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Comparative Genomics of *Bacillus* species and its Relevance in Industrial Microbiology

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Abstract: With the advent of high throughput sequencing platforms and relevant analytical tools, the rate of microbial genome sequencing has accelerated which has in turn led to better understanding of microbial molecular biology and genetics. The complete genome sequences of important industrial organisms provide opportunities for human health, industry, and the environment. *Bacillus* species are the dominant workhorses in industrial fermentations. Today, genome sequences of several *Bacillus* species are available, and comparative genomics of this genus helps in understanding their physiology, biochemistry, and genetics. The genomes of these bacterial species are the sources of many industrially important enzymes and antibiotics and, therefore, provide an opportunity to tailor enzymes with desired properties to suit a wide range of applications. A comparative account of strengths and weaknesses of the different sequencing platforms are also highlighted in the review.

Keywords: *Bacillus*, genome sequencing, comparative genomics, sequencing platforms, industrial enzymes

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Introduction

Whole genome sequencing is a powerful approach for gaining the reference sequence information of multiple organisms. It helps in identifying genomic variations associated with phenotypes. Whole genome sequencing enables the identification of individual nodes of multi-component genetic interaction networks simultaneously, and also helps in mapping the evolutionary pathways that can support the growth of a genetically compromised strain.

Whole genome sequences of industrially important organisms and bacterial pathogens provide prospectives for industry, human health, and the environment. A wide diversity is present in bacterial genomes. Most of the bacterial proteins are highly or moderately conserved in evolution as extensive gene shuffling occurs in a few conserved gene arrays in distantly related bacteria. The outcome of whole genome sequencing has revealed new insights into the evolution of bacterial lifestyles including strategies for adaptation to new niches and overcoming competitors.

Bacillus is the most important workhorse among industrial microorganisms. They have ancient history of more than thousand years since the production of natto (a traditional Japanese dish of fermented soya beans) using *B. subtilis*, and their roles are continuously expanding and evolving. *Bacillus* species are considered as generally regarded as safe (GRAS) in the list of Food and Drug Administration (FDA). They are known to secrete copious amounts of extracellular enzymes and have high growth rates and short fermentation cycles and therefore these are one of the most important industrial enzyme producers.^{1–5} For further development and exploitation of these bacteria in industrial processes, the complete genomes of several species of *Bacillus* have been sequenced in order to understand their biochemistry, physiology, and genetics. *B. subtilis* is the first gram positive bacterium whose genome was sequenced and since then, the genomes of several *Bacillus* species have been sequenced.

Strategies to Sequence Complete Bacterial Genomes

The random shotgun sequencing method was developed and perfected for prokaryotic genomes which are smaller in size and contain less repetitive DNA. Various methods are used to fragment DNA

including nebulization, ultrasonication, enzymatic fragmentation, and hydrodynamic shearing. After fragmentation, adaptors are ligated to these fragments. Template amplification is the next step and most of the platforms support mate pair sequencing, in which the ends of DNA fragments of size 3–20 kb are connected to form circular molecules. These molecules are then again fragmented, and the fragments flanking the joints are then selected and the end adaptors are added. Such sequencing offers significant information about the location of sequences scattered across the genome, which aids in assembling the genome.⁶ Another platform is paired end sequencing which is similar to mate pair sequencing however in the former DNA fragments are sequenced from each end with no requirement for additional library preparation steps. The pictorial representation of the whole genome sequencing is summarized in Figure 1.

In 1977, Frederick Sanger introduced DNA sequencing technology, based on chain-termination method (also known as Sanger sequencing). Walter Gilbert developed another sequencing technology which relies on chemical modification of DNA and successive cleavage at specific bases. Sanger sequencing was accepted as the primary technology in the ‘first generation’ of laboratory and commercial sequencing applications on the basis of its high efficiency and low radioactivity. During that time, DNA sequencing was tedious and radioactive materials were required. The first automatic sequencing machine (AB370) was launched by Applied Biosystems in 1987, with capillary electrophoresis making the sequencing faster and more accurate. With the advent of new informatic approaches, holistic integration, and significant analysis of the genome sequence data, the sequencing has become easy and large information can be extracted from the complete genome. A variety of sequencing methods, softwares for the assembly of contigs, and annotation of gene are employed for sequencing the genome. The next generation sequencing (NGS) reads millions of fragments in a single run. It offers several advantages such as extensive parallel sequencing of shotgun libraries, high throughput with maximum genome coverage, and cost effectiveness. The most popular NGS platform includes (Roche 454: GS FLX, XL+; Illumina: Genome analyzer, HiSeq2000; Life Technologies: Ion Torrent,

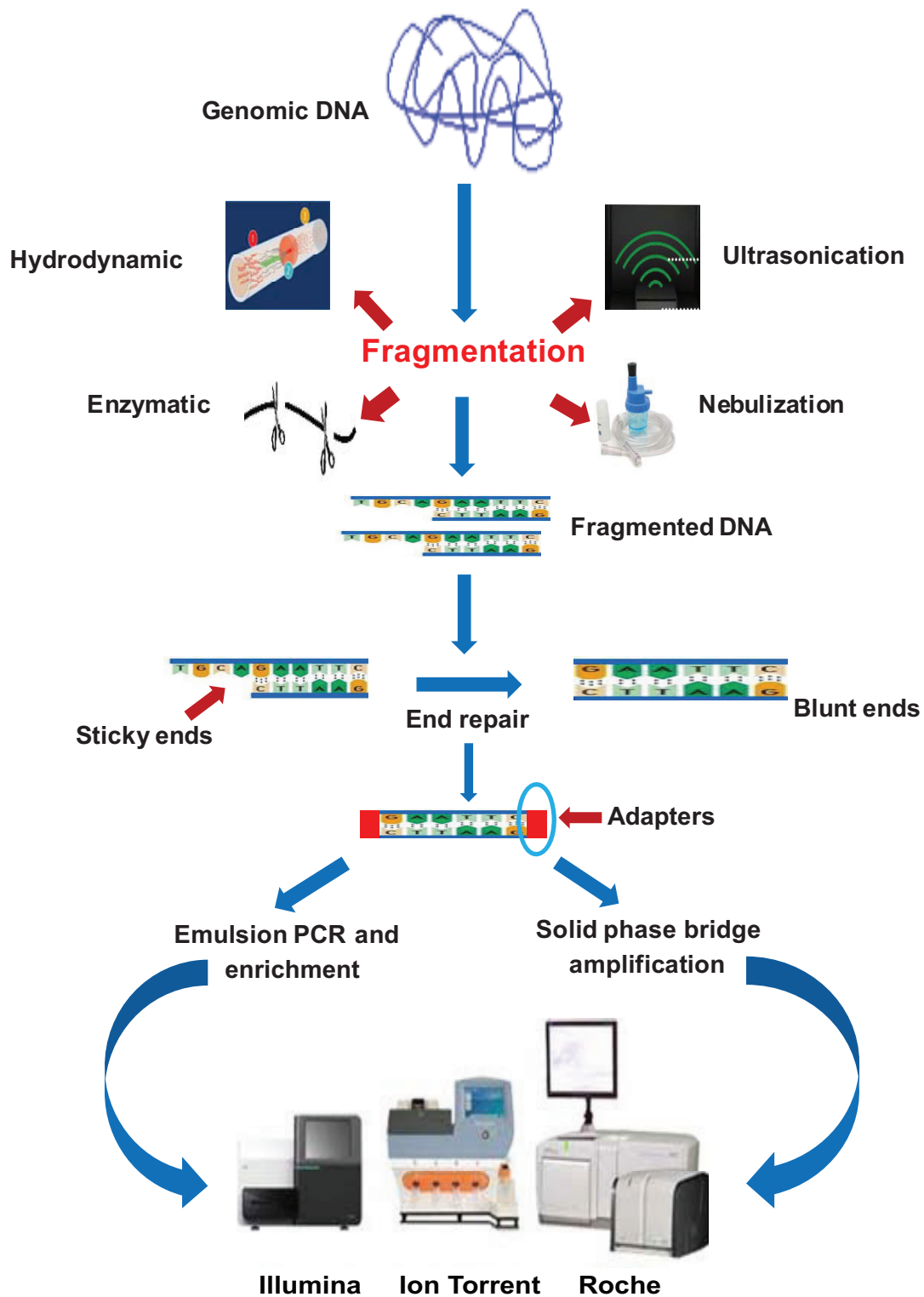


Figure 1. Pictorial representation of whole genome sequencing.

**Table 1.** Technical specifications of some important NGS platforms.

Platforms	Illumina MiSeq	Ion Torrent PGM	PacBio RS	Illumina GAllx	Illumina HiSeq 2000
Chemistry	Reversible terminator	Proton detection	Real time fluorescence DNA polymerization	Reversible terminator	Reversible terminator
Instrument Cost* (\$)	128 K	80 K (includes costing of PGM, server, OneTouch and OneTouch ES)	695 K	256 K	654 K
Sequence yield per run	1.5–2 Gb	20–50 Mb on 314 chip 100–200 Mb on 316 chip 1 Gb on 318 chip	100 Mb	30 Gb	600 Gb
Sequencing cost (\$) per Gb*	502	1000 (318 chip)	2000	148	41
Run Time	27 h (along with 2 h cluster generation)	2 h	2 h	10 days	11 days
Reported Accuracy	Mostly > Q30	Mostly Q20	<Q10	Mostly > Q30	Mostly > Q30
Observed Raw Error Rate (%)	0.80	1.71	12.86	0.76	0.26
Read length (bases)	Up to 150	~200	Average 1500**	Up to 150	Up to 150
Correct SNp calls (%)	76	~82	~71	70	69
Paired reads	Yes	Yes	No	Yes	Yes
Insert size	Up to 700 bases	Up to 250 bases	Up to 10 kb	Up to 700 bases	Up to 700 bases
Typical DNA Requirements	50–1000 ng	100–1000 ng	~1 µg	50–1000 ng	50–1000 ng

*All cost calculations are based on list price quotations obtained from the manufacturer and assume expected sequence yield.

**Mean mapped read length (adapter and reverse strand sequences). Subread lengths, i.e. the individual stretches of sequence from the sequenced fragment, are significantly shorter.

Adapted from Quail et al.⁵²

SOLiD, Pacific Biosciences: Pac Bio RS) sequencing. Illumina and Roche are the most commonly used platforms for sequencing genomes of *Bacillus* spp. The comparison of various sequencing platforms is depicted in Table 1.

The first bacterial genome project started in 1991 for sequencing the complete *Escherichia coli* genome.⁷ Since then, genome projects have been started on a number of bacteria, archaea, and eukaryotes. *Bacillus* is one of the best described genera in the genomic database. According to Alcaraz et al.⁸ more than 108 complete and draft genome sequences of *Bacillus* are available. The extensive research on *Bacilli* includes classical microbiology, biochemistry, and modern genomic and proteomic approaches. The details of genomes of various *Bacillus* spp. and their comparative analyses are highlighted in Tables 2 and 3.

The dendrogram drawn using 16S rDNA sequences suggests close phylogenetic relationship among industrially important (*B. licheniformis*, *B. subtilis*, *B. halodurans*, *B. megaterium*) and pathogenic (*B. anthracis*, *B. cereus*) *Bacillus* spp. (Fig. 2).

Metabolism of the Genus *Bacillus*

The type and range of metabolism provides information regarding the natural environment of the organism and biological activity. The key feature of *B. subtilis* metabolism includes the requirement of branched short chain carboxylic acids for lipid biosynthesis. It can also synthesize and utilize branched short chain carboxylic acids and alcohols.¹⁰ The high growth yield of *B. licheniformis* is due to its ability to utilize carbohydrates under conditions of varying oxygen tensions.¹¹ *B. anthracis* shows reduced

**Table 2.** Details of whole genome sequences of *Bacillus* spp.

S. no.	Microorganism	Genome size (Mbp)	GC (%)	Sequencing	Annotation	Fold coverage	Reference
1.	<i>Bacillus anthracis</i> Ames	5.22	35.4	TIGR microbial shotgun projects		13	5
2.	<i>Bacillus amyloliquefaciens</i> LL3	3.99	45.7	Roche 454 GS-FLX system	RAST	70	53
3.	<i>Bacillus anthracis</i> H9401	5.23	35.0	454 GS-FLX	UniRef90, NCBI nr, COG, KEGG	30	54
4.	<i>Bacillus cereus</i>	5.43	35.3	Applied Biosystems 3700 DNA sequencers	ERGO	6	34
5.	<i>Bacillus coagulans</i> 36D1	3.55	46.5	Combination of Roche 454 & Sanger	UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG	9	13
6.	<i>Bacillus halodurans</i> C-125	4.20	43.7	ABI Prism 377		7.1	9
7.	<i>Bacillus isronensis</i>	4.0	38.77	Roche 454 GS	PROKKA	34	35
8.	<i>Bacillus licheniformis</i> DSM13	4.22	46.2	Mega-BACE 1000/4000 ABI Prism 377 DNA	ERGO tool	7.2	4
9.	<i>Bacillus megaterium</i> WSH-002	4.14		454 Newbler	Phred/Phrap/Consed		30
10.	<i>Bacillus subtilis</i>	4.21	43.5			–	3
11.	<i>Bacillus subtilis</i> BSn5	4.09	43.85	Illumina Solexa GA IIx	PGAAP	169	55
12.	<i>Bacillus subtilis</i> subsp. spizizenii W23	3.60	43.89	Illumina HiSeq 2000	PGAAP	–	56

ability for sugar utilization as compared to *B. subtilis*. It lacks catabolic pathways for mannose, arabinose and rhamnose, less phosphotransferase system, and sugar transporters. However, the existence of genes for extracellular chitin and chitosan hydrolysis and N-acetylglucosamine utilization reflects the association of this bacterium with insects.¹² *B. cereus* has fewer genes for the degradation of carbohydrates and therefore this group lacks the metabolic versatility for the uptake and assimilation of plant-derived carbohydrates present in the soil as compared to *B. subtilis*.¹³

Horizontal Gene Transfer

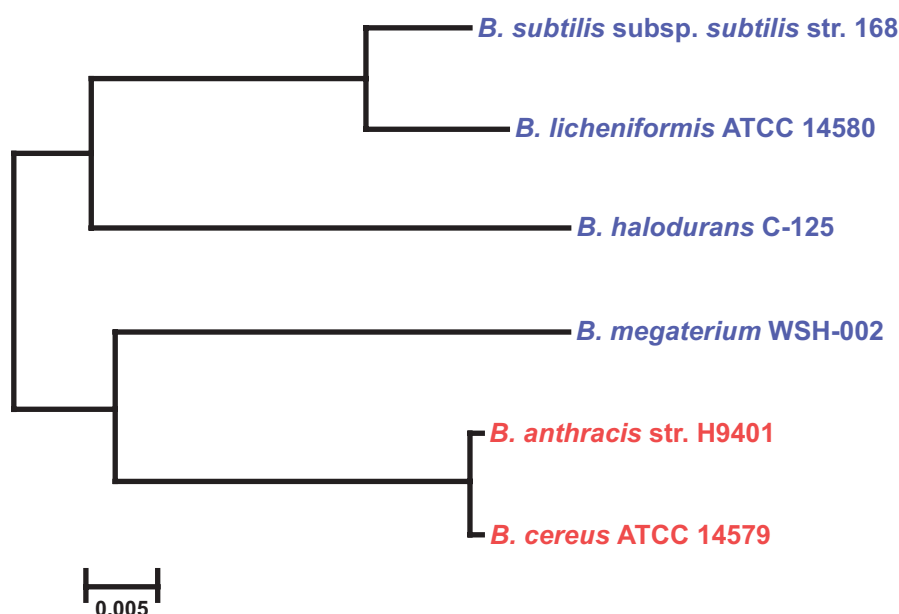
The comparisons among bacterial, archaeal, and eukaryotic genomes show that an important fraction of genes in the prokaryotic genomes have been subjected to horizontal gene transfer (HGT). The occurrence of HGT can be demonstrated by the discovery of pathogenicity islands, i.e., gene clusters that possess pathogenicity determinants in parasitic bacteria, and similar ‘symbiosis islands’ in symbiotic bacteria.^{14,15} The comparative genomic analysis of the enterohemorrhagic *E. coli* strain O157:H7 and the laboratory

K12 strain of *E. coli* has shown that nearly 30% of the genes in the pathogenic *E. coli* strain O157:H7 have been acquired by HGT.¹⁶ Massive archaeal-bacterial HGT has been shown between hyperthermophilic bacteria *Aquifex aeolicus*¹⁷ and *Thermotoga maritima*.¹⁸ Comparisons with mesophilic bacteria showed the presence of more ‘archaeal’ proteins in hyperthermophiles than in mesophiles.¹⁷ In another study, mesophilic archaea with relatively larger genomes, such as *Methanosarcina* and *Halobacterium*, had acquired more ‘bacterial’ genes than thermophilic archaea with smaller genomes.^{19–21} This implies that ~20% of the genes in an organism might have been acquired via archaeal-bacterial HGT in shared habitats.¹⁹

The presence of ten prophages and their remains in *B. subtilis* genome showed the evolutionary role in HGT, mainly in the propagation of bacterial pathogenesis.¹⁰ Alkaliphilic *Bacillus* strains cannot grow or grow poorly at neutral pH. The complete genome sequence of *B. halodurans* C125 has thrown light on the mechanism of adaptation of this strain to alkaline environments. The presence of a number of transposase genes (112 genes) played an evolutionary

**Table 3.** Comparative analysis of some industrially important *Bacillus* spp.

Characteristics	<i>B. subtilis</i>	<i>B. halodurans</i>	<i>B. licheniformis</i>	<i>B. amyloliquefaciens</i>	<i>B. megaterium</i>
Pathways	Embden-Meyerhof-Parnas Glycolytic pathway Tricarboxylic acid cycle (TCA)	TCA cycle aminoacyl-tRNA synthetases	Glycolysis, pentose cycle, TCA cycle glyoxylate bypass	—	Embden-Meyerhof pathway, Krebs cycle glyoxylate pathway
Open reading frames (%)	87	85	86	89.6	83.3
Genome coding					
Predicted number	4100	4066	4208	4325	5124
Conserved with function assigned	2379	2144	—	3691	—
Conserved with unknown function	668	1182	—	211	—
Non-conserved	1053	743	—	423	—
Gene start (%)					
ATG	78	78	—	—	—
TTG	13	10	—	—	—
GTG	9.0	12	—	—	—
Avg. gene Length (bp)	890	877	873	—	—
RNAs					
rRNAs	10	9	7	22	11
tRNAs	86	78	72	72	115
ABC transporters	77	75	—	—	—
Secondary Metabolism	4%	—	82 secreted protein & enzymes	—	—
Phage-associated genes	268	42	71	—	—
Reference	5	9	4	53	29

**Figure 2.** Phylogenetic relationships among *Bacillus* spp. Closely related industrially important *Bacillus* spp. are highlighted in blue and the pathogenic *Bacillus* spp. are highlighted in red.

role in HGT and internal genetic rearrangement in the genome.²² The HGT in two strains of *B. amyloliquefaciens* (DSM7^T and FZB42) has not affected the main metabolic pathways.²³ The role of HGT is unclear as several of these genes are annotated as conserved hypotheticals.

Comparative analysis of the genomes of *B. subtilis* and *E. coli*

The *B. subtilis* and *E. coli* genomes are similar in size. The evolutionary divergence of eubacteria into gram positive and gram negative groups has also been shown by sequencing *B. subtilis* and *E. coli* genomes. Nearly 1000 *B. subtilis* genes have orthologous counterparts in *E. coli* (one-quarter of the genome). These genes neither belong to the prophage-like regions nor to regions coding for secondary metabolism (15% of the *B. subtilis* genome), signifying that a huge portion of these genomes shared similar functions. One hundred putative operons or parts of the operons were conserved between *E. coli* and *B. subtilis*. Twelve of these operons showed a reshuffled gene order (typically, the arabinose operon is *araABD* in *B. subtilis* and *araBAD* in *E. coli*). Some other classes of operons, including major integrated functions like ATP synthesis (*atp* operon) and electron transfer (*cta* and *qox* operons), are also conserved among these microorganisms. Many operons with unknown functions are also conserved in *E. coli* and *B. subtilis*; these could be the main targets for functional analysis of these model genomes.¹⁰

Comparative Analysis of Genomes of the Genus *Bacillus*

The *B. subtilis* genome contains five signal peptidase genes along with the components of secretion apparatus which help in the secretion of macromolecular hydrolases (proteases and carbohydrases in g L⁻¹) and antibiotics.¹⁰ Brown et al²⁴ reported the evolution of a new strain of *B. subtilis*, named WN716, having different colony morphology as compared to known strains. This strain is also lacking sporulation, competence, acetoin production, motility, multiple auxotrophies, and enhanced competitive strength.²⁵ Genome sequencing of this strain revealed no large chromosomal rearrangements, 34 single-nucleotide polymorphisms (SNPs) and +1 frameshifts. In response, many genes were affected including biosynthetic

pathways, sporulation, competence and DNA repair. The whole genome sequencing within the species specified how genetic variation in the nucleotides add to the competitive robustness within species.

The genome sequence of *B. subtilis* natto was compared to its closely related strain *B. subtilis* 168. A number of insertion sequences harbored by *B. subtilis* natto and lacked by the latter strain, showing significant relation to natto production.²⁴ The genome of sporogenic lactic acid bacterium *B. coagulans* highlights the potential of this organism to produce biocatalysts for the production of fuels and chemicals. Comparative analysis of the genome of *B. coagulans* with other *Bacillus* and *Lactobacillus* spp. reveals the presence of some genes common to both genera however this strain falls into the genus *Bacillus*. The presence of D-lactate dehydrogenase (D-LDH) encoding gene marks the potential of this organism for probiotic use in humans.²⁶

The genome of industrially important *B. licheniformis* DSM 13 has been studied in detail. Some industrially significant genes include those which encode carbohydrate-, lipid-, and protein-degrading enzymes. The genes having extracellular protein secretory functions are presented in Table 4. The presence of conserved regulatory DNA motives, the glyoxylate bypass, and the anaerobic ribonucleotide reductase signifies that *B. licheniformis* can grow on acetate and 2, 3-butanediol as well as anaerobically on glucose.¹¹ The complete genome of *B. licheniformis* ATCC 14580 was sequenced and compared with closely related *B. subtilis*. It produces many extracellular enzymes useful in nature in nutrient cycling. The *B. licheniformis* and *B. subtilis* shared organizational similarities. However, their genomes differed in numbers and locations of prophages, transposable elements, a number of extracellular enzymes, and secondary metabolic pathway operons.²⁷ Many genes for exoenzyme production are also encoded in the genome including protease Subtilisin Carlsberg precursor,^{28,29} the glutamic acid-specific protease,^{30,31} the maltogenic α -amylase,³² and the temperature- and pH-stable α -amylase.^{33–36} The analysis of the genome of industrially important alkaliphilic *B. halodurans* offered remarkable and significant information.³⁷ This strain has been reported as a producer of β -galactosidase³⁸ and xylanase.³⁹

The establishment of relation between intermediary metabolism and genome structure, function, and



Table 4. Enzymes identified in the industrially important strain of *B. licheniformis* and the corresponding orthologs present in *B. subtilis*.

Gene ID	Gene function	Gene designation in <i>B. subtilis</i>
BLi00656	α -Amylase precursor (EC 3.2.1.1)	
BLi02117	α -Glucosidase (EC 3.2.1.20)	
BLi03021	α -L-Arabinofuranosidase	<i>abfA</i>
BLi01295	Arabinan endo-1,5-L-arabinase	<i>abnA</i>
BLi04220	Arabinan endo-1,5- α -L-arabinosidase	<i>yxIA</i>
BLi04276	Arabinogalactane endo-1,4- α -galactosidase	<i>yvfO</i>
BLi00447	β -Galactosidase	<i>lacA</i>
BLi04214	β -Glucosidase	<i>bglH</i>
BLi01882	Cellulase (EC 3.2.1.4)	
BLi01881	Cellulose 1,4- β -cellobiosidase	
BLi00338	Chitinase (EC 3.2.1.14)	
BLi02088	Endo-1,4- β -glucanase	<i>bglC</i>
BLi01883	Endo-1,4- β -mannosidase	
BLi00655	Endo-1,4- β -xylanase	<i>yjeA</i>
BLi01880	Endo-1,4-glucanase (EC 3.2.1.4)	
BLi00545	Esterase/lipase	
BLi00340	Glutamic acid-specific protease	<i>mpr</i>
BLi02827	Levanase	<i>sacC</i>
BLi03707	Levanase	<i>yveB</i>
BLi03706	Levansucrase	<i>sacB</i>
BLi03370	Lipase/esterase	
BLi00658	Maltogenic α -amylase (EC 3.2.1.1)	
BLi04019	Minor extracellular serine protease	<i>vpr</i>
BLi01123	Minor extracellular serine protease	<i>epr</i>
BLi01404	Pectate lyase	<i>pel</i>
BLi03053	Pectate lyase	<i>pelB</i>
BLi03741	Pectate lyase	<i>yvpA</i>
BLi03498	Pectin methylesterase	
BLi04177	Peptidase T	<i>pepT</i>
BLi01399	Polysugar-degrading enzyme	<i>ykfC</i>
BLi02863	Protease	<i>yrr</i>
BLi02862	Protease	<i>yrrO</i>

Adapted from Veith et al.⁴

evolution is important. Therefore, *B. subtilis* proteins were compared with themselves and with other complete genomes of *Bacillus* species. Nearly all of the essential genes in *B. subtilis* have orthologs in *B. licheniformis*, and many of them are present in a broad range of bacterial taxa. A number of paralogues are composed of big families of functionally associated proteins engaged in the transport of compounds in and out of the cell or in transcription regulation¹⁰ (Fig. 3).

B. subtilis possesses less genes involved in replication, recombination, and repair showing a relationship with the scarce repetitive elements. On the other hand, the average number of genes related to carbohydrate transport and metabolism are high, as it is a soil microbe

and is in close contact with plants and their products.⁴⁰ Some studies imply that the chromosome remodeling and genome reduction^{41–43} is not a common characteristic of *B. subtilis*. However, *B. pumilus* consists of fewer genes involved in DNA repair, oxidative stress, and acid soluble proteins that lessen the DNA damage due to desiccation and formation of UV resistant spores when compared to *B. subtilis* and related species.^{43,44}

B. megaterium is a commercially available, industrially important non-pathogenic host for the production of products such as vitamin B12, penicillin acylase, and amylases. It employs Sec and Tat systems for effective secretion of proteins into the medium and accounts for a total of 30 secreted proteases genes in the genome. It is also the first biotechnological

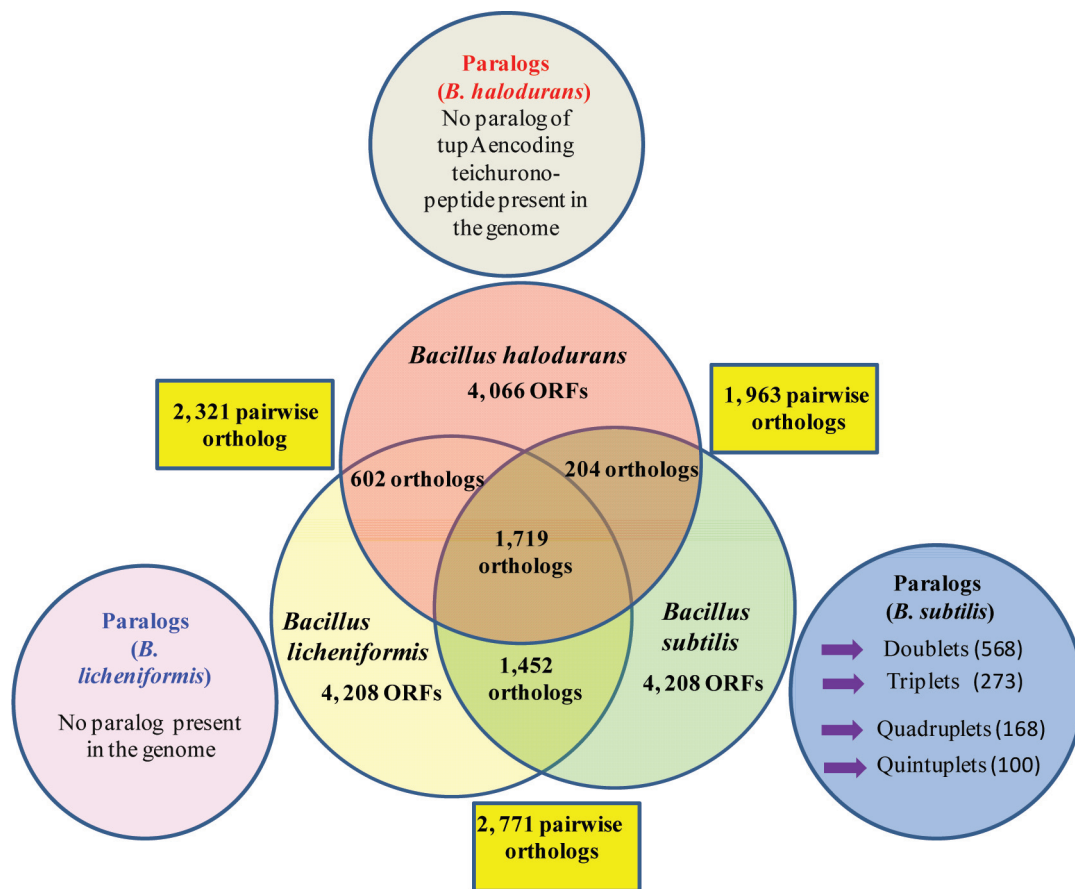


Figure 3. Comparison of the orthologous gene complements of *B. licheniformis* ATCC 14580, *B. subtilis* 168 and *B. halodurans* C-125. Numbers in the rectangular boxes shows the number of pairwise orthologs between neighboring species (BLAST threshold $E = 1 \times 10^{-5}$). Numbers in the outer circles indicates the total number of CDSs predicted in each genome, numbers in areas of overlap represents the number of orthologs predicted by reciprocal BLASTP analysis (threshold $E = 1 \times 10^{-5}$), and the number in the center presents the number of orthologous sequences common to all three genomes. The outer circles show the paralogs in the genome of these *Bacillus* spp (Modified from Rey et al).²⁷

vitamin B₁₂ producer. It is deep-rooted in the *Bacillus* phylogeny and is therefore significant in understanding genome evolution, dynamics, and agility in the Bacilli. The presence of an asymmetric region around the origin of replication was syntenic across the genus, a characteristic feature of the genome architecture of *Bacillus* spp. and sporulating lifestyle. *B. megaterium* is the largest of all Bacilli because of the presence of a second *ftsZ* gene.⁴⁵ The draft genome of *B. megaterium* WSH-002 contains 9.26% of genes responsible for the synthesis and secretion of proteins.⁴⁶

Read et al¹² sequenced and analyzed the complete genome sequence of the chromosome of *B. anthracis* Ames for understanding anthrax pathogenesis. Many proteins that contributed to pathogenicity (haemolysins, phospholipases, and iron acquisition functions) and surface proteins, as well as the targets for vaccines and drugs have been identified. The

B. anthracis genome was compared with the closely related *B. cereus* and *B. thuringiensis* which shared similarity of chromosomal genes but are not associated with anthrax. The high pathogenicity of *B. anthracis* H9401 is due to a tripartite exotoxin and a poly-D-glutamic acid capsule, the main virulence determinants, responsible for complete pathogenicity and are encoded by two plasmids, pXO1 and pXO2.^{47–49} *B. cereus* is an opportunistic pathogen that causes food poisoning and is closely related to *B. anthracis* (animal and human pathogen) and *B. thuringiensis* (insect pathogen). Ivanova et al¹³ reported sequencing and analysis of *B. cereus* ATCC 14579 and compared it with another pathogenic strain *B. anthracis* A2012. The pathogenicity related genes required for invasion, establishment, and propagation of bacteria in the host are well known in *B. anthracis* and are also present in *B. cereus*, showing the similarity among the



strains. Whole genome sequence of *B. cereus* reveals the presence of protein coding sequences (CDSs) for pathogenicity that indicates the relatedness of *B. cereus* to *B. anthracis* and *B. thuringiensis*. Nearly 75%–80% genes are conserved between *B. cereus* ATCC 14579 and *B. anthracis* A2012, signifying that both have a common ancestor. The analysis of the metabolic potential encoded by the sets of common genes challenges the assumption of the cereus group ancestor being a soil bacterium. The characteristic feature of soil bacteria (*Streptomyces* spp. or *B. subtilis*) is the existence of multiple carbohydrate catabolic pathways, as a variety of carbohydrates are present in the soil and plant-derived material is the major source of nutrients. A total of 41 genes for degradation of carbohydrate polymers were identified in the *B. subtilis* genome, in contrast to only 14 and 15 CDSs in *B. cereus* and *B. anthracis*, respectively. Furthermore, a total of 51 and 48 protease-encoding CDSs were identified in *B. cereus* and *B. anthracis*, respectively, as compared to only 30 in *B. subtilis*. It has been suggested on the basis of certain observations that the insect intestine may have been the natural habitat for the common ancestor of the cereus group. The major collection of antibiotic resistance genes are also the characteristic feature of *B. cereus* group. This underlines the probability of the cereus group ancestor as an opportunistic insect pathogen than a benign soil bacterium and the nature and origin of the *B. cereus*.

Shivaji et al⁵⁰ have recently sequenced the complete genome of *B. isronenes* isolated from an air sample collected at an altitude of 27 to 30 kilometers. As it survives in the upper atmosphere and exposed to UV radiation, it carries a *uvrE* gene encoding a UV DNA damage endonuclease enzyme responsible for a novel form of excision repair of DNA damaged by UV light.⁵¹ A number of antibiotic resistance proteins (penicillin acylase 2 precursor, putative niacin/nicotinamide, erythromycin esterase, putative vancomycin resistance protein, tunicamycin resistance protein, putative phosphinothricin acetyltransferase, daunorubicin/doxorubicin resistance ATP binding protein, daunorubicin, doxorubicin, and fosmidomycin resistance) are present in the genome of *B. isronenes*. The genome of this novel bacterial strain can be useful in comparative genomics among

phylogenetically related *Bacillus* isolates from different environments.

Conclusions

The genome sequences of *Bacillus* spp. provide a wealth of information related to gene conservation, diversity among species and systematic information, which cannot be obtained by any other approach. The understanding of the biochemistry of the organism also offers clues regarding its adaptation to the extreme environmental conditions. It can also be applied in genotype association studies, mutation screening, evolutionary studies, and environmental profiling of microorganisms. Genome sequencing has provided insights into the genetic framework of the microbial world and is a leading light of advancing technologies such as microarrays and proteomics, which have reinvigorated the field of microbiological research. There is still a need to explore new industrially important *Bacillus* species which possess novel genes which encode hitherto unknown products for a variety of applications.

Author Contributions

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Competing Interests

Authors disclose no potential conflicts of interest.

Disclosures and Ethics

As a requirement of publication the authors have provided signed confirmation of their compliance with ethical and legal obligations including but not limited to compliance with ICMJE authorship and competing interests guidelines, that the article is neither under consideration for publication nor published elsewhere, of their compliance with legal and ethical guidelines concerning human and animal research participants (if applicable), and that permission has been obtained for reproduction of any copyrighted

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