundation (DFG). The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

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