

Comparative Genomic Analyses of the Clinically-Derived *Winkia* Strain NY0527: the Reassignment of *W. neuii* subsp. *neuii* and *W. neuii* subsp. *antitratus* into Two Separate Species and Insights into Their Virulence Characteristics

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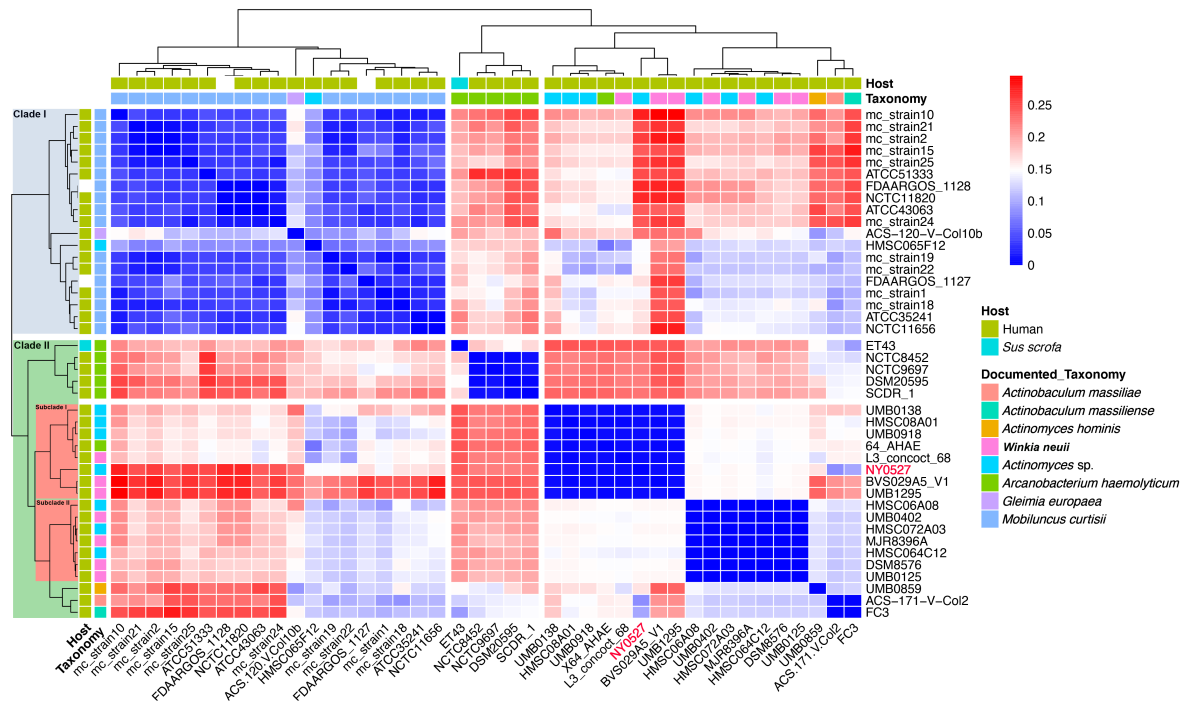


Figure S1 Heatmap displaying the genome distances between the strains phylogenomically close to strain NY0527.

Table S1 Taxonomic assignment of strain NY0527 using the MALDI Biotyper

Taxon	Strain	Score	Confidence Level
<i>W. neuii</i> subsp. <i>anitratus</i>	CIP104016T	2.171	Species
<i>W. neuii</i> subsp. <i>anitratus</i>	CCUG26929	2.161	Species
<i>W. neuii</i> subsp. <i>anitratus</i>	ENR_0422	2.057	Species
<i>W. neuii</i>	475RLT	2.051	Species
<i>W. neuii</i>	VA201_10 ERL	1.968	Genus
<i>W. neuii</i>	50_90 IBS	1.884	Genus
<i>W. neuii</i> subsp. <i>anitratus</i>	121 RLT	1.805	Genus
<i>W. neuii</i>	461 RLT	1.8	Genus
<i>W. neuii</i> subsp. <i>anitratus</i>	DSM 8577 ^T	1.581	Not significant
<i>W. neuii</i> subsp. <i>neuii</i>	DSM 8576 ^T	1.521	Not significant

Table S2 Sequence alignment of plasmid pNY0527 against the NCBI-nt database^a

Taxonomy	Strain	Query Coverage	Identity	Accession	Sequence Type
<i>Corynebacterium striatum</i>	M82B	53%	99.93%	AF024666.2	Plasmid
<i>Corynebacterium diphtheriae</i>	FRC0137	44%	99.92%	OV884287.1	Chromosome
<i>Corynebacterium diphtheriae</i>	FRC0375	44%	99.92%	OV884286.1	Chromosome
<i>Corynebacterium striatum</i>	KC-Na-01	40%	99.92%	CP021252.1	Chromosome
<i>Corynebacterium striatum</i>	FDAARGOS_1115	41%	99.87%	CP068158.1	Chromosome
<i>Corynebacterium diphtheriae</i>	FRC0402	52%	99.74%	OV884290.1	Plasmid
<i>Corynebacterium striatum</i>	215	54%	99.47%	CP024931.1	Chromosome
<i>Corynebacterium urealyticum</i>	FDAARGOS_995	50%	99.06%	CP066289.1	Chromosome
<i>Corynebacterium urealyticum</i>	DSM 7111	50%	98.61%	CP004085.1	Chromosome
<i>Corynebacterium urealyticum</i>	FDAARGOS_996	40%	98.61%	CP065982.1	Chromosome
<i>Corynebacterium urealyticum</i>	FDAARGOS_994	50%	98.4%	CP066064.1	Chromosome
<i>Corynebacterium urealyticum</i>	NCTC12011	50%	98.33%	LT906481.1	Chromosome
<i>Corynebacterium urealyticum</i>	DSM 7109	50%	98.33%	AM942444.1	Chromosome
<i>Corynebacterium kefirresidentialii</i>	FDAARGOS_1055	51%	95.69%	CP067011.1	Plasmid
<i>Corynebacterium striatum</i>	216	59%	95.43%	CP024932.1	Chromosome
<i>Corynebacterium striatum</i>	FDAARGOS_1197	59%	95.4%	CP069514.1	Chromosome
<i>Corynebacterium striatum</i>	KC-Na-01	40%	93.9%	CP021253.1	Plasmid

^a Only sequences with query-coverage higher than 40% are listed here.

Table S3 Information of the genomes downloaded for analysis in this study

Strain	Taxonomy	Assembly accession /Nucleotide accession
64_AHAE	<i>Arcanobacterium haemolyticum</i>	GCA_001055535.1
BVS029A5_V1	<i>Winkia neuui</i> subsp. <i>anitratus</i>	GCA_000296485.1
UMB1295	<i>Winkia neuui</i>	JAAUWI010000010,JAAUWI010000011,JAAUWI010000012,JAAUWI010000013,JAAUWI010000014,JAAUWI010000015,JAAUWI010000016

UMB0918	<i>Actinomyces</i> sp.	GCA_002872055.1
L3_concoct_68	<i>Winkia neuui</i>	GCA_018372675.1
HMSC08A01	<i>Actinomyces</i> sp.	GCF_001807435.1
UMB0138	<i>Actinomyces</i> sp.	GCA_002849225.1
HMSC06A08	<i>Actinomyces</i> sp.	LWOG01000001.1- LWOG01000045.1
UMB0125	<i>Winkia neuui</i>	GCA_002860645.1
HMSC064C12	<i>Actinomyces</i> sp.	GCF_001812345.1
MJR8396A	<i>Winkia neuui</i>	GCF_001546135.1
HMSC072A03	<i>Actinomyces</i> sp.	GCF_001812065.1
UMB0402	<i>Winkia neuui</i>	GCA_002860625.1
DSM8576	<i>Winkia neuui</i> subsp. <i>neuui</i>	GCA_000420405.1
ACS-171-V-Col2	<i>Actinobaculum massiliae</i>	GCA_000315465.1
mc_strain19	<i>Mobiluncus curtisii</i>	GCA_012976495.1
mc_strain1	<i>Mobiluncus curtisii</i>	GCA_012976845.1
FDAARGOS_1127	<i>Mobiluncus curtisii</i>	GCA_016725225.1
NCTC11656	<i>Mobiluncus curtisii</i>	GCA_900453315.1
FC3	<i>Actinobaculum massiliense</i>	GCA_001457435.1
UMB0859	<i>Actinomyces hominis</i>	GCA_002871945.1
HMSC065F12	<i>Actinomyces</i> sp.	GCF_001814535.1
mc_strain18	<i>Mobiluncus curtisii</i>	GCA_012976525.1
ACS-120-V-Col10b	<i>Gleimia europaea</i>	GCF_000411155.1
ATCC35241	<i>Mobiluncus curtisii</i>	GCA_000146285.1
ATCC43063	<i>Mobiluncus curtisii</i>	GCA_000196535.1
ATCC51333	<i>Mobiluncus curtisii</i>	GCA_000185425.1
DSM20595	<i>Arcanobacterium haemolyticum</i>	GCA_000092365.1
ET43	<i>Arcanobacterium haemolyticum</i>	GCA_021532125.1
FDAARGOS_1128	<i>Mobiluncus curtisii</i>	GCA_016726965.1
mc_strain10	<i>Mobiluncus curtisii</i>	GCA_012976565.1
mc_strain15	<i>Mobiluncus curtisii</i>	GCA_012976515.1

mc_strain2	<i>Mobiluncus curtisii</i>	GCA_012976795.1
mc_strain21	<i>Mobiluncus curtisii</i>	GCA_012976485.1
mc_strain22	<i>Mobiluncus curtisii</i>	GCA_012976465.1
mc_strain24	<i>Mobiluncus curtisii</i>	GCA_012976435.1
mc_strain25	<i>Mobiluncus curtisii</i>	GCA_012976425.1
NCTC11820	<i>Mobiluncus curtisii</i>	GCA_900450555.1
NCTC8452	<i>Arcanobacterium haemolyticum</i>	GCA_900475915.1
NCTC9697	<i>Arcanobacterium haemolyticum</i>	GCA_900445275.1
NY0527	<i>Winkia neuui</i> subsp. <i>anitratu</i> s	
SCDR_1	<i>Arcanobacterium haemolyticum</i>	GCA_006088775.1

Table S4 Presence of the four homologs of beta-lactamase expression repressor coding gene in *Winkia* spp.

Strain	Homolog1	Homolog2	Homolog3	Homolog4
64_AHAE	A	P	A	A
BVS029A5_V1	A	A	A	A
DSM8576	P	A	A	A
HMSC064C12	P	A	A	A
HMSC06A08	A	P	A	A
HMSC072A03	P	A	A	A
HMSC08A01	A	A	P	A
L3_concoct_68	A	P	A	A
MJR8396A	P	A	A	A
NY0527	A	A	A	P
UMB0125	P	A	A	A
UMB0138	A	P	A	A
UMB0402	P	A	A	A
UMB0918	A	A	P	A
UMB1295	A	A	A	A

A and P represent absence and presence, respectively.