

Table S5. MLST allelic profiles and resulting sequence types of *Vibrio cholerae* non-O1, non-O139 isolates from German coastal waters and from German clinical samples analyzed in this study.^a

Strain	Source code ^b	Allelic profile							Sequence type
		<i>adk</i>	<i>gyrB</i>	<i>mdh</i>	<i>metE</i>	<i>pntA</i>	<i>purM</i>	<i>pyrC</i>	
Environmental - Baltic Sea									
VN-00278	E-BS-sw	68	73	14	131	84	62	94	488
VN-00455	E-BS-sw	60	75	69	120	87	1	n.d. ^c	n.d.
VN-00456	E-BS-sw	72	38	14	126	79	60	92	497
VN-00457	E-BS-sw	48	84	46	127	88	1	105	467
VN-00458	E-BS-sw	14	30	66	91	66	41	73	454
VN-00459	E-BS-sw	18	61	67	156	71	1	35	330
VN-00460	E-BS-sw	3	48	29	36	25	1	12 ^d	445
VN-00461	E-BS-sw	72	65	11	113	91	60	92	498
VN-00462	E-BS-sw	70	36	14	117	85	60	102	492
VN-00463	E-BS-sw	60	70	69	122	87	1	113	475
VN-00464	E-BS-sw	61	55	14	146	75	1	94	479
VN-00465	E-BS-sw	14	49	15	47	77	1	120	455
VN-00466	E-BS-sw	2	23	57	9	59	1	35	441
VN-00468	E-BS-sw	58	48	73	139	47	63	90	472
VN-00469	E-BS-sw	78	86	14	138	1	52	115	504
VN-00470	E-BS-sw	72	65	45	113	91	60	92	499
VN-00471	E-BS-sw	70	36	14	117	85	60	102	492
VN-00472	E-BS-sw	70	36	14	117	85	60	102	492
VN-00473	E-BS-sw	70	65	14	129	92	60	102	493
VN-00474	E-BS-sw	66	86	14	143	47	1	92	485
VN-00475	E-BS-sw	49	1	74	147	93	56	119	468
VN-00476	E-BS-sw	14	5	14	123	84	60	91	456
VN-00477	E-BS-sw	60	75	69	120	87	1	n.d. ^c	n.d.
VN-02995	E-BS-sw	68	73	14	131	84	62	94	488
VN-03901	E-BS-sw/sd	18	5	14	43	71	58	35	462
VN-03902	E-BS-sw/sd	38	5	75	152	62	1	121	465
VN-03903	E-BS-sw	48	84	46	127	88	1	105	467
VN-03907	E-BS-sw/sd	3	48	29	36	25	3	12 ^d	446
VN-03908	E-BS-sw	2	5	14	122	91	1	103 ^d	442
VN-03911	E-BS-sw	63	5	14	129	6	1	67	481
VN-03916	E-BS-sd	1	38	14	122	91	60	103	433
VN-03918	E-BS-sw/sd	53	36	7	9	90	1	65	469
VN-03939	E-BS-sd	63	5	14	129	6	1	67	481
VN-03942	E-BS-sw/sd	66	5	8	36	6	1	92	486
VN-03944	E-BS-sw/sd	14	5	74	137	5	64	110	458
VN-03949	E-BS-sw/sd	18	5	15	48	17	1	45	463
VN-03951	E-BS-sw/sd	73	85	14	149	19	1	96	303
VN-03954	E-BS-sw/sd	1	5	14	116	6	1	92	434
VN-03955	E-BS-sd	1	5	14	142	6	1	92	435
VN-03958	E-BS-sw/sd	13	38	11	148	64	59	118	451
VN-03963	E-BS-sw	70	65	73	116	13	60	117	494
VN-04241	E-BS-sw	18	81	14	130	86	41	43	464
VN-04250	E-BS-sw	14	38	14	117	47	60	116	459
VN-05169	E-BS-sw	65	5	2	131	80	60	103	484
VN-05172	E-BS-sw	74	5	62	129	6	1	67	500
VN-05174	E-BS-sw	53	5	62	129	6	1	67	470
VN-05176	E-BS-sw	70	36	14	117	85	60	102	492
VN-05177	E-BS-sw	13	77	14	151	66	61	122	452
VN-05185	E-BS-sw	1	70	74	157	38	1	111	436
VN-05301	E-BS-sw	14	5	14	192	18	60	96	460

Table continued									
Strain	Source code ^b	Allelic profile							Sequence type
		<i>adk</i>	<i>gyrB</i>	<i>mdh</i>	<i>metE</i>	<i>pntA</i>	<i>purM</i>	<i>pyrC</i>	
Environmental - North Sea									
VN-02808	E-NS-sw	57	76	14	115	18	1	101	336
VN-02825	E-NS-sw	57	76	14	115	18	1	101	336
VN-02923	E-NS-sw	57	76	14	115	18	1	101	336
VN-03012	E-NS-sw	1	5	74	119	80	53	106	432
VN-03213	E-NS-sw	65	1	14	140	93	62	90	483
VN-03301	E-NS-sw/sd	14	68	75	19	9	56	114	457
VN-03361	E-NS-sw/sd	76	82	76	150	83	65	67	502
VN-03377	E-NS-sw/sd	13	5	15	59	73	1	67	449
VN-03405	E-NS-sw/sd	57	38	70	125	18	54	95	471
VN-03407	E-NS-sw/sd	57	38	70	125	18	54	95	471
VN-03428	E-NS-sw/sd	79	5	68	159	81	57	109	505
VN-03460	E-NS-sw/sd	1	5	74	119	80	53	106	432
VN-03469	E-NS-sw/sd	1	5	74	119	80	53	106	432
VN-03470	E-NS-sw/sd	13	1	64	144	5	1	108	450
VN-03471	E-NS-sw/sd	1	5	74	119	80	53	106	432
VN-03472	E-NS-sw/sd	1	5	74	119	80	53	106	432
VN-03475	E-NS-sw/sd	1	5	74	119	80	53	106	432
VN-03492	E-NS-sw/sd	1	5	74	119	80	53	106	432
VN-03503	E-NS-sw/sd	77	38	65	154	91	1	93	503
VN-04219	E-NS-sw	58	78	63	128	61	8	100	473
VN-04223	E-NS-sw	69	41	15	47	74	1	83	489
VN-04226	E-NS-sw	3	79	14	153	66	41	98	447
VN-04231	E-NS-sw	58	78	63	128	61	8	100	473
VN-04233	E-NS-sw	2	38	14	123	13	60	103	443
VN-10012	E-NS-bm	71	74	76	133	3	9	39	495
VN-10013	E-NS-bm	71	74	76	133	3	9	39	495
VN-10127	E-NS-bm	66	5	8	36	6	1	92	486
VN-10130	E-NS-bm	60	65	71	136	80	1	104	476
VN-10131	E-NS-bm	60	65	71	136	80	1	104	476
VN-10133	E-NS-bm	60	83	14	126	76	63	91	477
VN-10137	E-NS-bm	65	1	14	140	93	62	90	483
VN-10143	E-NS-bm	13	71	62	124	3	9	39	453
VN-10144	E-NS-bm	13	71	62	124	3	9	39	453
VN-10145	E-NS-bm	13	71	62	124	3	9	39	453
VN-10146	E-NS-bm	13	71	62	124	3	9	39	453
VN-10150	E-NS-bm	47	1	14	160	18	17	66	466
VN-10156	E-NS-bm	60	36	61	134	82	56	89	478
VN-10159	E-NS-bm	60	36	61	134	82	56	89	478
VN-10162	E-NS-bm	60	36	61	134	82	56	89	478
VN-10191	E-NS-bm	13	71	62	124	3	9	39	453
VN-10192	E-NS-bm	13	71	62	124	3	9	39	453
VN-10196	E-NS-bm	59	23	14	135	3	1	97	474
VN-10197	E-NS-bm	14	64	15	121	3	8	99	461
VN-10198	E-NS-bm	14	64	15	121	3	8	99	461
VN-10204	E-NS-bm	67	44	14	132	66	55	88	487
VN-10205	E-NS-bm	67	44	14	132	66	55	88	487
VN-10206	E-NS-bm	67	44	14	132	66	55	88	487
VN-10207	E-NS-bm	67	44	14	132	66	55	88	487
VN-10208	E-NS-bm	1	69	14	1	64	1	93	437
VN-10320	E-NS-bm	59	23	14	135	3	1	97	474

Table continued									
Strain	Source code ^b	Allelic profile							Sequence type
		<i>adk</i>	<i>gyrB</i>	<i>mdh</i>	<i>metE</i>	<i>pntA</i>	<i>purM</i>	<i>pyrC</i>	
Clinical - Germany									
VN-00168	C-G-ext	72	65	45	114	91	60	92	496
VN-00169	C-G-ext	72	65	45	114	91	60	92	496
VN-00297	C-G-ext	70	65	14	129	92	1	107	490
VN-00298	C-G-ext	70	38	14	155	85	60	102	491
VN-00300	C-G-int	13	74	76	133	3	9	39	448
VN-00302	C-G-int	2	44	11	64	3	8	43	438
VN-00305	C-G-ext	64	65	11	141	2	60	112	482
VN-00307	C-G-ext	70	65	14	129	92	1	107	490
VN-00533 ^c	C-G-ext	70	65	14	218	5	60	102	589
VN-00534 ^c	C-G-ext	60	83	14	143	76	53	91	590

n.d., not determined.

^a Alleles and sequence types that were new to PubMLST database are in bold print.

^b The source code is explained in Table 1.

^c PCR amplification of *pyrC* failed.

^d Fixed maximum length of *Vibrio cholerae pyrC* allele sequences in PubMLST database (449 bp) required the removal of a 6-nt insertion (GCCACA) between nucleotide 23 and 24. The resulting *pyrC* allele is given.

^e MLST alleles were determined from *de novo* assemblies of genomes with the web-based tool “MLST 1.8” of the Center for Genomic Epidemiology (Larsen et al., 2012). New allele sequences were verified by PCR amplification and partial gene sequencing and finally submitted to the PubMLST database for assignment of new allele numbers (see Material and Methods).

References

Larsen, M. V., Cosentino, S., Rasmussen, S., Friis, C., Hasman, H., Marvig, R. L., et al. (2012). Multilocus sequence typing of total-genome-sequenced bacteria. *J. Clin. Microbiol.* 50, 1355-1361. doi: 10.1128/JCM.06094-11