

Table S1 Detection rates and mean counts of target groups of *Clostridium difficile* in healthy Belgian infants by qPCR

Stool specimen (N)	CD16SrRNA-F/R/P			tcdA-F/R/P			tcdB-F/R/P		
	Detection rate (%)	Count ^a (Mean ± SD)		Detection rate (%)	Count ^a (Mean ± SD)		Detection rate (%)	Count ^a (Mean ± SD)	
Meconium (99)	0/99 (0)	-		0/99 (0)	-		0/99 (0)	-	
Day 3 (83)	5/83 (6)	7.6 ± 1.1		2/83 (2)	7.2		2/83 (2)	7.0	
Day 7 (100)	6/100 (6)	6.9 ± 1.9		2/100 (2)	7.4		2/100 (2)	7.3	
Day 30 (108)	10/108 (9)	6.7 ± 1.1		3/108 (3)	7.0 ± 1.5		3/108 (2)	6.9 ± 1.4	
Day 90 (107)	13/107 (12)	6.8 ± 0.9		4/107 (4)	7.0 ± 1.3		5/107 (5)	7.0 ± 1.3	
Weaning (75)	23/75 (31)	7.0 ± 1.0		8/75 (11)	7.4 ± 1.1		10/75 (13)	7.3 ± 1.0	
Day 180 (105)	47/105 (45)	6.7 ± 1.0		14/105 (13)	6.9 ± 0.6		16/105 (15)	6.9 ± 0.7	

^a log₁₀ cells/g of stool

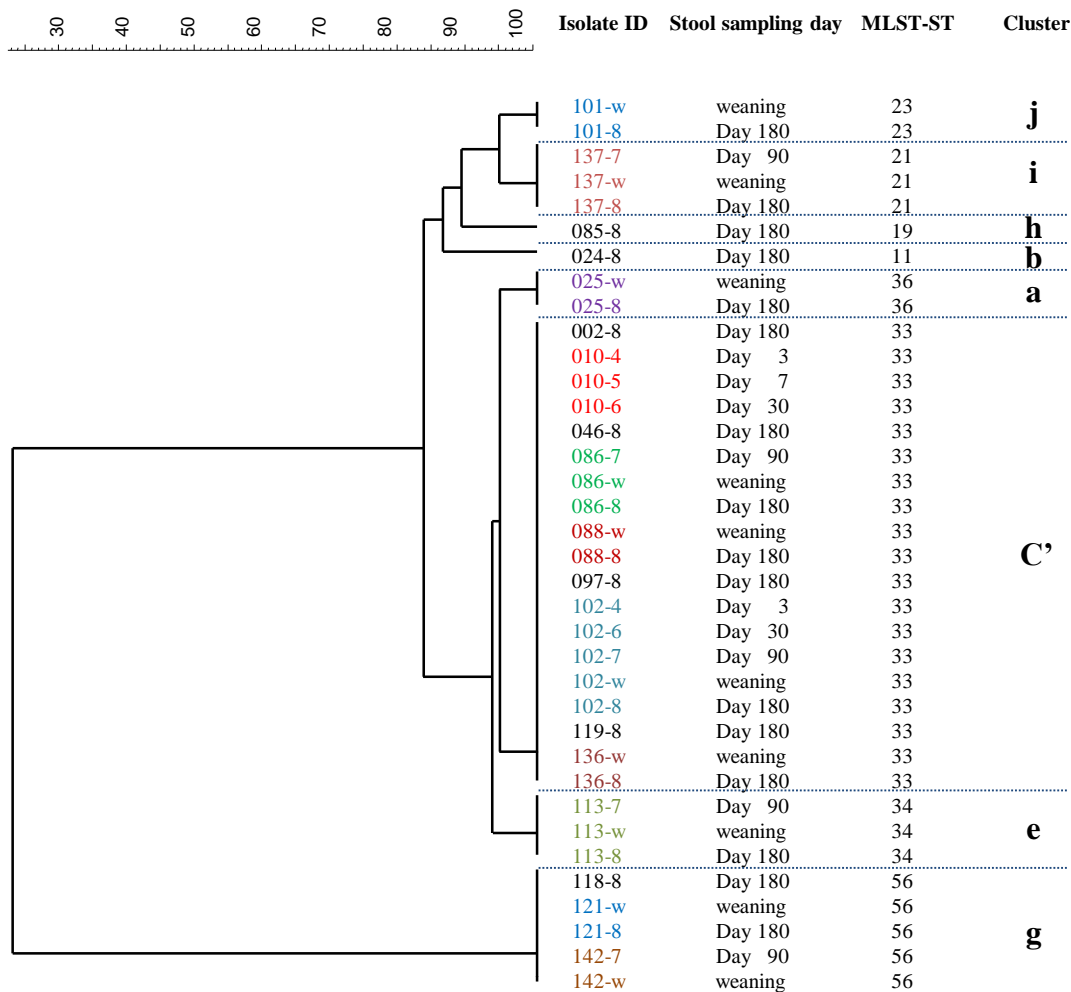


Fig. S1 Dendrogram of toxigenic *Clostridium difficile* isolates from infants, as determined by MLST analysis

The dendrogram was created with a multiscale setting for comparison and the unweighted pair group method with arithmetic mean for clustering. Isolate ID is composed of the subject ID (3 digits) and a number indicating the day of sampling of the stool specimen (#4: day 3; #5: day 7; #6: day 30; #7: day 90; #8: day 180; #w: weaning). The MLST database was queried for the sequences of 7 genes of each isolate of *C. difficile*, and a matched sequencing type (ST) of 2 digits was assigned to each strain. The compositions of clusters with the same cluster letters in the MLST analysis were equivalent to those in CGE-PCR ribotyping. The cluster C' was composed of isolates that belonged to clusters c, d and f in CGE-PCR ribotyping.

Table S2 Counts of total bacteria and *Clostridium difficile* in stools of 55 *C. difficile*-positive infants

Subject ID	Day 3			Day 7			Day 30			Day 90			Weaning			Day 180		
	Total bacterial counts ^a	<i>C. difficile</i> counts ^b	Toxigenic type	Total bacterial counts ^a	<i>C. difficile</i> counts ^b	Toxigenic type	Total bacterial counts ^a	<i>C. difficile</i> counts ^b	Toxigenic type	Total bacterial counts ^a	<i>C. difficile</i> counts ^b	Toxigenic type	Total bacterial counts ^a	<i>C. difficile</i> counts ^b	Toxigenic type	Total bacterial counts ^a	<i>C. difficile</i> counts ^b	Toxigenic type
001	9.8	-	-	9.9	-	-	9.4	-	-	10.8	-	-	No sample	-	-	10.1	5.6	A-B-
002	10.4	-	-	10.3	-	-	10.6	-	-	10.9	-	-	No sample	-	-	9.9	7.4	A+B+
004	8.8	-	-	10.3	-	-	10.5	-	-	10.6	-	-	10.5	7.9	A-B-	10.1	5.1	A-B-
008	-	No sample	-	10.7	-	-	10.4	-	-	10.9	-	-	10.5	7.4	A-B-	10.8	7.2	A-B-
010	9.3	8.3	A+B+	9.9	8.7	A+B+	10.3	8.3	A+B+	10.6	-	-	No sample	-	-	10.3	-	-
013	11.0	-	-	10.9	-	-	10.7	-	-	10.9	-	-	10.9	5.7	A-B-	10.9	7.5	A-B-
014	10.0	-	-	10.8	-	-	11.2	-	-	10.8	-	-	No sample	-	-	10.4	7.7	A-B-
018	10.0	-	-	9.9	-	-	9.9	-	-	11.1	-	-	10.7	-	-	11.2	8.7	A-B-
019	9.7	-	-	No sample	-	-	10.9	8.3	A-B-	11.3	-	-	No sample	-	-	10.3	-	-
024	10.7	-	-	10.3	-	-	10.9	-	-	11.3	-	-	No sample	-	-	11.0	8.0	A+B+
025	-	No sample	-	No sample	-	-	10.7	-	-	No sample	-	-	10.3	4.5	A+B+	10.0	6.9	A+B+
028	10.2	-	-	No sample	-	-	-	-	-	11.3	-	-	11.0	-	-	10.5	5.4	A-B-
029	10.4	-	-	10.3	-	-	10.9	-	-	9.5	5.6	A-B-	9.8	-	-	10.4	7.2	A-B-
030	-	No sample	-	9.9	-	-	10.5	-	-	10.4	-	-	10.7	-	-	10.3	7.2	A-B-
033	-	No sample	-	10.0	-	-	10.7	7.2	A-B-	10.4	-	-	10.9	-	-	9.7	7.4	A-B-
037	9.8	-	-	9.4	-	-	10.0	-	-	10.5	-	-	No sample	-	-	10.6	8.0	A-B-
039	-	No sample	-	10.4	-	-	10.7	-	-	11.1	7.2	A-B-	10.7	7.0	A-B-	10.0	7.1	A-B-
040	9.7	8.3	A-B-	-	No sample	-	10.7	6.2	-	10.5	7.4	A-B-	No sample	-	-	9.6	-	-
041	9.8	7.7	A-B-	9.8	4.3	A-B-	10.6	5.2	A-B-	10.3	-	-	No sample	-	-	No sample	-	-
043	9.9	-	-	9.6	-	-	10.0	-	-	10.9	-	-	No sample	-	-	10.3	6.3	A-B-
044	-	No sample	-	10.3	-	-	10.2	-	-	10.8	7.0	A-B-	11.2	8.2	A-B-	10.6	4.8	A-B-
046	-	No sample	-	10.7	8.8	A-B-	10.4	6.6	A-B-	10.5	7.5	A-B-	10.8	5.8	A-B-	10.0	6.1	A+B+
052	7.7	-	-	9.9	-	-	10.3	-	-	10.4	-	-	No sample	-	-	10.2	7.4	A-B-
055	-	No sample	-	10.5	-	-	10.2	-	-	10.4	-	-	No sample	-	-	9.9	6.5	A-B-
060	-	No sample	-	10.0	8.3	A-B-	10.4	5.7	A-B-	10.5	6.0	A-B-	No sample	-	-	10.2	-	-
061	-	No sample	-	10.5	-	-	10.3	-	-	10.9	-	-	10.4	7.4	A-B-	10.5	7.3	A-B-
065	10.4	-	-	10.1	-	-	10.3	-	-	10.7	6.9	A-B-	10.3	-	-	10.4	-	-
068	9.8	8.2	A-B-	10.4	5.6	A-B-	10.5	7.7	A-B-	10.5	-	-	10.1	-	-	10.3	4.6	A-B-
071	-	No sample	-	No sample	-	-	10.9	-	-	No sample	-	-	10.0	5.4	A-B-	10.2	7.4	A-B-
074	10.7	-	-	11.1	-	-	10.4	-	-	10.7	-	-	10.6	-	-	9.6	5.9	A-B-
078	-	No sample	-	No sample	-	-	9.8	-	-	10.4	-	-	10.4	-	-	10.8	7.3	A-B-
080	9.8	-	-	10.4	-	-	No sample	-	-	10.9	-	-	10.7	6.6	A-B-	7.6	-	-
085	9.8	-	-	9.9	-	-	10.0	-	-	10.4	-	-	10.1	7.0	A-B-	10.4	7.3	A+B+
086	10.3	-	-	10.6	-	-	10.5	-	-	10.2	6.4	A+B+	10.6	7.4	A+B+	10.1	5.7	A+B+
088	10.1	-	-	10.2	-	-	9.9	-	-	9.9	-	-	10.2	6.9	A+B+	10.3	6.4	A+B+
092	9.5	-	-	10.5	-	-	10.2	-	-	9.7	-	-	10.4	5.0	A-B-	10.3	6.2	A-B-
097	10.1	-	-	10.1	-	-	9.9	-	-	10.3	-	-	10.4	-	-	10.7	6.7	A+B+
101	9.1	-	-	No sample	-	-	10.1	-	-	9.4	-	-	10.3	7.5	A+B+	10.2	6.6	A+B+
102	10.1	5.8	A+B+	10.4	-	-	10.1	5.6	A+B+	10.3	5.4	A+B+	10.5	7.2	A+B+	10.7	6.0	A+B+
105	10.5	-	-	10.5	-	-	10.9	-	-	10.6	-	-	No sample	-	-	10.3	5.1	A-B-
109	9.8	-	-	10.0	-	-	10.8	-	-	10.8	-	-	10.6	-	-	10.7	7.1	A-B-
110	-	No sample	-	9.6	-	-	9.9	-	-	10.4	-	-	10.3	-	-	10.2	5.5	A-B-
113	-	No sample	-	9.6	5.8	A+B+	10.0	6.4	A+B+	9.9	6.8	A+B+	10.3	7.6	A+B+	10.7	6.7	A+B+
117	9.9	-	-	10.1	-	-	9.9	-	-	9.7	-	-	10.7	-	-	10.6	6.8	A-B-
118	10.1	-	-	9.6	-	-	10.0	-	-	10.0	-	-	10.4	-	-	10.8	7.9	A+B+
119	10.1	-	-	10.3	-	-	No sample	-	-	No sample	-	-	No sample	-	-	10.6	7.3	A+B+
121	9.4	-	-	9.6	-	-	10.0	-	-	10.2	-	-	10.4	6.7	A-B+	10.0	5.9	A-B+
123	9.5	-	-	9.2	-	-	10.1	-	-	10.5	6.8	A-B-	10.5	7.4	A-B-	10.5	7.2	A-B-
126	9.8	-	-	9.7	-	-	10.2	-	-	10.4	-	-	10.7	8.1	A-B-	10.3	7.0	A-B-
130	9.6	-	-	9.9	-	-	10.6	-	-	11.1	-	-	10.8	-	-	10.2	4.9	A-B-
133	-	No sample	-	10.0	-	-	10.5	-	-	10.2	-	-	11.0	-	-	10.8	7.9	A-B-
136	-	No sample	-	10.0	-	-	9.8	-	-	10.6	-	-	10.7	8.1	A+B+	10.4	6.9	A+B+
137	-	No sample	-	10.2	-	-	10.2	-	-	10.6	8.8	A+B+	10.6	7.9	A+B+	10.4	7.0	A+B+
138	10.0	-	-	9.7	-	-	9.8	-	-	9.9	-	-	No sample	-	-	10.8	7.8	A-B-
142	-	No sample	-	10.1	-	-	9.6	-	-	10.9	7.2	A-B+	10.7	7.8	A-B+	No sample	-	-

^a The number of total stool bacteria was determined by 4', 6-diamidino-2-phenylindole (DAPI) staining method.

^b The number of *C. difficile* was determined by qPCR for 16S rRNA gene.