



# Complete genome and plasmid sequence of a novel *Bacillus* sp. BD59S, a parasporal protein synthesizing bacterium

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## Abstract

Parasporal crystalline inclusion proteins of some *Bacillus* spp. are of paramount importance due to their insecticidal, nematocidal, and cancer cell killing capabilities. Here, we present a brief report of the complete genome sequence of *Bacillus* sp. BD59S, a bacterium that produced HeLa cell-killing parasporal crystalline inclusion proteins. From genome sequencing and assembly, we found that the bacterium has one circular chromosome and two large plasmids, pBTBD59S1 and pBTBD59S2. The size of the chromosome is 5283,933 bp with a 35.4% GC content, consisting of 5938 genes and 5550 protein-coding sequences (CDSs), 25 complete rRNAs (5S, 16S, 23S), 98 tRNAs, 5 ncRNAs, 260 pseudo-genes, and 356 subsystems. Complete plasmid sequence of pBTBD59S1 comprises a total size of 162,149 bp with 33.4% GC content, 192 CDSs, and 13 subsystems. The other plasmid pBTBD59S2, is 199,209 bp long with 32.9% GC content, 179 CDSs, and 11 subsystems. Analyses by NCBI microbial genome BLAST, phylogenetic genome tree, and BLAST ring image generator (BRIG) revealed that BD59S belongs to *Bacillus cereus* group, and is more close to *B. thuringiensis*. Further, the strain possesses 57.04 kDa and 54.42 kDa Cry protein-coding genes, which show significant similarities with cancer cell-killing parasporin proteins of *B. thuringiensis* strains.

**Keywords** Genome sequence · *Bacillus* sp. BD59S · Parasporal protein · HeLa cell

## Introduction

The genus *Bacillus* comprises Gram-positive, rod-shaped, and endospore-forming bacteria that could be either facultative or obligate aerobe (Drobniewski 1993). *Bacillus thuringiensis* (*Bt*) is a member of the *B. cereus* group, and phenotypically and genotypically are very close to *B. cereus* and *B. anthracis* (Guttmann and Ellar 2000). Among *B. cereus* group, only certain *Bt* can synthesize large proteinaceous parasporal crystalline (Cry) inclusions (Stahly et al. 2006).

These inclusions are visible under microscope and become water soluble in an alkaline solution of sodium carbonate ( $\text{Na}_2\text{CO}_3$ ) and dithiothreitol (DTT) (Brasseur et al. 2015). They are genealogically heterogeneous (<http://parasporin.ftc.pref.fukuoka.jp/>) and to date more than 800 different Cry proteins have been reported ([http://www.lifesci.susx.ac.uk/home/Neil\\_Crickmore/Bt/toxins2.html](http://www.lifesci.susx.ac.uk/home/Neil_Crickmore/Bt/toxins2.html)) from different *Bt* strains. Each of them has unique and selective biocidal activity on different insects, nematodes or human cancer cells (Mizuki et al. 1999). In the present study, we reported complete genome sequence of a bacterium named *Bacillus* sp. BD59S isolated from a soil sample (Shishir et al. 2014) of an agricultural field (Latitude: 24.1344°N, Longitude: 90.7860°E) with shadowed and slightly moistened places generally not exposed to sunlight of Bangladesh. We found the strain as an endospore forming, hemolytic, Gram-positive, and rod-shaped bacterium, which is motile, citrate, Voges Proskauer (VP), indole, starch, and gelatin hydrolysis positive, and Methyl Red (MR) negative. It produced parasporal Cry inclusion proteins during its sporulation phase of life cycle. The solubilized and activated Cry proteins

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