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Draft Genome Sequence of *Turicibacter sanguinis* PC909, Isolated from Human Feces▽

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While the microbiota resident in the human gut is now known to provide a range of functions relevant to host health, many of the microbial members of the community have not yet been cultured or are represented by a limited number of isolates. We describe here the draft genome sequence of *Turicibacter sanguinis* PC909, isolated from a pooled healthy human fecal sample as part of the Australian Human Gut Microbiome Project.

Turicibacter spp. belong to a deeply branching, low-DNA G+C class of the *Firmicutes* termed the *Erysipelotrichia* that is comprised of the single order *Erysipelotrichiales* and the family *Erysipelotrichaceae* (3). *Turicibacter* spp. have been detected in the gastrointestinal tracts of several animals, including humans (e.g., references 4 and 7), suggesting that they may be important members of the gut microbiota. Consistent with this, *Turicibacter* spp. have been found to constitute part of the core measurable microbiota in mice, where they have also been shown to vary quantitatively in association with the host genotype (1). To date, only one axenic isolate has been described, *Turicibacter sanguinis* MOL361, a strain that was recovered from the bloodstream of a patient with acute appendicitis (2). However, it has been suggested that an uncultured murine phylotype, *Turicibacter* 458, may possess putative immunomodulatory and invasive properties (9) and that *Turicibacter* spp. may cause subclinical infections in piglets (10).

The *rrs* gene of *T. sanguinis* PC909 displays 100% sequence identity to the corresponding region of *T. sanguinis* MOL361 (NR_028816) and that of *Turicibacter* 458 (EU375462). In order to better understand the interaction of *T. sanguinis* with the host, we performed whole-genome sequencing using a 454 Life Sciences GS FLX system at the J. Craig Venter Institute (JCVI). The sequence data consists of 2,953,411 bp of DNA sequence at 70.6× coverage. Contig assembly was performed using the Newbler Assembler v. 2.3. The sequences assembled into 125 individual contigs, with a contig N50 of approximately 40.7 kb and with the largest contig approximately 146.6 kb. The DNA sequences were annotated using JCVI's prokaryotic annotation pipeline.

The draft genome has a G+C content of 34% and contains 2,851 genes with 2,781 protein coding genes and 70 structural RNAs. The annotated genome sequence revealed the presence of three internalin related proteins, including a protein with sequence similarity to internalin A from *Listeria monocytogenes*, which has been shown to be necessary for gastrointestinal (6) and intracellular invasion (5). Comparison with the Virulence Factor Database (11) revealed the presence of proteins with suspected roles in binding to host structural factors (e.g., fibronectin, laminin, HSP60), the production of a collagen binding pilus, and capsule biosynthesis. Interestingly, genes related to sporulation and tolerance to oxygen species were also identified in the *T. sanguinis* PC909 genome sequence, which contrasts with the original phenotypic description for the genus and species (2).

Two other *Turicibacter* sp. genomes are currently being sequenced, *T. sanguinis* MOL361 and *Turicibacter* sp. HGF1, and in addition to that of *T. sanguinis* PC909, these genome sequences will provide a greater insight into the functional repertoire and potential pangenome of *Turicibacter* spp.

Nucleotide sequence accession numbers. The Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ADMN00000000. The version described here is the first version, accession number ADMN01000000. The genome project data are also available at GenBank under the genome project ID 42765. The *rrs* sequence of *T. sanguinis* PC909 has been deposited in GenBank under accession number HQ428099.

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