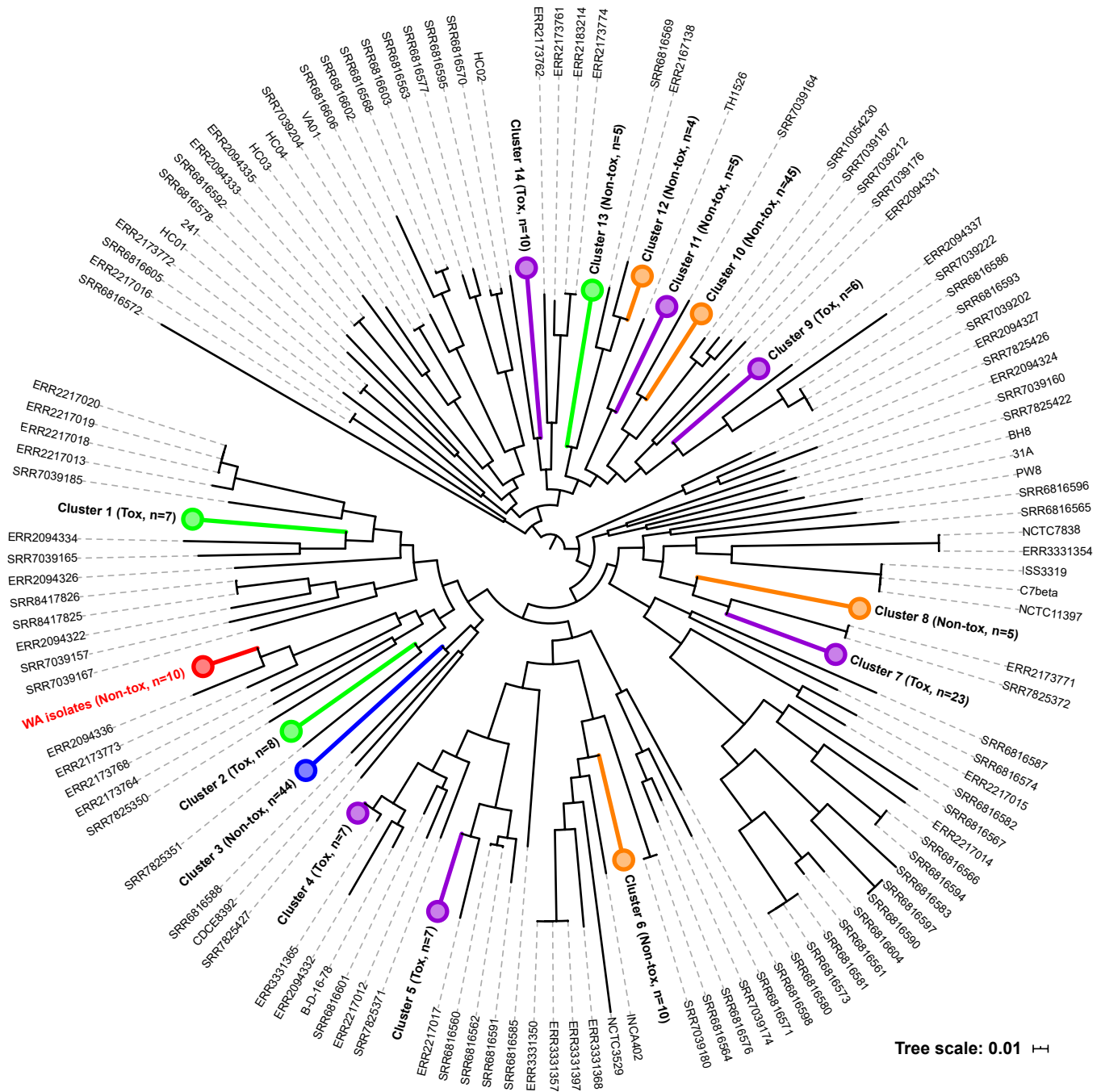


Supplemental Material

Figure S1: Phylogenetic reconstruction of the WA *C. diphtheriae* isolates and additional publicly available genomic data from 305 isolates using 136180 core, variable sites with maximum likelihood. The cluster of WA isolates is indicated in red. Previously reported clusters from Switzerland (green) [1], Canada (blue) [2], and Germany (orange) [3] are indicated with their toxigenicity and isolate count. Details for additional geographically defined clusters (purple) are listed in Table S4.



Tree scale: 0.01

Table S1: *C. diphtheriae* isolates within clustered highlighted in Figure S1.

Cluster	Run	Alias Name	ST	Toxin gene presence (Yes/No)	Project	Country
WA	SRR12270040	PC0646	445	N	PRJNA541849	USA
WA	SRR12270039	PC0647	445	N	PRJNA541849	USA
WA	SRR12270038	PC0648	445	N	PRJNA541849	USA
WA	SRR12270037	PC0649	445	N	PRJNA541849	USA
WA	SRR12270036	PC0650	445	N	PRJNA541849	USA
WA	SRR12270035	PC0651	445	N	PRJNA541849	USA
WA	SRR12270034	PC0652	NT*	N	PRJNA541849	USA
WA	SRR12270033	PC0653	445	N	PRJNA541849	USA
WA	SRR12270032	PC0654	445	N	PRJNA541849	USA
WA	SRR12270031	PC0655	445	N	PRJNA541849	USA
1	ERR2173765	Cd_6	486	Y	PRJNA541849	Switzerland
1	ERR2173769	Cd_18	486	Y	PRJEB14914	Switzerland
1	ERR2173770	Cd_19	486	Y	PRJEB14914	Switzerland
1	SRR7825355	KL0652	486	Y	PRJNA490531	Germany
1	SRR7825367	KL0613	486	Y	PRJNA490531	Germany
1	SRR7825368	KL0625	486	Y	PRJNA490531	Germany
1	SRR7825369	KL0623	486	Y	PRJNA490531	Germany
2	ERR2173763	Cd_3	473	Y	PRJEB14914	Switzerland
2	ERR2173767	Cd_9	473	Y	PRJEB14914	Switzerland
2	ERR2173855	Cd-11	473	Y	PRJEB14914	Switzerland
2	SRR7825356	KL0654	473	Y	PRJNA490531	Germany
2	SRR7825358	KL0663	473	Y	PRJNA490531	Germany
2	SRR7825359	KL0670	473	Y	PRJNA490531	Germany
2	SRR7825364	KL0633	473	Y	PRJNA490531	Germany
2	SRR7825365	KL0631	473	Y	PRJNA490531	Germany
3	SRR10054201	CD35	76	N	PRJNA563223	Canada
3	SRR10054202	CD36	76	N	PRJNA563223	Canada
3	SRR10054203	CD37	76	N	PRJNA563223	Canada
3	SRR10054204	CD38	76	N	PRJNA563223	Canada
3	SRR10054211	CD44	76	N	PRJNA563223	Canada
3	SRR10054217	CD50	76	N	PRJNA563223	Canada
3	SRR10054218	CD6	76	N	PRJNA563223	Canada
3	SRR10054219	CD51	76	N	PRJNA563223	Canada
3	SRR10054220	CD52	76	N	PRJNA563223	Canada
3	SRR10054221	CD53	76	N	PRJNA563223	Canada
3	SRR10054222	CD54	76	N	PRJNA563223	Canada
3	SRR10054223	CD55	76	N	PRJNA563223	Canada
3	SRR10054224	CD56	76	N	PRJNA563223	Canada
3	SRR10054225	CD7	76	N	PRJNA563223	Canada
3	SRR10054226	CD8	76	N	PRJNA563223	Canada
3	SRR10054227	CD9	76	N	PRJNA563223	Canada
3	SRR10054228	CD10	76	N	PRJNA563223	Canada
3	SRR10054229	CD34	76	N	PRJNA563223	Canada
3	SRR10054231	CD32	76	N	PRJNA563223	Canada
3	SRR10054232	CD31	76	N	PRJNA563223	Canada
3	SRR10054233	CD4	76	N	PRJNA563223	Canada
3	SRR10054234	CD30	76	N	PRJNA563223	Canada
3	SRR10054235	CD29	76	N	PRJNA563223	Canada
3	SRR10054236	CD28	76	N	PRJNA563223	Canada
3	SRR10054237	CD27	76	N	PRJNA563223	Canada
3	SRR10054238	CD26	76	N	PRJNA563223	Canada
3	SRR10054239	CD25	76	N	PRJNA563223	Canada
3	SRR10054240	CD24	76	N	PRJNA563223	Canada
3	SRR10054241	CD23	76	N	PRJNA563223	Canada
3	SRR10054242	CD22	76	N	PRJNA563223	Canada
3	SRR10054243	CD21	76	N	PRJNA563223	Canada
3	SRR10054244	CD3	76	N	PRJNA563223	Canada
3	SRR10054245	CD20	76	N	PRJNA563223	Canada
3	SRR10054246	CD19	76	N	PRJNA563223	Canada
3	SRR10054247	CD18	76	N	PRJNA563223	Canada
3	SRR10054248	CD17	76	N	PRJNA563223	Canada
3	SRR10054249	CD16	76	N	PRJNA563223	Canada
3	SRR10054250	CD15	76	N	PRJNA563223	Canada
3	SRR10054251	CD14	76	N	PRJNA563223	Canada
3	SRR10054252	CD13	76	N	PRJNA563223	Canada
3	SRR10054253	CD12	76	N	PRJNA563223	Canada

3	SRR10054254	CD11	76	N	PRJNA563223	Canada
3	SRR10054255	CD2	76	N	PRJNA563223	Canada
3	SRR10054256	CD1	76	N	PRJNA563223	Canada
4	ERR3331362	SAMEA5615640	209	Y	PRJEB32654	UK and vietnam
4	ERR3331366	SAMEA5615644	209	Y	PRJEB32654	UK and vietnam
4	ERR3331372	SAMEA5615650	209	Y	PRJEB32654	UK and vietnam
4	ERR3331384	SAMEA5615662	209	Y	PRJEB32654	UK and vietnam
4	ERR3331386	SAMEA5615664	209	Y	PRJEB32654	UK and vietnam
4	ERR3331387	SAMEA5615665	209	Y	PRJEB32654	UK and vietnam
4	ERR3331395	SAMEA5615674	209	Y	PRJEB32654	UK and vietnam
5	BQ11	NA	125	Y	PRJNA224116	Australia
5	SRR7223801	Cdiphth_UnIn-R1	125	Y	PRJNA473263	Australia
5	SRR7223802	Cdiphth_UnIn-R2	125	Y	PRJNA473263	Australia
5	SRR7223803	Cdiphth_UnIn-R3	125	Y	PRJNA473263	Australia
5	SRR7223805	Cdiphth_In-R1	125	Y	PRJNA473263	Australia
5	SRR7223806	Cdiphth_In-R2	125	Y	PRJNA473263	Australia
5	SRR7223807	Cdiphth_In-R3	125	Y	PRJNA473263	Australia
6	SRR7039158	KL0371	130	N	PRJNA416260	Germany
6	SRR7039159	KL0330	130	N	PRJNA416260	Germany
6	SRR7039162	KL0438	130	N	PRJNA416260	Germany
6	SRR7039163	KL0372	130	N	PRJNA416260	Germany
6	SRR7039178	KL0507	130	N	PRJNA416260	Germany
6	SRR7039208	KL0939	130	N	PRJNA416260	Germany
6	SRR7039210	KL0937	130	N	PRJNA416260	Germany
6	SRR7039216	KL0660	130	N	PRJNA416260	Germany
6	SRR7039221	KL0943	130	N	PRJNA416260	Germany
6	SRR7039228	KL0932	130	N	PRJNA416260	Germany
7	ERR3331348	SAMEA5615626	67	Y	PRJEB32654	UK and vietnam
7	ERR3331349	SAMEA5615627	67	Y	PRJEB32654	UK and vietnam
7	ERR3331351	SAMEA5615629	67	Y	PRJEB32654	UK and vietnam
7	ERR3331353	SAMEA5615631	67	Y	PRJEB32654	UK and vietnam
7	ERR3331355	SAMEA5615633	67	Y	PRJEB32654	UK and vietnam
7	ERR3331358	SAMEA5615636	67	Y	PRJEB32654	UK and vietnam
7	ERR3331359	SAMEA5615637	67	Y	PRJEB32654	UK and vietnam
7	ERR3331360	SAMEA5615638	67	Y	PRJEB32654	UK and vietnam
7	ERR3331363	SAMEA5615641	67	Y	PRJEB32654	UK and vietnam
7	ERR3331370	SAMEA5615648	67	Y	PRJEB32654	UK and vietnam
7	ERR3331375	SAMEA5615653	67	Y	PRJEB32654	UK and vietnam
7	ERR3331376	SAMEA5615654	67	Y	PRJEB32654	UK and vietnam
7	ERR3331377	SAMEA5615655	67	Y	PRJEB32654	UK and vietnam
7	ERR3331378	SAMEA5615656	67	Y	PRJEB32654	UK and vietnam
7	ERR3331382	SAMEA5615660	67	Y	PRJEB32654	UK and vietnam
7	ERR3331388	SAMEA5615666	67	Y	PRJEB32654	UK and vietnam
7	ERR3331389	SAMEA5615667	67	Y	PRJEB32654	UK and vietnam
7	ERR3331391	SAMEA5615670	67	Y	PRJEB32654	UK and vietnam
7	ERR3331392	SAMEA5615671	67	Y	PRJEB32654	UK and vietnam
7	ERR3331393	SAMEA5615672	67	Y	PRJEB32654	UK and vietnam
7	ERR3331394	SAMEA5615673	67	Y	PRJEB32654	UK and vietnam
7	ERR3331396	SAMEA5615675	67	Y	PRJEB32654	UK and vietnam
7	ERR3331398	SAMEA5615677	67	Y	PRJEB32654	UK and vietnam
8	SRR7039170	KL0964	439	N	PRJNA416260	Germany
8	SRR7039175	KL0522	439	N	PRJNA416260	Germany
8	SRR7039193	KL0954	439	N	PRJNA416260	Germany
8	SRR7039206	KL0947	439	N	PRJNA416260	Germany
8	SRR7039214	KL0676	439	N	PRJNA416260	Germany
9	ERR3331390	SAMEA5615669	455	Y	PRJEB32654	UK and vietnam
9	ERR3331352	SAMEA5615630	455	Y	PRJEB32654	UK and vietnam
9	ERR3331371	SAMEA5615649	455	Y	PRJEB32654	UK and vietnam
9	ERR3331373	SAMEA5615651	455	Y	PRJEB32654	UK and vietnam
9	ERR3331381	SAMEA5615659	455	Y	PRJEB32654	UK and vietnam
9	ERR3331399	SAMEA5615678	455	Y	PRJEB32654	UK and vietnam
10	NCTC13129	NA	8	Y	PRJNA224116	UK
10	SRR4271515	FDAARGOS 197	8	Y	PRJNA231221	USA
10	SRR7039153	KL0811	8	N	PRJNA490531	Germany
10	SRR7039154	KL0945	8	N	PRJNA490531	Germany
10	SRR7039156	KL0812	8	N	PRJNA490531	Germany
10	SRR7039161	KL0759	8	N	PRJNA490531	Germany
10	SRR7039166	KL0788	8	N	PRJNA490531	Germany
10	SRR7039168	KL0768	8	N	PRJNA490531	Germany

10	SRR7039169	KL0770	8	N	PRJNA490531	Germany
10	SRR7039171	KL0649	8	N	PRJNA490531	Germany
10	SRR7039172	KL0659	8	N	PRJNA490531	Germany
10	SRR7039173	KL0813	8	N	PRJNA490531	Germany
10	SRR7039179	KL0628	8	N	PRJNA490531	Germany
10	SRR7039181	KL0585	8	N	PRJNA490531	Germany
10	SRR7039182	KL0599	8	N	PRJNA490531	Germany
10	SRR7039183	KL0854	8	N	PRJNA490531	Germany
10	SRR7039184	KL0899	8	N	PRJNA490531	Germany
10	SRR7039186	KL0891	8	N	PRJNA490531	Germany
10	SRR7039188	KL0881	8	N	PRJNA490531	Germany
10	SRR7039189	KL0848	8	N	PRJNA490531	Germany
10	SRR7039190	KL0872	8	N	PRJNA490531	Germany
10	SRR7039191	KL0935	8	N	PRJNA490531	Germany
10	SRR7039192	KL0953	8	N	PRJNA490531	Germany
10	SRR7039195	KL0833	8	N	PRJNA490531	Germany
10	SRR7039198	KL0929	8	N	PRJNA490531	Germany
10	SRR7039199	KL0823	8	N	PRJNA490531	Germany
10	SRR7039200	KL0844	8	N	PRJNA490531	Germany
10	SRR7039201	KL0847	8	N	PRJNA490531	Germany
10	SRR7039203	KL0834	8	N	PRJNA490531	Germany
10	SRR7039205	KL0798	8	N	PRJNA490531	Germany
10	SRR7039209	KL0871	8	N	PRJNA490531	Germany
10	SRR7039211	KL0845	8	N	PRJNA490531	Germany
10	SRR7039213	KL0678	8	N	PRJNA490531	Germany
10	SRR7039215	KL0675	8	N	PRJNA490531	Germany
10	SRR7039217	KL0705	8	N	PRJNA490531	Germany
10	SRR7039218	KL0698	8	N	PRJNA490531	Germany
10	SRR7039219	KL0693	8	N	PRJNA490531	Germany
10	SRR7039220	KL0691	8	N	PRJNA490531	Germany
10	SRR7039223	KL0747	8	N	PRJNA490531	Germany
10	SRR7039224	KL0713	8	N	PRJNA490531	Germany
10	SRR7039225	KL0865	8	N	PRJNA490531	Germany
10	SRR7039226	KL0858	8	N	PRJNA490531	Germany
10	SRR7039227	KL0933	8	N	PRJNA490531	Germany
10	SRR7825441	KL0927	8	N	PRJNA490531	Germany
11	SRR6816589	SAMN08624601	32	N	PRJNA436425	Australia
11	SRR6816584	SAMN08624601	32	N	PRJNA436425	Australia
11	SRR6816575	SAMN08624601	32	N	PRJNA436425	Australia
11	SRR6816599	SAMN08624601	32**	N	PRJNA436425	Australia
11	SRR6816600	SAMN08624601	32**	N	PRJNA436425	Australia
12	SRR7039155	KL0476	295	N	PRJNA416260	Germany
12	SRR7039194	KL0961	509	N	PRJNA416260	Germany
12	SRR7039196	KL0965	295	N	PRJNA416260	Germany
12	SRR7039207	KL0895	295	N	PRJNA416260	Germany
13	ERR2173766	Cd_8	398	N	PRJEB14914	Switzerland
13	ERR2173856	Cd-15	398	N	PRJEB14914	Switzerland
13	ERR2173857	Cd-16	398	N	PRJEB14914	Switzerland
13	ERR2173858	Cd-17	398	N	PRJEB14914	Switzerland
13	SRR7825357	KL0655	398	N	PRJNA490531	Germany
14	ERR3331346	SAMEA5615624	258	N	PRJEB32654	UK and vietnam
14	ERR3331347	SAMEA5615625	258	N	PRJEB32654	UK and vietnam
14	ERR3331361	SAMEA5615639	258	N	PRJEB32654	UK and vietnam
14	ERR3331364	SAMEA5615642	258	N	PRJEB32654	UK and vietnam
14	ERR3331369	SAMEA5615647	258	N	PRJEB32654	UK and vietnam
14	ERR3331374	SAMEA5615652	258	N	PRJEB32654	UK and vietnam
14	ERR3331379	SAMEA5615657	258	N	PRJEB32654	UK and vietnam
14	ERR3331380	SAMEA5615658	258	N	PRJEB32654	UK and vietnam
14	ERR3331383	SAMEA5615661	258	N	PRJEB32654	UK and vietnam
14	ERR3331385	SAMEA5615663	258	N	PRJEB32654	UK and vietnam

NT: new type

* one SNP in *fusA*

** one SNP in *dnaK*

Table S2: Available complete genomes of *C. diphtheriae* isolates used in this study.

Strain	MLST	Accession No.
NCTC11397	ST26	NZ_LN831026.1
NCTC 13129	ST8	NC_002935.2
31A	ST584	NC_016799.1
241	ST175	NC_016782.1
INCA 402	ST173	NC_016783.1
BH8	ST172	NC_016800.1
HC03	ST171	NC_016787.1
HC02	ST176	NC_016802.1
C7 (beta)	ST26	NC_016801.1
HC04	ST128	NC_016788.1
CDCE 8392/CD174	ST50	NC_016785.1
HC01	ST175	NC_016786.1
VA01	ST80	NC_016790.1
PW8	ST44	NC_016789.1
B-D-16-78	ST453	NZ_CP018331.1
FDAARGOS_197	ST8	NZ_CP020410.2
ISS 3319	ST26	NZ_CP025209.1
BQ11	ST125	NZ_CP029644.1
TH1526	ST377	CP038504.1
NCTC3529	ST452	NZ_LR134538.1
NCTC7838	ST10	NZ_LR134537.1

Table S3: Pairwise SNP distance among the WA *C. diphtheriae* isolates

	PC0646	PC0647	PC0648	PC0649	PC0650	PC0651	PC0652	PC0653	PC0654	PC0655
PC0646	0	8	8	7	9	10	2	14	15	15
PC0647	8	0	0	9	1	2	8	16	17	17
PC0648	8	0	0	9	1	2	8	16	17	17
PC0649	7	9	9	0	10	11	7	15	16	10
PC0650	9	1	1	10	0	3	9	17	18	18
PC0651	10	2	2	11	3	0	10	18	19	19
PC0652	2	8	8	7	9	10	0	14	15	15
PC0653	14	16	16	15	17	18	14	0	1	23
PC0654	15	17	17	16	18	19	15	1	0	24
PC0655	15	17	17	10	18	19	15	23	24	0

Table S4: Pairwise SNP distances for the WA isolates and other clusters in Figure S1

Cluster ¹	No. of isolates	MLST	Reference	Average pairwise SNP distance and range	Country
WA	10	ST445/NT	PC0646	11.6 (0-24)	United States
3	44	ST76	SRR10054211	19.2 (0-157)	Canada [2]
4	7	ST209	ERR3331366	36.6 (0-51)	Vietnam and UK
5	7	ST125	BQ11	0.6 (0-1)	Australia
6	10	ST130	SRR7039158	36.3 (1-78)	Germany
7	23	ST67	ERR3331348	144.3 (0-282)	Vietnam and UK
8	5	ST439	SRR7039170	74.6 (10-119)	Germany
9	6	ST455	ERR3331371	32.3 (15-52)	Vietnam and UK
10	45	ST8	NCTC13129	63.8 (0-113)	Germany [3]
11	5	ST32	SRR6816589	77.4 (0-98)	Australia
12	4	ST295 & 509	SRR7039155	160.5 (101-186)	Germany
14	10	ST258	ERR3331346	143.3 (4-363)	Vietnam and UK

¹cluster 1,2,13 contained isolates from Switzerland outbreak and they pairwise SNP distances were up to 150 SNPs [1].

NT: new type

Table S5: Detected mutations among the WA *C. diphtheriae* isolates relative to the closed genome assembly of PC0646.

Position	Ref	Alt	Count	Mutation Type	Locus Tag	AA Change	Gene Annotation	PC0647	PC0648	PC0649	PC0650	PC0651	PC0652	PC0653	PC0654	PC0655
4708	CG	C	8	CDS_frameshift	FGA20_00015	p.Gly393fs	DNA replication/repair protein RecF	x	x	x	x	x		x	x	x
144412	C	CG	3	Intergenic					x			x		x		
175418	C	T	4	CDS_nonsynonymous	FGA20_01015	p.Leu94Phe	sugar-binding transcriptional regulator	x	x		x	x				
208374	A	G	9	CDS_synonymous	FGA20_01185	p.Val336Val	penicillin-binding protein	x	x	x	x	x	x	x	x	x
212404	T	TG	1	Intergenic						x						
219339	AC	A	3	Intergenic						x				x	x	
338731	T	C	2	CDS_nonsynonymous	FGA20_01905	p.Leu277Ser	ABC transporter permease							x	x	
370633	C	T	1	CDS_synonymous	FGA20_02030	p.Ser314Ser	elongation factor G fusA						x			
385202	TA	AC	1	Intergenic												x
397459	A	G	2	CDS_nonsynonymous	FGA20_02185	p.Val289Ala	nitrate reductase subunit beta narH							x	x	
432888	A	AT	2	CDS_frameshift	FGA20_02350	p.Cys158fs	sugar ABC transporter permease							x	x	
441663	C	T	1	CDS_nonsynonymous	FGA20_02390	p.Ala23Val	exo-alpha-sialidase									x
519404	GC	G	8	Intergenic				x		x	x	x	x	x	x	x
546196	C	CG	9	Intergenic				x	x	x	x	x	x	x	x	x
646360	A	G	2	CDS_nonsynonymous	FGA20_03370	p.Glu21Gly	biotin/lipoyl-binding protein							x	x	
665317	C	G	8	CDS_synonymous	FGA20_03465	p.Arg45Arg	transposase	x	x	x	x	x		x	x	x
696524	C	A	2	CDS_nonsynonymous	FGA20_03635	p.Ala111Ser	phosphoserine transaminase serC							x	x	
709710	G	C	1	Intergenic												x
742909	G	A	1	CDS_nonsynonymous	FGA20_03870	p.Gly454Glu	HAMP domain-containing histidine kinase					x				
808375	T	C	9	Intergenic				x	x	x	x	x	x	x	x	x
817405	A	T	2	CDS_nonsynonymous	FGA20_04245	p.Lys245Met	serine hydroxymethyltransferase							x	x	
907208	C	T	2	CDS_synonymous	FGA20_04680	p.Asp207Asp	DEAD/DEAH box helicase							x	x	
943722	C	T	1	CDS_synonymous	FGA20_04835	p.Ser235Ser	F0F1 ATP synthase subunit delta								x	
959126	A	G	1	CDS_synonymous	FGA20_04930	p.Tyr676Tyr	DUF3416 domain-containing protein									x
1023707	AC	A	1	Intergenic					x							
1023707	ACCC	A	1	Intergenic											x	
1106552	G	A	2	CDS_nonsynonymous	FGA20_05605	p.Val1Met	dethiobiotin synthetase							x	x	
1164411	G	T	2	CDS_nonsynonymous	FGA20_05870	p.Ser13Ile	tRNA (cytidine(34)-2'-O)-methyltransferase							x	x	
1171833	A	AT	1	CDS_frameshift	FGA20_05910	p.Cys447fs	proteasome ATPase arc					x				

1219451	C	T	4	CDS_synonymous	FGA20_06115	p.Leu135Leu	metal-sulfur cluster assembly factor	x	x		x	x			
1408510	A	G	2	CDS_synonymous	FGA20_07025	p.Cys82Cys	CinA family protein							x	x
1499299	G	A	1	Intergenic											x
1506899	T	G	1	CDS_nonsynonymous	FGA20_07460	p.Lys405Thr	transposase family protein								x
1650645	T	A	2	CDS_nonsynonymous	FGA20_08120	p.Tyr234Phe	alpha/beta hydrolase						x	x	
1650923	T	C	1	CDS_synonymous	FGA20_08120	p.Glu141Glu	alpha/beta hydrolase				x				
1663026	GA	G	2	CDS_frameshift	FGA20_08200	p.Asp148fs	TPM domain-containing protein						x	x	
1691345	T	C	1	CDS_nonsynonymous	FGA20_08340	p.Ile349Val	HNH endonuclease								x
1692391	T	C	2	Intergenic						x					x
1758345	G	GC	2	CDS_frameshift	FGA20_08650	p.Pro65fs	DsbA family protein			x					x
1765503	G	A	4	CDS_synonymous	FGA20_08680	p.Ile106Ile	energy-dependent translational throttle protein ettA	x	x		x	x			
1874191	G	T	1	Intergenic											x
1877963	C	A	1	Intergenic					x						
1973285	T	G	2	CDS_nonsynonymous	FGA20_09680	p.Glu465Asp	isopeptide-forming domain-containing fimbrial				x				x
2027854	T	C	2	Intergenic							x				x
2060141	G	A	4	CDS_nonsynonymous	FGA20_10060	p.His5Tyr	hypothetical protein	x	x		x	x			
2060161	T	TG	4	CDS_frameshift	FGA20_10065	p.Ile76fs	hypothetical protein	x	x		x	x			
2060266	T	A	1	CDS_synonymous	FGA20_10065	p.Gly40Gly	hypothetical protein		x						
2060284	T	C	4	CDS_synonymous	FGA20_10065	p.Arg34Arg	hypothetical protein	x	x		x	x			
2063716	T	A	2	Intergenic										x	x
2133313	G	T	1	Intergenic							x				
2323370	G	T	1	CDS_nonsynonymous	FGA20_11260	p.Leu508Met	Cell surface protein				x				

Table S6: BLASTp query results for the unique 8.7kb region detected in PC0653 and PC0654

Nucleotide sequence position in the 8.7 kb region	VF analyzer prediction	BLASTp top hit (NCBI accession no.)	Amino acid sequence identity to isolate FRC0435
1257-442 bp	NA	Cell surface protein (CAB0925098.1)	95%
2195-1257 bp	SrtC	Class C sortase (CAB0925096.1)	99%
3893-2346 bp	SpaD	Isopeptide_forming domain-containing fimbriae protein (CAB0925093.1)	99%
4566-5504 bp	SrtB	Class C sortase (CAB0925087.1)	100%
6917-8710 bp	NA	Membrane protein (CAB0925084.1)	100%

NA: not applicable

References:

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2. Chorlton, S.D., et al., *Whole-Genome Sequencing of Corynebacterium diphtheriae Isolates Recovered from an Inner-City Population Demonstrates the Predominance of a Single Molecular Strain*. J Clin Microbiol, 2020. **58**(2).
3. Dangel, A., et al., *Geographically Diverse Clusters of Nontoxigenic Corynebacterium diphtheriae Infection, Germany, 2016-2017*. Emerg Infect Dis, 2018. **24**(7): p. 1239-1245.