



Draft Genome Sequence of “*Candidatus Arthromitus*” UMNCA01, a Suspected Commensal Isolated from the Gut Microbiome of Commercial Turkey

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ABSTRACT “*Candidatus Arthromitus*” UMNCA01 was recovered from ileal samples of commercial turkey poults and may have probiotic capabilities. The complete genome was determined using the Illumina MiSeq and HiSeq sequencing platforms. The complete genome consists of 1,631,326 bp and has a G+C content of 26.14%, 1,540 coding sequences (CDS), and 37 RNA coding genes.

A candidate genus of segmented filamentous bacteria, “*Candidatus Arthromitus*” belongs to the family *Clostridiaceae*. These commensal organisms promote adaptive and innate immune responses in murine models in a host-specific manner, prevent diseases, and promote animal growth (1, 2). Different strains of “*Candidatus Arthromitus*” inhabit the ileum region in many vertebrate animals, such as cattle, pigs, chickens, humans, and, as shown more recently, turkeys (3). In an attempt to discern the microbial basis of light turkey syndrome (LTS), a condition where commercial turkey flocks fail to meet their genetic potential weights despite standardized diets and growth conditions (4), Danzeisen et al. performed 16S rRNA sequencing of intestinal microbiome analysis of high-performing and low-performing (based upon flock weights) turkey flocks (5). This analysis revealed that at the age of 2 to 3 weeks, high-performing turkey flocks harbored significantly higher proportions of “*Candidatus Arthromitus*” bacteria than their low-performing counterparts (5). In this study, the genome of a turkey-specific strain of “*Candidatus Arthromitus*” was sequenced from the gut microbiome.

“*Candidatus Arthromitus*” UMNCA01, a Gram-positive bacterium, was recovered from ileal samples harvested from 2-week-old turkey poults from a research turkey flock in barns at the University of Minnesota. The sample was identified for shotgun sequencing by previous 16S rRNA amplicon profiling indicating a high relative abundance of “*Candidatus Arthromitus*” bacteria and light microscopy confirming the presence of high levels of segmented filamentous bacteria. For metagenomic shotgun sequencing, the total genomic DNA was isolated using a Qiagen stool kit (Hilden, Germany). The quantity of the genomic DNA was determined by measuring A_{260} using a UV-visible (UV-Vis) spectrophotometer ($A_{260} = 1$ corresponds to 50 ng/ μ l of double-stranded DNA [dsDNA]). The quality of the genomic DNA was determined by measuring the A_{260}/A_{280} ratio, and a value of 1.8 indicated pure DNA preparation as described (6). Twenty micrograms of metagenomic DNA was used to prepare a paired-end (PE) sequencing library (Nextera XT, Illumina, San Diego, CA), and a PCR amplified library was sequenced using the Illumina MiSeq and HiSeq platforms. The shotgun data were assembled using CLC Genomics Workbench v. 9.0/APRIL-2016, with default parameters, and then contigs were mapped to an existing mouse

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TABLE 1 Global statistics of the “*Candidatus Arthromitus*” UMNCA01 genome

Parameter ^a	Value
Total sequence length (bp)	1,631,326
No. of genes (total)	1,577
No. of CDS (total)	1,540
No. of genes (coding)	1,480
No. of CDS (coding)	1,480
No. of genes (RNA)	37
No. of rRNAs (16S)	1
No. of partial rRNAs (16S)	1
No. of tRNAs	33
No. of ncRNAs	3
No. of pseudogenes	60
No. of scaffolds	41
Scaffold N_{50} (bp)	68,513
Scaffold L_{50} (bp)	9
No. of contigs	44
Contig N_{50} (bp)	57,760
Contig L_{50} (bp)	10

^a CDS, coding DNA sequences; ncRNAs, noncoding RNAs.

“*Candidatus Arthromitus*” genome using Mauve (7) to retrieve and arrange “*Candidatus Arthromitus*” sequences (sourced from turkeys) that mapped to those genomes. Following manual curation, unmapped contigs were then filtered from the metagenomic assembly. The final “*Candidatus Arthromitus*” assembly resulted in an average 100× genome coverage with a total number of 1,631,326 bp arranged into 41 contigs. The G+C content of these contigs was 26.14%, with an average contig size of 39,788 bp and an N_{50} value of 57,760 bp. The draft genome contains 1,480 protein coding sequences, 37 RNA genes, and 60 pseudogenes. The genome sequence of “*Candidatus Arthromitus*” UMNCA01 was annotated using the National Center for Biological Information (NCBI) Prokaryotic Genome Annotation Pipeline and the best-placed reference protein set of GeneMarkS+ (annotation software v. 4.6) as described (8, 9); the results are summarized in Table 1.

Data availability. This “*Candidatus Arthromitus*” UMNCA01 whole-genome shotgun (WGS) project has the GenBank accession number [NZ_LXFF00000000](#). The version of this project is NZ_LXFF01000000 and consists of sequences [LXFF01000001](#) through [LXFF01000041](#). The filtered assembly and raw sequencing reads can be accessed through BioProject accession number [PRJNA319431](#) and BioSample accession numbers [SAMN04889864](#) and [SAMN13392129](#), respectively.

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