

Figure S1. 16S rRNA bootstrap consensus phylogenetic tree of MMM721<sup>T</sup>, ISU324, PIG517, and publicly available 16S rRNA gene sequences from cultured *Turicibacter* isolates on the Ribosomal Database Project as of September 2021 (1). The tree is rooted by *Eggerthia catenaformis* DSM 20559. The phylogenetic tree was constructed in MEGA the neighbor-joining algorithm (2).

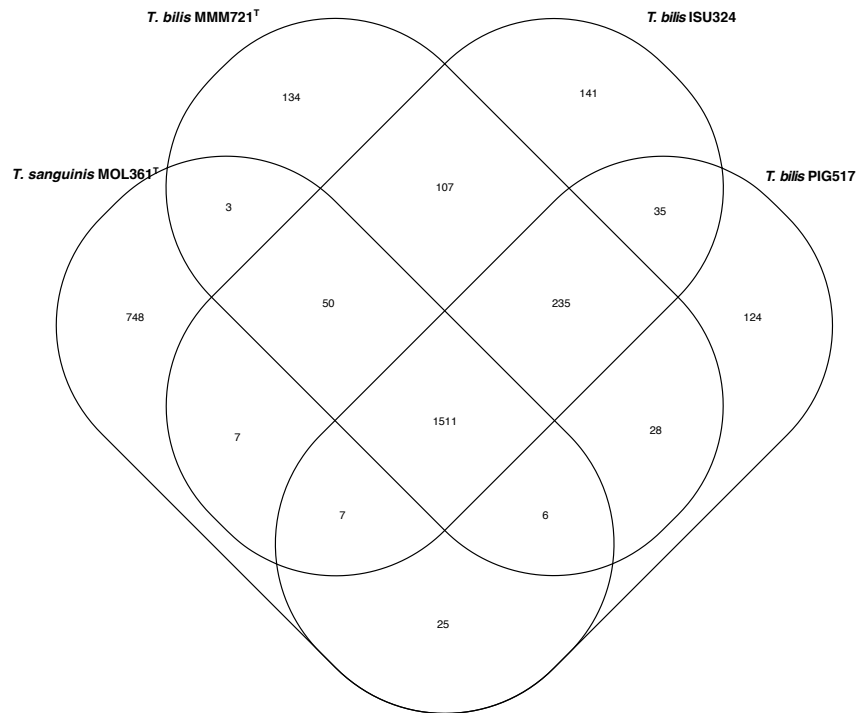


Figure S2. Venn diagram indicating shared ORFs between MMM721<sup>T</sup>, ISU324, PIG517, and *T. sanguinis* MOL361<sup>T</sup>. Genome features were downloaded from annotated genomes on the PathoSystems Resource Integration Center (PATRIC) genome database and submitted to eggNOG-mapper and annotated with default settings. The resultant data frames were imported into R and the “seed\_eggNOG\_orthologs” (the best matching gene sequence) for each ORF were compared using the venn function in R

	<i>T. sanguinis</i> MOL361 <sup>T</sup>	<i>T. bilis</i> MMM721 <sup>T</sup>	<i>T. bilis</i> ISU324	<i>T. bilis</i> PIG517
Biochemical reactivity:				
a,D-glucoside	+	-	-	+
a,D-galactoside	+	-	-	-
Glycine-b	+	-	-	-
Arginine-b	-	+	-	+
Serine-b	+	-	-	w
gelatin	+	+	+	+
esculin	±	±	+	+
Methyl-beta-D-xylopyranoside	-	-	-	w
D-glucose	-	-	-	w
Arbutin	-	-	-	w
Salicin	-	-	-	w
D-cellobiose	-	-	-	w
D-maltose	+	-	-	w
D-lactose (bovine origin)	-	-	-	w
Potassium 5-ketogluconate	w	-	-	-
*SCFAs	Ac, Lac	Ac, But, Lac, Val, Cap, Phen	Ac, But, Lac, Cap, Ox, Suc	Ac, But, Lac, Cap, Suc
Genome Length (Mb)	2.9	2.7	2.8	2.6
Genome G+C content (mol%)	34.2	34.3	34.1	34.3

Table S1. Comparison of biochemical reactivity, fermentation end products, and genome characteristics of MMM721<sup>T</sup>, ISU324, and PIG517 with *Turicibacter sanguinis* MOL361<sup>T</sup>.

+, positive; -, negative; w, weak; ±, variable. Characteristics for *T. sanguinis* MOL361<sup>T</sup> were taken from Bosshard *et al.* (3).

SCFAs: Ac, Acetic acid; But, Butyric acid; Cap, Caproic acid; Lac, Lactic acid; Ox, Oxalic acid; Phen, Phenylacetic acid; Suc, Succinic acid; Val, Valeric acid.

Strain	Substrate	Formate	Acetate	Propionate	Isobutyrate	Butyrate	Lactate 1	Lactate 2	Isovalerate	Valerate	Caproate	Oxalate	Succinate	Phenylacetate
<b>MMM</b>	BHIGL	-	++	-	-	++	+++	+++	-	-	+	-	-	-
	Gelatin	-	++	-	-	++	+++	+++	-	-	+	-	-	+
	Arginine	-	++	-	-	++	+++	+++	-	+++	+	-	-	-
<b>Pig</b>	BHIGL	-	-	-	-	+	+++	+++	-	-	-	-	-	-
	Arginine	-	++	-	-	++	+++	+++	-	-	-	-	-	-
	Gelatin	-	+	-	-	++	+++	+++	-	-	+	-	+	-
	Dextrose	-	++	-	-	++	+++	+++	-	-	+	-	-	-
<b>ISU</b>	BHIGL	-	++	-	-	++	+++	+++	-	-	+	-	-	-
	Gelatin	-	++	-	-	++	+++	+++	-	-	+	+	+	-

Table S2. Fermentation end products of MMM721<sup>T</sup>, ISU324, and PIG517 as measured by gas chromatograph (GC). Strains were grown in supplemented BHIGL broth for 48 hr at 42°C prior to extractions of fermentation end products. Measurements were normalized to uninoculated control tubes and all analyses were conducted in duplicate. -, <0.01 mM; +, 0.01-0.1 mM; ++, 0.1-1.0 mM, +++, >1.0 mM.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>T. sanguinis</i> MGYG-HGUT-00143 (1)	*	86.01	<b>99.74</b>	85	<b>99.73</b>	<b>99.69</b>	84.81	85.91	<b>99.7</b>	83.53	85.03	85.87	86.01	85.84
<i>Turicibacter</i> sp. H121 (2)	85.98	*	85.74	85.25	85.65	85.59	85.11	<b>98.62</b>	85.71	<b>83.85</b>	84.48	<b>98.52</b>	<b>98.88</b>	<b>98.47</b>
<i>T. sanguinis</i> PC909 (3)	<b>99.74</b>	85.77	*	84.92	<b>99.76</b>	<b>99.67</b>	84.74	85.74	<b>99.79</b>	84.32	84.9	86.07	85.89	85.94
<i>Turicibacter</i> sp. UBA1159 (4)	85	85.26	84.92	*	84.95	84.92	86.49	85.32	84.84	83.08	84.03	85.32	85.25	85.46
<i>T. sanguinis</i> am_0171 (5)	<b>99.72</b>	85.67	<b>99.76</b>	84.96	*	<b>99.64</b>	84.78	85.66	<b>99.75</b>	83.04	84.79	85.58	85.7	85.52
<i>Turicibacter</i> sp. HGF1 (6)	<b>99.69</b>	85.6	<b>99.68</b>	84.92	<b>99.64</b>	*	84.86	85.57	<b>99.65</b>	83.11	84.95	85.57	85.66	85.46
<i>Turicibacter</i> sp. UBA7094 (7)	84.81	85.11	84.74	86.48	84.79	84.86	*	85.05	84.8	83.07	84.46	85.13	85.06	85.14
<i>T. sanguinis</i> MGYG-HGUT-00037 (8)	85.89	<b>98.62</b>	85.73	85.32	85.65	85.56	85.05	*	85.84	83.85	84.63	<b>98.63</b>	<b>98.63</b>	<b>98.57</b>
<i>T. sanguinis</i> MOL361 <sup>T</sup> (9)	<b>99.7</b>	85.72	<b>99.78</b>	84.84	<b>99.74</b>	<b>99.65</b>	84.8	85.85	*	83.52	85.01	86.07	85.8	86
<i>Turicibacter</i> sp. Lab288P1bin27 (10)	83.53	83.85	84.32	83.08	83.04	83.11	83.07	83.85	83.52	*	86.81	83.85	83.85	83.85
<i>Turicibacter</i> sp. Nc150P1bin9 (11)	85.09	84.47	84.9	84.03	84.8	84.93	84.46	84.66	85.02	86.81	*	84.66	84.34	84.49
<i>T. bilis</i> ISU324 (12)	85.86	<b>98.53</b>	86.04	85.31	85.55	85.54	85.13	<b>98.62</b>	86.04	83.85	84.66	*	<b>98.51</b>	<b>99.14</b>
<i>T. bilis</i> PIG517 (13)	85.99	<b>98.88</b>	85.88	85.23	85.68	85.65	85.06	<b>98.62</b>	85.79	83.85	84.34	<b>98.51</b>	*	<b>98.44</b>
<i>T. bilis</i> MMM721 <sup>T</sup> (14)	85.81	<b>98.48</b>	85.91	85.44	85.49	85.44	85.14	<b>98.57</b>	85.97	83.85	84.49	<b>99.14</b>	<b>98.42</b>	*

Table S3. Pairwise comparison of ANIm values between MMM721<sup>T</sup>, ISU324, PIG517, and all publicly available genomes on the PathoSystems Resource Integration Center (PATRIC) genome database. Bolded values exceed the 95-96% threshold for species assignment. The \* indicates 100% similarity when genomes were compared against themselves.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>T. sanguinis</i> MGYG-HGUT-00143 (1)	*	23.1	<b>97.7</b>	21.2	<b>97.8</b>	<b>97.2</b>	20.7	22.3	<b>97.3</b>	17.2	25.3	22.4	22.5	22.5
<i>Turicibacter</i> sp. H121 (2)	23.1	*	22.8	22.7	22.6	22.1	22.2	<b>86.8</b>	22.7	23.5	25.9	<b>86.2</b>	<b>90.2</b>	<b>85.9</b>
<i>T. sanguinis</i> PC909 (3)	<b>97.7</b>	22.8	*	21.1	<b>97.9</b>	<b>97.1</b>	20.7	22.1	<b>98.3</b>	16.9	24.7	22.5	22.2	22.5
<i>Turicibacter</i> sp. UBA1159 (4)	21.2	22.7	21.1	*	21.0	21.1	26.5	22.8	21.0	21.9	23.4	22.8	22.6	22.7
<i>T. sanguinis</i> am_0171 (5)	<b>97.8</b>	22.6	<b>97.9</b>	21.0	*	<b>97.1</b>	20.5	22.0	<b>98.0</b>	17.0	24.5	21.9	22.0	21.9
<i>Turicibacter</i> sp. HGF1 (6)	<b>97.2</b>	22.1	<b>97.1</b>	21.1	<b>97.1</b>	*	20.7	21.9	<b>96.9</b>	16.8	24.7	22.0	22.0	22.1
<i>Turicibacter</i> sp. UBA7094 (7)	20.7	22.2	20.7	26.5	20.5	20.7	*	22.3	20.5	21.2	22.8	22.3	22.2	22.3
<i>T. sanguinis</i> MGYG-HGUT-00037 (8)	22.3	<b>86.8</b>	22.1	22.8	22.0	21.9	22.3	*	22.1	22.6	26.0	<b>87.1</b>	<b>86.6</b>	<b>86.2</b>
<i>T. sanguinis</i> MOL361 <sup>T</sup> (9)	<b>97.3</b>	22.7	<b>98.3</b>	21.0	<b>98.0</b>	<b>96.9</b>	20.5	22.1	*	17.1	24.8	22.5	22.1	22.5
<i>Turicibacter</i> sp. Lab288P1bin27 (10)	17.2	23.5	16.9	21.9	17.0	16.8	21.2	22.6	17.1	*	15.7	23.0	23.2	23.1
<i>Turicibacter</i> sp. Nc150P1bin9 (11)	25.3	25.9	24.7	23.4	24.5	24.7	22.8	26.0	24.8	15.7	*	25.8	25.7	25.8
<i>T. bilis</i> ISU324 (12)	22.4	<b>86.2</b>	22.5	22.8	21.9	22.0	22.3	<b>87.1</b>	22.5	23.0	25.8	*	<b>85.9</b>	<b>92.3</b>
<i>T. bilis</i> PIG517 (13)	22.5	<b>90.2</b>	22.2	22.6	22.0	22.0	22.2	<b>86.6</b>	22.1	23.2	25.7	<b>85.9</b>	*	<b>84.2</b>
<i>T. bilis</i> MMM721 <sup>T</sup> (14)	22.5	<b>85.9</b>	22.5	22.7	21.9	22.1	22.3	<b>86.2</b>	22.5	23.1	25.8	<b>92.3</b>	<b>84.2</b>	*

Table S4. Pairwise comparison of dDDH values between MMM721<sup>T</sup>, ISU324, PIG517, and all publicly available genomes on the PathoSystems Resource Integration Center (PATRIC) genome database. Bolded values exceed the 70% threshold for species assignment. The \* indicates 100% similarity when genomes were compared against themselves.

References:

1. Cole JR, Wang Q, Fish JA, Chai B, McGarrell DM, Sun Y, et al. Ribosomal Database Project: data and tools for high throughput rRNA analysis. *Nucleic Acids Res.* 2014;42(Database issue):D633-42.
2. Tamura K, Stecher G, Kumar S. MEGA11: Molecular Evolutionary Genetics Analysis Version 11. *Mol Biol Evol.* 2021;38(7):3022-7.
3. Bosshard PP, Zbinden R, Altwegg M. *Turicibacter sanguinis* gen. nov., sp. nov., a novel anaerobic, Gram-positive bacterium. *Int J Syst Evol Microbiol.* 2002;52(4):1263-6.