



Molecular characterization and genotyping of *Bacillus cereus* isolated from buffalo raw milk and milk products

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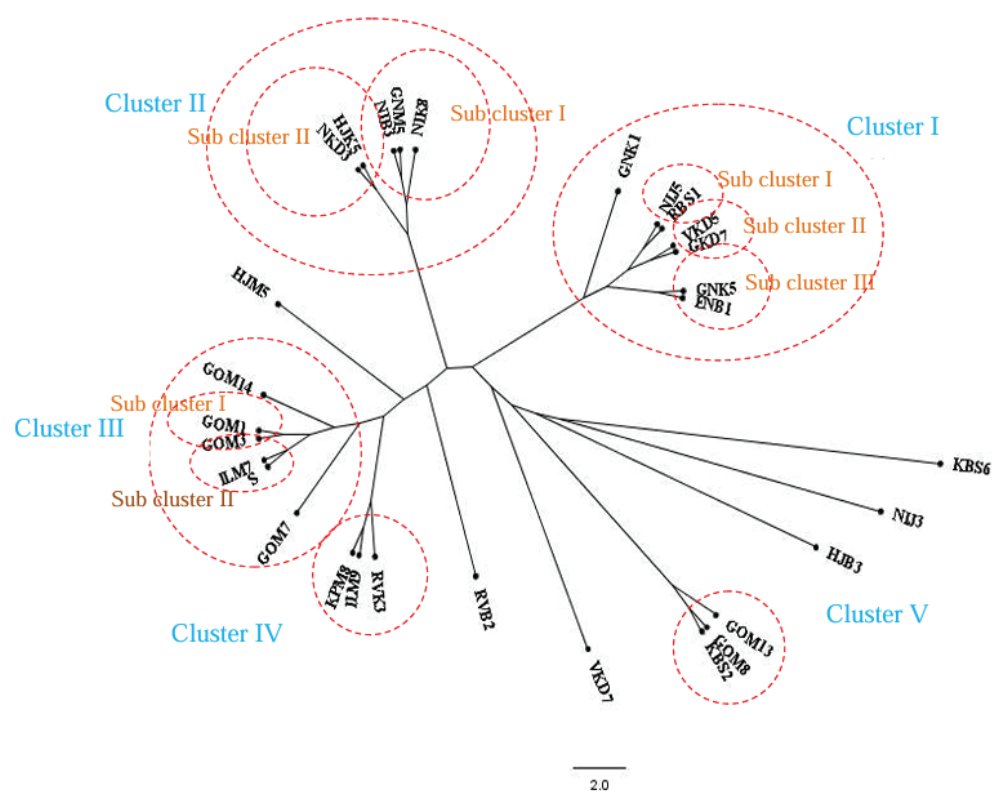
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Supplementary Table 1. Primers used for detection of virulence genes in *B. cereus* isolates

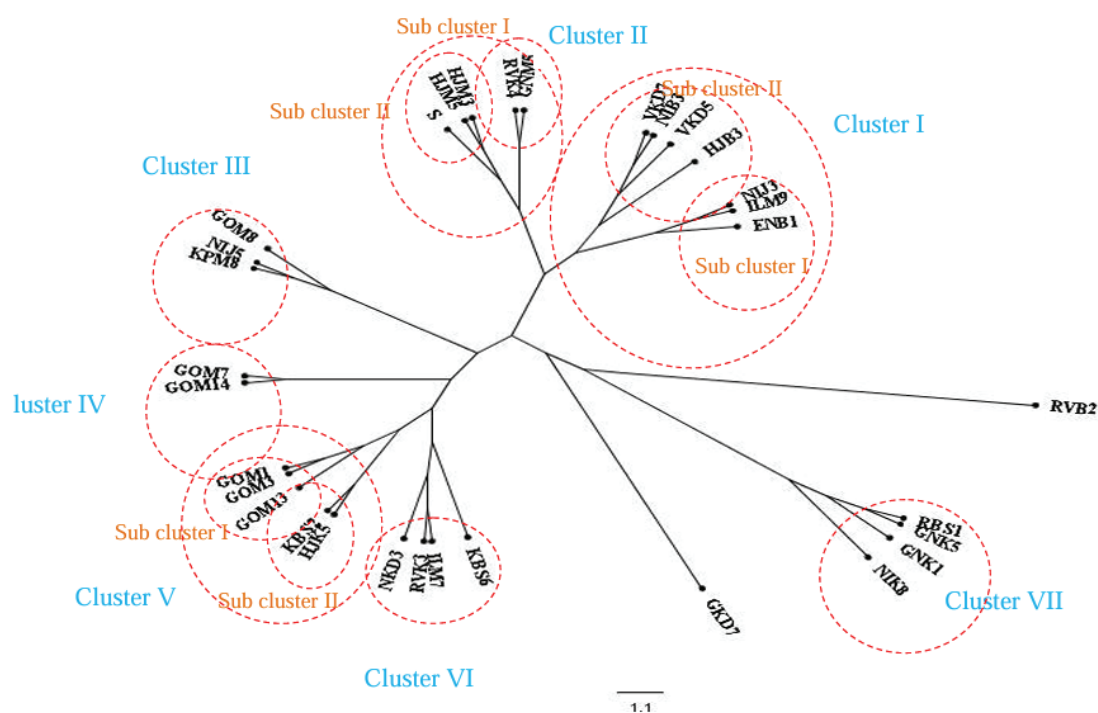
Target gene	Primer	Sequence of the primer	Amplicon size (bp)
<i>hblC</i>	FHbIC	CCTATCAATACTCTCGCAA	695 bp
	RHbIC	TTTCCTTTGTTATACGCTGC	
<i>hblD</i>	FHD	GAAACAGGGTCTCATATTTT	1018 bp
	RHD2	CTGCATCTITATGAATATCA	
<i>hblA</i>	FhblA	GCAAAATCTATGAATGCCTA GCATCTGTTCGTAATGTTTT	884 bp
	RhblA		
<i>nheA</i>	F2nheB	TAAGGAGGGGCAAACAGAAG TGAATGCGAAGAGCTGCTTC	759 bp
	RnheB		
<i>nheB</i>	F2nheB	CAAGCTCCAGTTCATGCGG GATCCCATTGTGTACCATTG	935 bp
	RnheB		
<i>nheC</i>	FnheC	ACATACCTTTTGCAGCAGAAC CCACCAGCAATGACCATATC	618 bp
	R2nheC		
<i>cytK</i>	FcytK	CGACGTCACAAGTTGTAACA CGTGTGTAAATACCCAGTT	565 bp
	R2cytK		
<i>entFM</i>	FentFM	GTTCGTTTCAGGTGCTGGTAC AGCTGGGCCTGTACGTACIT	486 bp
	RentFM		

Supplementary Table 2. Antimicrobial susceptibility patterns of *B. cereus* isolates

Antibiotic class	Antimicrobial agent	Pattern of antibiogram of <i>B. cereus</i> isolates		
		Sensitive (%)	Intermediate (%)	Resistant (%)
Pencillins	Amoxicillin+Clavulanicacid	0	0	31 (100%)
	Pencillin-G	0	0	31 (100%)
Cephalosporins	Cefepime	1 (3.2%)	3 (9.7%)	27 (87.1%)
Amphenicols	Chloramphenicol	26 (83.8%)	3 (9.7%)	2 (6.5%)
Lincosamides	Clindamycin	7 (22.6%)	14 (45.2%)	10 (32.3%)
Polypeptides	Colistin	4 (12.9%)	21 (67.7%)	6 (19.4%)
Flouroquinolones	Ciprofloxacin	25 (80.6%)	4 (12.9%)	2 (6.5%)
Macrolide	Erythromycin	27 (87.1%)	2 (6.5%)	2 (6.5%)
Aminoglycosides	Gentamicin	31 (100%)	0	0
Rifamycins	Rifampicin	2 (6.5%)	20 (64.5%)	9 (29%)
Tetracyclines	Tetracycline	31 (100%)	0	0
Glycopeptides	Vancomycin	6 (19.4%)	17 (54.8%)	8 (25.8%)



Supplementary Fig. 1. Cluster analysis of ERIC-PCR fingerprints of *B. cereus* isolates from different sources. An unrooted phylogenetic tree was constructed using dollop program of phylip 3.6 version branch



Supplementary Fig. 2. Cluster analysis of REP-PCR fingerprints of *B. cereus* isolates from different sources. An unrooted phylogenetic tree was constructed using dollop program of phylip 3.6 version branch