

Table S1: analysis of *cotH* locus in *Bacillus* species with completely sequenced genomes

Species ^a	CotH orthologue ^b	CotG orthologue ^b	Divergent gene ^c	Tax ID ^d	Accession number ^e
1. <i>B. subtilis spizizenii</i>	+	+	+	655816	NC_014479.1
2. <i>B. amyloliquefaciens</i>	+	+	+	326423	NC_014551.1
3. <i>B. atrophaeus</i>	+	+	+	720555	NC_014639.1
4. <i>B. methylotrophicus</i>	+	+	+	326423	NC_009725.1
5. <i>B. sp. Pc3</i>	+	+	+	1446792	CP010406.1
6. <i>B. sp. BH072</i>	+	+	+	1570330	CP009938.1
7. <i>B. sp. BS34A</i>	+	+	+	1639654	LN680001.1
8. <i>B. licheniformis</i>	+	-	+	279010	NC_006270.3
9. <i>B. anthracis</i>	+	-	+	1392	NC_005945.1
10. <i>B. cereus</i>	+	-	+	396343	NC_003909.8
11. <i>B. thuringiensis</i>	+	-	+	714359	NC_014171.1
12. <i>B. cytotoxicus</i>	+	-	+	315749	NC_009674.1
13. <i>B. weihenstephanensis</i>	+	-	+	315730	NC_010184.1
14. <i>B. toyonensis</i>	+	-	+	155322	NC_022781.1
15. <i>B. mycoides</i>	+	-	+	1405	CP007626.1
16. <i>B. pumilus</i>	+	-	+	536229	NC_009848.1
17. <i>B. megaterium</i>	+	-	+	545693	NC_014019.1
18. <i>B. smithii</i>	+	-	+	1479	CP012024.1
19. <i>B. bombysepticus</i>	+	-	+	658666	CP007512.1
20. <i>B. sp. JS</i>	+	-	+	1127744	NC_017743.1
21. <i>B. sp. 1NLA3E</i>	+	-	+	666686	NC_021171.1
22. <i>B. sp. YP1</i>	+	-	+	1574141	CP010014.1
23. <i>B. sp. WP8</i>	+	-	-	756828	CP010075.1
24. <i>B. sp. LM 4-2</i>	+	-	-	1628753	CP011101.1
25. <i>B. sp. X1</i>	-	ND	ND	498382	CP008855.1
26. <i>B. sp. OxB-1</i>	-	ND	ND	98228	AP013294.1
27. <i>B. halodurans</i>	-	ND	ND	86665	NC_002570.2
28. <i>B. clausii</i>	-	ND	ND	79880	NC_006582
29. <i>B. pseudofirmus</i>	-	ND	ND	79885	NC_013791.2
30. <i>B. cellulolyticus</i>	-	ND	ND	1413	CP002394.1
31. <i>B. coagulans</i>	-	ND	ND	1121088	CP009709.1
32. <i>B. infantis</i>	-	ND	ND	324767	NC_022524.1
33. <i>B. iehensis</i>	-	ND	ND	300825	CP003923.1
34. <i>B. methanolicus</i>	-	ND	ND	1471	CP007739.1
35. <i>B. endophyticus</i>	-	ND	ND	135735	CP011974.1

^a List of *Bacillus* species whose genomes have been completely sequenced (source KEGG, Kyoto Encyclopedia of Genes and Genomes database http://www.genome.jp/kegg/catalog/org_list.html);

^b presence (+) or absence (-) of a protein sharing a minimum of 40% sequence identity respect to CotH and CotG of *B. subtilis* 168

^c presence (+) or absence (-) of an adjacent and divergent *orf* respect to *cotH*;

^d Taxonomy ID from NCBI (<http://www.ncbi.nlm.nih.gov/taxonomy>)

^e accession numbers of the respective genomic sequences

ND, not determined