

Preplanned Studies

Isolation and Characterization of Botulinum Neurotoxin-Producing *Clostridium caccae* from Meat and Soil — China, 1990–2025

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Summary

What is known about this topic?

Botulinum neurotoxin (BoNT)-producing clostridia are categorized into six physiologically and phylogenetically distinct groups (Groups I–VI). Increasing genomic evidence indicates that *bont* genes are distributed across multiple clostridial lineages, highlighting the taxonomic complexity of BoNT-producing clostridia. *Clostridium caccae* (*C. caccae*), first described in 2020 from human stool, was originally described as a strain lacking the *bont* gene; however, its association with BoNT production has not been previously recognized.

What is added by this report?

Six isolates originally identified as Group II *C. botulinum* in China were assigned to *C. caccae* based on the average nucleotide identity (ANI) analysis. In addition, 140 publicly available genomes of *C. caccae* were analyzed. Among the 146 *C. caccae* strains, 63% carried *bont* genes (subtypes B4, E9, E12, and F6), with geographical distribution patterns differing by subtype.

What are the implications for public health practice?

A subset of Group II *C. botulinum* strains should be considered as *C. caccae*, indicating that this species represents a previously under-recognized reservoir of multiple BoNT subtypes. To our knowledge, this is the first study to link BoNT-producing *C. caccae* to both soil contamination and human botulism, highlighting that BoNT-producing *C. caccae* may be an under-recognized contributor to the risk of botulism.

genomic evidence indicates that *bont* genes are distributed across multiple clostridial lineages. *Clostridium caccae* (*C. caccae*) was first described in human stool in 2020, and the originally described strain lacked the *bont* gene; thus, its association with BoNT production remains poorly characterized.

Methods: Phenotypic characterization using API 20A and mouse bioassays was performed on two soil isolates. *Clostridium* genomes were screened for *C. caccae* and *bont* genes using average nucleotide identity (ANI) analysis and BLASTP. Phylogenetic and latitudinal distribution analyses were performed.

Results: ANI analysis identified 146 strains of *C. caccae*. Phylogenetic analysis revealed two major lineages, with 63.01% carrying *bont* genes. Four BoNT subtypes were identified, all belonging to Group II. Geographic analysis revealed a broad latitudinal distribution with subtype-specific patterns.

Conclusion: To the best of our knowledge, this is the first study to link BoNT-producing *C. caccae* with both soil and human botulism. Our findings further demonstrate that a subset of Group II *C. botulinum* should be identified as *C. caccae*. These results highlight the potential public health significance of *C. caccae* as a contributor to botulinum infections in humans.

Botulinum neurotoxin (BoNT)-producing clostridia are traditionally categorized into six physiologically and phylogenetically distinct groups (Groups I–VI). Groups I, II, and III are currently classified as *C. botulinum*, whereas Group IV corresponds to *Clostridium argentinense* (1). Group V comprises the BoNT-producing strains of *Clostridium baratii*, and Group VI comprises the BoNT-producing strains of *Clostridium butyricum* (2). To date, BoNTs encompass at least seven serotypes (A–G) and 46 subtypes.

ABSTRACT

Introduction: Botulinum neurotoxin (BoNT)-producing clostridia are traditionally categorized into six groups (Groups I–VI). However, increasing

Increasing genomic evidence suggests that *bont* genes are not restricted to a single clostridial lineage. Consequently, several taxonomic revisions have been proposed, including designating proteolytic Group I *C. botulinum* strains as *Clostridium parabotulinum* and Group III strains as *Clostridium novyi sensu lato* (2). In addition, *bont* genes have been identified in toxigenic *Clostridium sporogenes* strains (3).

Recent taxonomic advances have led to the identification of novel clostridial species closely related to the human gut microbiota. In 2020, Tall et al. proposed *Clostridium cagae* sp. nov. (renamed *C. caccae* in 2026), an anaerobic species originally isolated from human stool (4). The strain used for the original description of this species did not harbor the *bont* gene. However, the potential association between *C. caccae* and botulinum neurotoxin production has not been previously recognized, and its role as a reservoir of *bont* genes remains largely unexplored.

In 2025, we reported two *C. botulinum* strains producing BoNT/B4, which were isolated from the soil in Qinghai Province (5). In the same year, a foodborne botulism outbreak associated with the consumption of homemade dried beef occurred in Qinghai from which a BoNT/E12-producing *C. botulinum* strain was isolated. However, preliminary genomic analyses suggested that these isolates were phylogenetically distinct from classical *C. botulinum* strains. ANI analysis further demonstrated that all three Qinghai isolates showed high genomic similarity with *C. caccae*. This finding prompted us to further investigate the global distribution of *C. caccae* and the prevalence of *bont* genes within this species, which may have important implications for the control of botulism.

Two soil isolates (FZSY032906030011 and FZSY032906030023) collected from the Qinghai Province in 2024 were included in this study for phenotypic characterization. Pure colonies were cultured on blood agar and egg yolk agar plates and incubated under anaerobic conditions at 10 °C, 28 °C, 35 °C, and 40 °C for 12 h, 24 h, 36 h, and 48 h to assess growth characteristics. Biochemical profiles were determined using API 20A strips (bioMérieux, France) according to the manufacturer's instructions. Mouse bioassays were performed according to the National Food Safety Standard GB 4789.12-2025. The minimum lethal dose (MLD/mL) was defined as the highest dilution of the toxin that resulted in the death of all tested mice.

Genome sequences of historical surveillance and newly sequenced *C. botulinum* isolates from China, along with all publicly available *Clostridium* genomes (up to May 2025), were retrieved from the NCBI GenBank and RefSeq databases. ANI analysis was conducted using PyANI (version 0.3.0-alpha; University of Strathclyde, Glasgow, UK) to assess genomic relatedness, with a threshold >95% ANI used to define *C. caccae* (6). Reference genomes included the *C. caccae* (GenBank: GCF_900290265.1), Group I *C. botulinum* (GenBank: GCF_000063585.1), Group II *C. botulinum* (GenBank: GCF_002798035.1), Group III *C. botulinum* (GenBank: GCF_000204565.1), Group IV *C. botulinum* (GenBank: GCF_002074155.1), Group V *C. botulinum* (GenBank: GCF_001991075.2) and Group VI *C. botulinum* (GenBank: GCF_014131795.1). Core genome alignment of *C. caccae* strains was performed using Roary (version 3.13.0; Wellcome Sanger Institute, Hinxton, UK), and a maximum-likelihood phylogenetic tree was constructed using FastTree (version 2.2.0; Lawrence Berkeley National Laboratory, Berkeley, CA, USA). BoNT subtyping was performed using BLASTP (version 2.15.0+; National Center for Biotechnology Information, Bethesda, MD, USA) for BoNT protein sequence alignment. The default BLOSUM62 matrix was applied as the scoring matrix, with the default gap penalties set to 11 for gap existence and 1 for gap extension. An E-value threshold of 1×10^{-5} was used to filter out significant hits. A cutoff difference of 2.6% difference was applied to discriminate subtypes (7). Metadata, including sample source and geographic origin, were collected for all *C. caccae* strains when available. Statistical analyses and visualization were performed using ggplot2 (version 4.0.2), and phylogenetic trees were visualized using ggtree (version 4.0.5).

Colonies of the two soil isolates on blood agar were circular, translucent to opalescent, hemolytic, and reached 1–2 mm in diameter (Figure 1A). On egg yolk agar, the colonies were circular and opalescent, measuring 1–2 mm in diameter and surrounded by an opaque precipitation halo (Figure 1B). Single colony subcultures grew only at 28 °C under anaerobic conditions after 48 h, with no growth observed at 10 °C, 35 °C, or 40 °C. Biochemical characterization using API 20A strips showed that both isolates fermented glucose (GLU+), glycerol (GLY+) and mannose (MNE+), but not maltose (MAL-) or trehalose (TRE-), and were negative for gelatin

hydrolysis (GEL-), esculin hydrolysis (ESC-), and catalase activity (Supplementary Table S1, available at <https://weekly.chinacdc.cn/>). Mouse bioassays confirmed toxicity at 10,000 MLD/mL, and the

toxicity was completely neutralized by the type B antitoxin, confirming BoNT/B production.

ANI analysis revealed that six surveillance isolates exhibited high ANI values (97.4%–97.6%) relative to

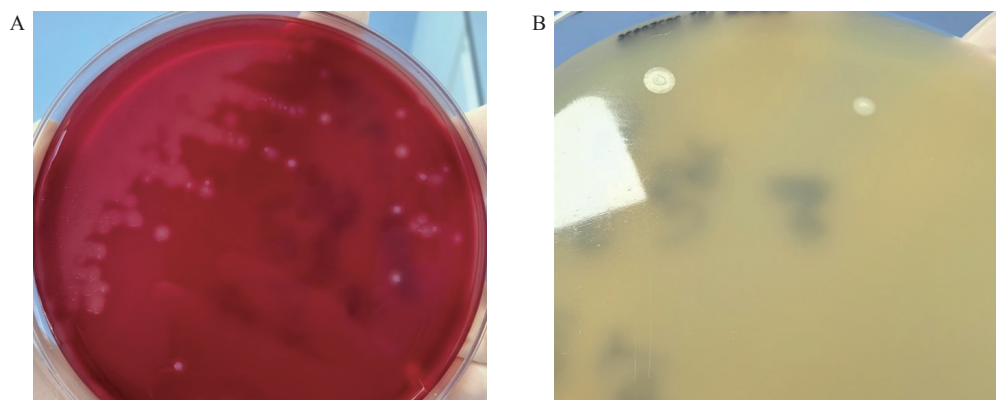


FIGURE 1. Colony morphology of soil isolate. (A) Colonies on blood agar after 48 h of anaerobic incubation at 28 °C. (B) Colonies on egg yolk agar after 48 h of anaerobic incubation at 28 °C.

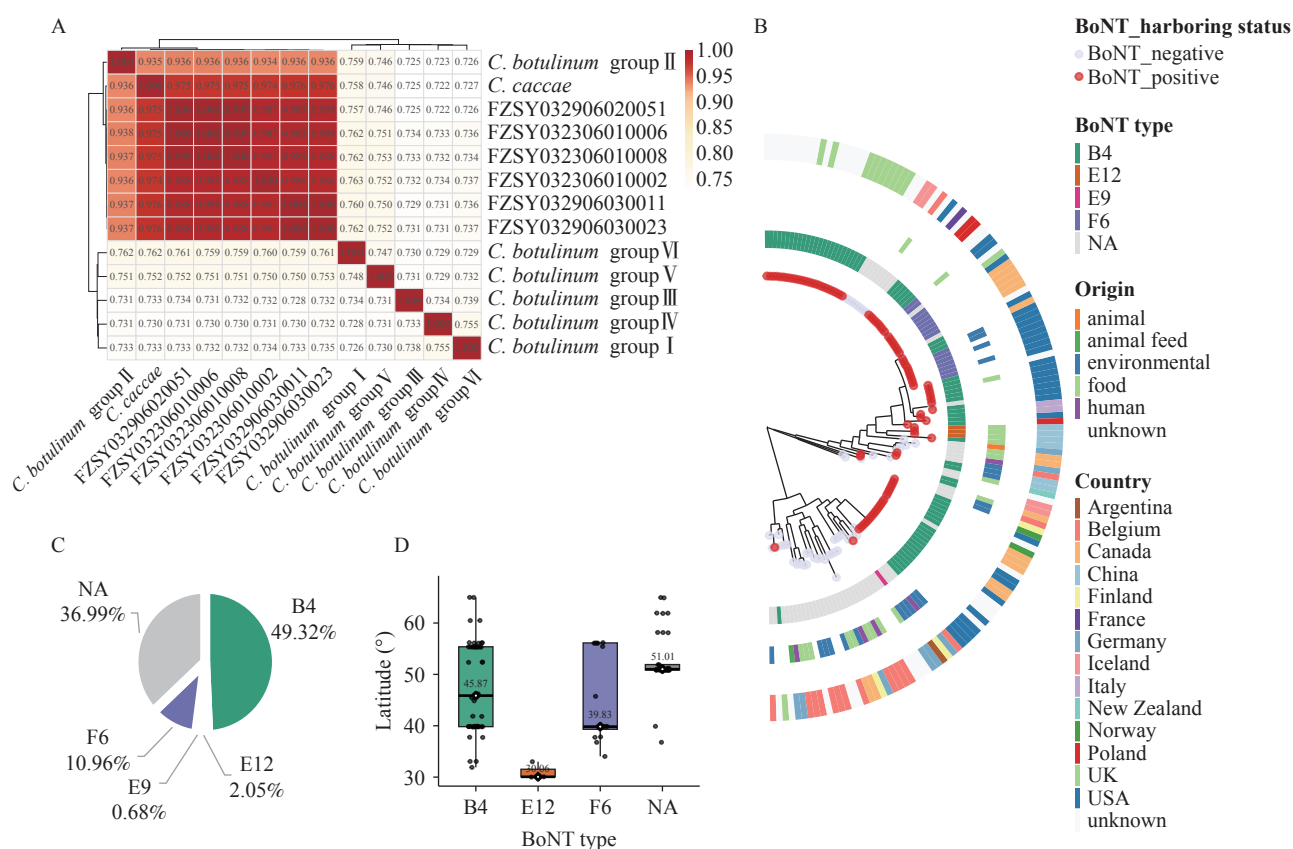


FIGURE 2. Genomic taxonomy, phylogeny, toxin profiles, and geographic distribution of *Clostridium caccae*. (A) ANI heatmap and phylogenetic tree of representative *C. botulinum* I–VI and *C. caccae* isolates. (B) Core genome-based maximum-likelihood phylogenetic tree of 146 *C. caccae* strains, with concentric rings from inner to outer denoting BoNT presence, toxin subtypes, sample sources and country of origin. (C) Pie chart showing the proportion of *bont* gene carriage and toxin subtypes distributions. (D) Box plots showing the latitudinal distribution of *bont*-positive *C. caccae* strains by toxin subtype.

Abbreviation: BoNT=botulinum neurotoxin.

the reference *C. caccae* strain, exceeding the generally accepted threshold of 95% (Figure 2A). Based on these results, six isolates were assigned as *C. caccae*, including two soil isolates from Qinghai Province (BoNT/B4), one meat isolate associated with a botulism outbreak in Qinghai Province (BoNT/E12), and three meat isolates from botulism outbreaks in Sichuan Province (one BoNT/B4 and two BoNT/E12) (Supplementary Table S2, available at <https://weekly.chinacdc.cn/>). In contrast, these *C. caccae* isolates showed low ANI values (72.2%–76.2%) relative to representative genomes of Groups I, III–VI *C. botulinum* (Figure 2A). Notably, higher ANI values (93.6%–93.8%) were observed relative to the representative Group II *C. botulinum* genome but remained below the 95% species threshold.

Comprehensive ANI-based screening of publicly available *Clostridium* genomes identified 140 *C. caccae* strains originating from 13 countries, excluding China, predominantly from environmental and food sources (Supplementary Table S2). Core genome-based phylogenetic analysis revealed that 146 *C. caccae* strains formed two main clusters (Figure 2B), with 92 strains (63.01%) carrying *bont* genes. Notably, *bont*-positive strains were predominantly clustered within one major lineage, with only a single sublineage identified in the other cluster. Four toxin subtypes were identified among *C. caccae* strains: B4 (72/146, 49.32%), E9 (1/146, 0.68%), E12 (3/146, 2.05%), and F6 (16/146, 10.96%), all belonging to Group II (Figure 2C).

Geographic analysis revealed a wide latitudinal range of *bont*-positive *C. caccae* strains (Figure 2D). The B4 subtype exhibited the broadest distribution, spanning approximately 30°N to 65°N, with a median latitude of 45.87°N. Only three E12 strains were identified, all of which were exclusively detected in the Qinghai and Sichuan Provinces, China (approximately 30°N–33°N). The F6 strains showed a relatively narrow distribution (approximately 34°N–56°N), with a median latitude of 39.83°N. *bont*-negative *C. caccae* strains were also widely distributed, ranging from approximately 36°N to 65°N, with a higher median latitude (51.01°N), suggesting a tendency toward more northern regions.

DISCUSSION

Increasing genomic evidence shows that *bont* genes are distributed across multiple clostridial lineages, reflecting the genetic mobility and complex

evolutionary history of BoNT-producing clostridia (2–3). Previous studies demonstrated that *bont* genes are often located on plasmids or bacteriophages and can be horizontally transferred between species, leading to discordance between toxin production and phylogeny (1). Consequently, it has become increasingly recognized that toxin production alone is not a reliable taxonomic criterion for species identification.

In the present study, we combined phenotypic, biochemical, toxigenic, and genomic analyses to demonstrate that a subset of strains historically classified as Group II, *C. botulinum*, is phylogenetically affiliated with *C. caccae*. Specifically, we found that *C. caccae* strains were capable of producing multiple BoNT subtypes, including B4, E9, E12, and F6, thereby expanding the known diversity of BoNT-producing clostridia. These findings further highlight the taxonomic complexity of BoNT-producing clostridia and are consistent with previous observations that toxin production and phylogenetic relationships may not always be fully concordant (8).

Phenotypic variability among the BoNT-producing *C. caccae* strains highlights the limitations of conventional identification methods. Phenotypic and biochemical characterization of the two Qinghai soil-derived isolates revealed partial inconsistencies with the previously reported characteristics of *C. caccae*. Both isolates were catalase-negative and did not hydrolyze gelatin, in contrast to earlier descriptions of *C. caccae* and the typical Group II *C. botulinum* (4,9). However, mouse bioassays have confirmed their ability to produce BoNT/B, indicating that BoNT-producing *C. caccae* may exhibit phenotypic variability and that reliance on biochemical traits alone may lead to misidentification. Besides, the single colonies of the two isolates grew only at 28 °C, indicating that detection using the GB 4789.12-2025 method, which recommends 36 °C±1 °C for incubation, may lead to false-negative results.

Genomic analysis revealed that *bont*-positive *C. caccae* may be widespread and epidemiologically relevant. Three isolates previously reported as *C. botulinum* from foodborne botulism outbreaks in Sichuan from 1990 to 2024 (10), and one isolate from a 2025 outbreak in Qinghai showed high genomic similarity to *C. caccae* based on ANI analysis. Together with the two soil-derived isolates identified in this study, these findings provide direct evidence that BoNT-producing *C. caccae* occur in both

environmental reservoirs and confirmed foodborne botulism outbreaks. To our knowledge, this is the first report linking BoNT-producing *C. caccae* to both soil contamination and human botulism, suggesting that BoNT-producing *C. caccae* may represent an under-recognized contributor to the risk of botulism.

The distribution of *bont* genes in *C. caccae* reflects the underlying evolutionary dynamics shaping the maintenance of toxin genes. Globally, the high prevalence of *bont* genes (63.01%) among *C. caccae* strains further suggests that toxin carriage is a common feature of *C. caccae* rather than a sporadic event. Moreover, the phylogenetic distribution of *bont*-positive strains, predominantly clustered within a major lineage, indicated that the acquisition and maintenance of *bont* genes may be shaped by evolutionary processes within specific genetic backgrounds. Given the known mobility of *bont* genes, horizontal gene transfer, potentially mediated by plasmids or bacteriophages, is likely to play a key role in their dissemination across clostridial species (11).

Geographic patterns of *bont* subtypes may reflect the underlying ecological or environmental influences. Geographic analysis revealed that *bont*-positive *C. caccae* strains are distributed across a broad latitudinal range with subtype-specific differences. Notably, in China, all six isolates were derived from high-altitude regions, including Yushu in Qinghai Province and the Aba and Ganzi prefectures in Sichuan Province. These regions are characterized by low temperatures, hypoxic conditions, and arid environments, which may facilitate the long-term survival and persistence of anaerobic spore-forming bacteria. Although the specific mechanisms underlying these patterns remain to be fully elucidated, these observations suggest that environmental and ecological factors influence the distribution and persistence of *bont*-positive *C. caccae*. Further studies that integrate environmental metadata and functional analyses are necessary to elucidate these relationships.

This study had several limitations. First, the use of publicly available genomic data may have introduced sampling bias. Second, the number of isolates available for phenotypic and biochemical characterization was limited. Finally, incomplete geographic metadata limited the detailed spatial analysis.

In conclusion, this study demonstrates that a subset of strains originally identified as Group II *C. botulinum* should be considered *C. caccae*, and that this species serves as a previously underrecognized

reservoir of multiple BoNT subtypes. These findings highlight the potential public health significance of *C. caccae* as a contributor to botulinum outbreaks in humans.

Conflicts of interest: No conflicts of interest.

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SUPPLEMENTARY MATERIAL

SUPPLEMENTARY TABLE 1. Biochemical characteristics of two soil isolates using API 20A strips.

Abbreviation	Reaction	FZSY032906030011	FZSY032906030023
IND	Indole production	-	-
URE	Urease	-	-
GLU	Glucose fermentation	+	+
MAN	Mannitol fermentation	-	-
LAC	Lactose fermentation	-	-
SAC	Sucrose fermentation	-	-
MAL	Maltose fermentation	-	-
SAL	Salicin fermentation	-	-
XYL	Xylose fermentation	-	-
ARA	Arabinose fermentation	-	-
GEL	Gelatin hydrolysis	-	-
ESC	Esculin hydrolysis	-	-
GLY	Glycerol fermentation	+	+
CEL	Cellobiose fermentation	-	-
MNE	Mannose fermentation	+	+
MLZ	Melezitose fermentation	-	-
RAF	Raffinose fermentation	-	-
SOR	Sorbitol fermentation	-	+
RHA	Rhamnose fermentation	-	-
TRE	Trehalose fermentation	-	-
CAT	Catalase	-	-
SPOR	Spore	+	+
GRAM	Gram reaction	+	+
COCC	Morphology	-	-

SUPPLEMENTARY TABLE 2. Metadata of 146 *C. caccae* strains analyzed in this study.

Isolate ID	Assembly Accession	Subtype	Sample	Country	Year	Latitude
GCA_011012265.1	GCA_011012265.1	B4	unknown	unknown	unknown	unknown
GCA_011012415.1	GCA_011012415.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011012495.1	GCA_011012495.1	B4	unknown	USA	1965	39.8283° N
GCA_011012515.1	GCA_011012515.1	F6	unknown	UK	unknown	55.3781° N
GCA_011012715.1	GCA_011012715.1	B4	unknown	Norway	1970	60.4720° N
GCA_011013445.1	GCA_011013445.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011013745.1	GCA_011013745.1	F6	unknown	USA	1965	39.8283° N
GCA_011014075.1	GCA_011014075.1	B4	unknown	USA	1965	39.8283° N
GCA_011014605.1	GCA_011014605.1	B4	unknown	USA	1981	39.8283° N
GCA_011014625.1	GCA_011014625.1	B4	unknown	Iceland	1981	64.9631° N
GCA_011014645.1	GCA_011014645.1	B4	unknown	USA	1977	39.8283° N
GCA_011014695.1	GCA_011014695.1	B4	unknown	unknown	unknown	unknown
GCA_011014705.1	GCA_011014705.1	B4	unknown	unknown	unknown	unknown
GCA_011014795.1	GCA_011014795.1	B4	unknown	Poland	2012	52.3792° N
GCA_011014805.1	GCA_011014805.1	B4	unknown	Poland	2013	52.3792° N
GCA_011015055.1	GCA_011015055.1	B4	unknown	UK	2012	55.3781° N
GCA_011015115.1	GCA_011015115.1	B4	unknown	unknown	unknown	unknown
GCA_011015125.1	GCA_011015125.1	B4	unknown	unknown	unknown	unknown
GCA_011015145.1	GCA_011015145.1	B4	unknown	Poland	2005	52.3792° N
GCA_011015235.1	GCA_011015235.1	F6	unknown	Canada	2006	56.1304° N
GCA_011015255.1	GCA_011015255.1	F6	unknown	Canada	2006	56.1304° N
GCA_011015265.1	GCA_011015265.1	F6	unknown	Canada	2006	56.1304° N
GCA_011015295.1	GCA_011015295.1	F6	unknown	Canada	2006	56.1304° N
GCA_011015345.1	GCA_011015345.1	F6	unknown	Canada	2006	56.1304° N
GCA_011015755.1	GCA_011015755.1	B4	unknown	UK	2005	55.3781° N
GCA_011015765.1	GCA_011015765.1	B4	unknown	UK	2005	55.3781° N
GCA_011015815.1	GCA_011015815.1	B4	unknown	UK	2005	55.3781° N
GCA_011015835.1	GCA_011015835.1	B4	unknown	UK	2005	55.3781° N
GCA_011015845.1	GCA_011015845.1	B4	unknown	UK	2005	55.3781° N
GCA_011015875.1	GCA_011015875.1	B4	unknown	UK	2005	55.3781° N
GCA_011015895.1	GCA_011015895.1	B4	unknown	UK	2005	55.3781° N
GCA_011015915.1	GCA_011015915.1	B4	unknown	UK	2005	55.3781° N
GCA_011015925.1	GCA_011015925.1	B4	unknown	Canada	2005	56.1304° N
GCA_011015935.1	GCA_011015935.1	B4	unknown	UK	2005	55.3781° N
GCA_011015955.1	GCA_011015955.1	B4	unknown	Canada	2005	56.1304° N
GCA_011015995.1	GCA_011015995.1	B4	unknown	Canada	2005	56.1304° N
GCA_011016025.1	GCA_011016025.1	B4	unknown	Canada	2005	56.1304° N
GCA_011016035.1	GCA_011016035.1	B4	unknown	Canada	2005	56.1304° N
GCA_011016145.1	GCA_011016145.1	B4	unknown	unknown	unknown	unknown
GCA_011016185.1	GCA_011016185.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011017435.1	GCA_011017435.1	B4	unknown	unknown	unknown	unknown
GCA_011018055.1	GCA_011018055.1	no <i>bont</i>	unknown	Iceland	1983	64.9631° N
GCA_011018065.1	GCA_011018065.1	no <i>bont</i>	unknown	USA	unknown	39.8283° N

Continued

Isolate ID	Assembly Accession	Subtype	Sample	Country	Year	Latitude
GCA_011018075.1	GCA_011018075.1	B4	unknown	USA	1981	39.8283° N
GCA_011018135.1	GCA_011018135.1	B4	unknown	USA	1981	39.8283° N
GCA_011018185.1	GCA_011018185.1	B4	unknown	USA	1981	39.8283° N
GCA_011018235.1	GCA_011018235.1	B4	unknown	Italy	1986	41.8719° N
GCA_011018255.1	GCA_011018255.1	B4	unknown	France	unknown	46.2276° N
GCA_011018335.1	GCA_011018335.1	no <i>bont</i>	unknown	Iceland	1983	64.9631° N
GCA_011018355.1	GCA_011018355.1	B4	unknown	Italy	1986	41.8719° N
GCA_011018375.1	GCA_011018375.1	B4	unknown	Iceland	1981	64.9631° N
GCA_011018455.1	GCA_011018455.1	F6	unknown	USA	1965	39.8283° N
GCA_011018505.1	GCA_011018505.1	B4	unknown	Norway	unknown	60.4720° N
GCA_011018515.1	GCA_011018515.1	F6	unknown	USA	1965	39.8283° N
GCA_011018615.1	GCA_011018615.1	B4	unknown	USA	1965	39.8283° N
GCA_011018715.1	GCA_011018715.1	B4	unknown	UK	unknown	55.3781° N
GCA_011019155.1	GCA_011019155.1	F6	unknown	USA	unknown	39.8283° N
GCA_011019315.1	GCA_011019315.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011019325.1	GCA_011019325.1	B4	unknown	unknown	unknown	unknown
GCA_011019335.1	GCA_011019335.1	B4	unknown	unknown	unknown	unknown
GCA_011019615.1	GCA_011019615.1	B4	unknown	unknown	unknown	unknown
GCA_011019705.1	GCA_011019705.1	B4	unknown	unknown	unknown	unknown
GCA_011020025.1	GCA_011020025.1	B4	unknown	USA	1965	39.8283° N
GCA_011020095.1	GCA_011020095.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020105.1	GCA_011020105.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020155.1	GCA_011020155.1	B4	unknown	USA	1965	39.8283° N
GCA_011020325.1	GCA_011020325.1	B4	unknown	unknown	unknown	unknown
GCA_011020335.1	GCA_011020335.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020375.1	GCA_011020375.1	B4	unknown	unknown	unknown	unknown
GCA_011020395.1	GCA_011020395.1	B4	unknown	unknown	unknown	unknown
GCA_011020415.1	GCA_011020415.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020425.1	GCA_011020425.1	B4	unknown	unknown	unknown	unknown
GCA_011020445.1	GCA_011020445.1	B4	unknown	unknown	unknown	unknown
GCA_011020495.1	GCA_011020495.1	B4	unknown	unknown	unknown	unknown
GCA_011020515.1	GCA_011020515.1	B4	unknown	unknown	unknown	unknown
GCA_011020615.1	GCA_011020615.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020775.1	GCA_011020775.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020855.1	GCA_011020855.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011020925.1	GCA_011020925.1	B4	unknown	unknown	unknown	unknown
GCA_011021045.1	GCA_011021045.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011021075.1	GCA_011021075.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011021085.1	GCA_011021085.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011021115.1	GCA_011021115.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCA_011021235.1	GCA_011021235.1	B4	unknown	unknown	unknown	unknown
GCA_011021275.1	GCA_011021275.1	F6	unknown	USA	1965	39.8283° N
GCA_011021395.1	GCA_011021395.1	B4	unknown	unknown	unknown	unknown

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Isolate ID	Assembly Accession	Subtype	Sample	Country	Year	Latitude
GCA_011022005.1	GCA_011022005.1	B4	unknown	USA	1965	39.8283° N
GCA_011363195.1	GCA_011363195.1	B4	unknown	unknown	unknown	unknown
GCA_016925805.1	GCA_016925805.1	no <i>bont</i>	environmental	Finland	1996	61.9241° N
GCA_016925935.1	GCA_016925935.1	no <i>bont</i>	environmental	Finland	1996	61.9241° N
GCA_016925955.1	GCA_016925955.1	no <i>bont</i>	environmental	Finland	1996	61.9241° N
GCA_019836585.1	GCA_019836585.1	B4	unknown	Canada	1905	45.5088° N
GCA_019836715.1	GCA_019836715.1	B4	unknown	unknown	unknown	unknown
GCA_019836745.1	GCA_019836745.1	B4	unknown	USA	unknown	44.8000° N
GCA_019836765.1	GCA_019836765.1	no <i>bont</i>	unknown	USA	1905	36.7783° N
GCA_019837835.1	GCA_019837835.1	B4	unknown	USA	1905	37.7739° N
GCA_019838725.1	GCA_019838725.1	B4	unknown	USA	1968	39.8283° N
GCA_019838785.1	GCA_019838785.1	F6	unknown	USA	unknown	37.7739° N
GCA_019838865.1	GCA_019838865.1	B4	unknown	USA	1905	37.7739° N
GCA_024608455.1	GCA_024608455.1	B4	unknown	unknown	unknown	unknown
GCA_025232875.1	GCA_025232875.1	F6	food	USA	1966	45.6667° N
GCA_025232915.1	GCA_025232915.1	B4	environmental	USA	1960	39.8283° N
GCA_025233355.1	GCA_025233355.1	no <i>bont</i>	food	Canada	2002	58.1500° N
GCA_025234305.1	GCA_025234305.1	no <i>bont</i>	food	Canada	2002	58.1500° N
GCA_025234565.1	GCA_025234565.1	no <i>bont</i>	food	Canada	1980	51.9167° N
GCA_025234595.1	GCA_025234595.1	no <i>bont</i>	food	Canada	1980	51.9167° N
GCA_025258105.1	GCA_025258105.1	no <i>bont</i>	food	Canada	2002	58.1500° N
GCF_000309805.1	GCF_000309805.1	E9	environmental	Argentina	1993	38.4161° S
GCF_000750055.1	GCF_000750055.1	B4	food	USA	1981	39.8283° N
GCF_000750065.1	GCF_000750065.1	B4	environmental	USA	1968	39.8283° N
GCF_000789355.1	GCF_000789355.1	F6	environmental	USA	1965	37.7739° N
GCF_001273195.1	GCF_001273195.1	F6	environmental	USA	1965	36.7783° N
GCF_002797995.1	GCF_002797995.1	F6	environmental	USA	1965	34.0522° N
GCF_011065855.2	GCF_011065855.2	no <i>bont</i>	food	New Zealand	2019	40.3528° S
GCF_023845495.1	GCF_023845495.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCF_023845565.1	GCF_023845565.1	no <i>bont</i>	unknown	unknown	unknown	unknown
GCF_023845605.1	GCF_023845605.1	no <i>bont</i>	food	Germany	2015	51.1657° N
GCF_023845655.1	GCF_023845655.1	no <i>bont</i>	animal feed	Germany	2015	51.1657° N
GCF_023845665.1	GCF_023845665.1	no <i>bont</i>	human	Germany	2015	51.1657° N
GCF_023845725.1	GCF_023845725.1	no <i>bont</i>	human	Germany	2014	51.1657° N
GCF_023845735.1	GCF_023845735.1	no <i>bont</i>	human	Germany	2014	51.1657° N
GCF_023845775.1	GCF_023845775.1	no <i>bont</i>	animal	Germany	2014	51.1657° N
GCF_023845795.1	GCF_023845795.1	no <i>bont</i>	human	Germany	2013	51.1657° N
GCF_023845835.1	GCF_023845835.1	no <i>bont</i>	environmental	Germany	2012	51.1657° N
GCF_023845865.1	GCF_023845865.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023845895.1	GCF_023845895.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023845915.1	GCF_023845915.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023845935.1	GCF_023845935.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023845955.1	GCF_023845955.1	no <i>bont</i>	food	Belgium	2018	50.8503° N

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Isolate ID	Assembly Accession	Subtype	Sample	Country	Year	Latitude
GCF_023845975.1	GCF_023845975.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023845995.1	GCF_023845995.1	no <i>bont</i>	food	Belgium	2018	50.8503° N
GCF_023846015.1	GCF_023846015.1	no <i>bont</i>	food	Belgium	2018	50.8503° N
GCF_023846035.1	GCF_023846035.1	no <i>bont</i>	food	Belgium	2018	50.8503° N
GCF_023846055.1	GCF_023846055.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023846075.1	GCF_023846075.1	no <i>bont</i>	food	Belgium	2018	50.8503° N
GCF_023846095.1	GCF_023846095.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023846115.1	GCF_023846115.1	no <i>bont</i>	environmental	Belgium	2018	50.8503° N
GCF_023846135.1	GCF_023846135.1	no <i>bont</i>	food	Belgium	2018	50.8503° N
GCF_023846155.1	GCF_023846155.1	no <i>bont</i>	human	Belgium	2018	50.8503° N
GCF_023846175.1	GCF_023846175.1	no <i>bont</i>	food	Belgium	2018	50.8503° N
FZSY032906030023	NA	B4	environmental	China	2024	33.0060° N
FZSY032906030011	NA	B4	environmental	China	2024	33.0060° N
FZSY032306010002	GCA_051906095.1	B4	food	China	2014	31.9100° N
FZSY032906020051	NA	E12	food	China	2025	33.0060° N
FZSY032306010008	GCA_051906055.1	E12	food	China	1990	30.0563° N
FZSY032306010006	GCA_051906075.1	E12	food	China	2005	30.0563° N