Print this Page

Looking for the most current news, updates, and articles relating to microbiology, go to The American Society for Microbiology educational website **Microbe World**.

To search the entire book, enter a term or phrase in the form below

Search

Google™ Custom Search

Web Review of Todar's Online Textbook of Bacteriology. *"The Good, the Bad, and the Deadly"*.

Tag words: bacteria, aerobic bacteria, endospore, spores, Bacillus, B. cereus, B. anthracis, B. thuringiensis, B. subtilis

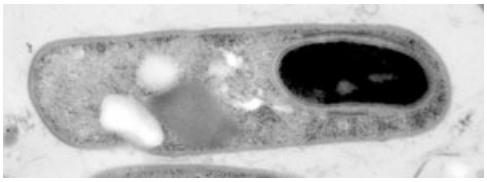
Gram-positive, aerobic endospore-forming bacteria

TAXONOMY: THE GENUS BACILLUS

Kingdom: Bacteria
Phylum: Firmicutes
Class: Bacilli
Order: Bacillales
Family: Bacillaceae
Genus: Bacillus

The Genus *Bacillus* (page 1)

(This chapter has 6 pages)

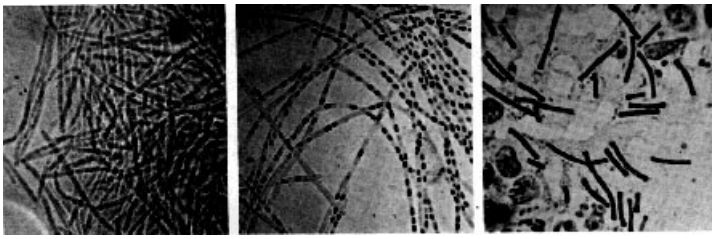


Transmission E.M. of *Bacillus megaterium*.

Gram-positive, Aerobic or Facultative Endospore-forming Bacteria

In 1872, Ferdinand Cohn, a contemporary of Robert Koch, recognized and named the bacterium ***Bacillus subtilis.*** The organism is **Gram-positive**, capable of **growth in the presence of oxygen**, and forms a unique type of resting cell called an **endospore**. The organism represented what was to become a large and diverse **genus** of bacteria named ***Bacillus***, in the Family ***Bacillaceae.***

Koch relied on Cohn's observations in his classic work (1876), *The etiology of anthrax based on the life history of Bacillus anthracis*, which provided the first proof that a specific microorganism could cause a specific disease.



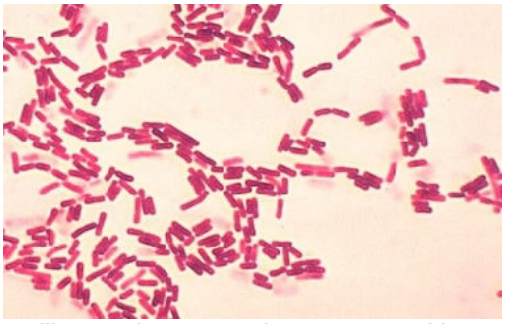
Robert Koch's original photomicrographs of *Bacillus anthracis.* In 1876, Koch established by careful microscopy that the bacterium was always present in the blood of animals that died of anthrax. He took a small amount of blood from such an animal and injected it into a healthy mouse, which subsequently became diseased and died. He was able to recover the original anthrax organism from the dead mouse, demonstrating for the first time that a specific bacterium is the cause of a specific disease.

The genus *Bacillus* remained intact until 2004, when it was split into several families and genera of endospore-forming bacteria, justifiable on the basis of ssRNA analysis. In order to accommodate former members of the genus *Bacillus* covered in this chapter, its title has been changed to "**Gram-positive aerobic or facultative endospore-forming bacteria**".

The unifying characteristic of these bacteria is that they are **Gram-positive**, form **endospores**, and **grow in the presence of O_2**. The trivial name assigned to them is **aerobic sporeformers**.

The ubiquity and diversity of these bacteria in nature, the unusual resistance of their endospores to chemical and physical agents, the developmental cycle of endospore formation, the production of antibiotics, the toxicity of their spores and protein crystals for many insects, and the pathogen *Bacillus anthracis,* have attracted ongoing interest in these bacteria since and Cohn and Koch's discoveries in the 1870s.

There is great diversity of physiology among the aerobic sporeformers, not surprising considering their recently-discovered phylogenetic diversity. Their collective features include degradation of most all substrates derived from plant and animal sources, including cellulose, starch, pectin, proteins, agar, hydrocarbons, and others; antibiotic production; nitrification; denitrification; nitrogen fixation; facultative lithotrophy; autotrophy; acidophily; alkaliphily; psychrophily; thermophily; and parasitism. Endospore formation, universally found in the group, is thought to be a strategy for survival in the soil environment, wherein these bacteria predominate. Aerial distribution of the dormant spores probably explains the occurrence of aerobic sporeformers in most habitats examined.



Bacillus coagulans. **Gram stain. CDC. Gram-positive or Gram-negative? The cell wall structure of endospore-forming bacteria is consistent with that of Gram-positive bacteria, and young cultures stain as expected. However, many sporeformers rapidly become Gram-negative when entering the stationary phase of growth.**

Classification and Phylogeny

Early attempts at classification of *Bacillus* species were based on two characteristics: aerobic growth and endospore formation. This resulted in tethering together many bacteria possessing different kinds of physiology and occupying a variety of habitats. Hence, the heterogeneity in physiology, ecology, and genetics, made it difficult to categorize the genus *Bacillus* or to make generalizations about it.

In **Bergey's Manual of Systematic Bacteriology (1st ed. 1986),** the G+C content of known species of *Bacillus* ranges from 32 to 69%. This observation, as well as DNA hybridization tests, revealed the genetic heterogeneity of the genus. Not only was there variation from species to species, but there were sometimes profound differences in G+C content within strains of a species. For example, the G+C content of the *Bacillus megaterium* group ranged from 36 to 45%.

In **Bergey's Manual of Systematic Bacteriology (2nd ed. 2004)**, phylogenetic classification schemes landed the two most prominent types of endospore-forming bacteria, clostridia and bacilli, in two different **Classes** of **Firmicutes**, **Clostridia** and **Bacilli**. **Clostridia** includes the Order ***Clostridiales*** and Family ***Clostridiaceae*** with 11 genera including, ***Clostridium.*** **Bacilli** includes the Order ***Bacillales*** and the Family ***Bacillaceae.*** In this family there 37 new genera on the level with ***Bacillus.*** This explains the heterogeneity in G+C content observed in the 1986 genus *Bacillus.*

The phylogenetic approach to *Bacillus* taxonomy has been accomplished largely by analysis of 16S rRNA molecules by oligonucleotide sequencing. This technique, of course, also reveals phylogenetic relationships. Surprisingly, *Bacillus* species showed a kinship with certain nonsporeforming species, including *Enterococcus, Lactobacillus*, and *Streptococcus* at the Order level, and *Listeria* and *Staphylococcus* at the Family level. Otherwise, some former members of the genus *Bacillus* were gathered into new Families, including *Acyclobacillaceae*, *Paenibacillaceae* and *Planococcaceae*, now on the level with *Bacillaceae*. Most of the bacteria discussed in this article come from one of these four Families. Their taxonomic hierarchy (Bergey's 2004) is Kingdom: **Bacteria**; Phylum: **Firmicutes**; Class: **Bacilli**; Order: **Bacillales**; Family: **Acyclobacillaceae** (genus: **Acyclobacillus**); Family: **Bacillaceae** (genus: **Bacillus**, **Geobacillus**); Family: **Paenibacillaceae** (genus: **Paenibacillus**, **Brevibacillus**); Family: **Planococcaceae** (genus: **Sporosarcina**).

Notable former members of the genus *Bacillus* that have been moved to new families and/or genera are given in the table below.

Table 1. Important taxonomic reassignments in the Genus *Bacillus* (1986-2004).

Bergey's Manual of Systematic Bacteriology (1st ed. 1986)	**Bergey's Manual of Systematic Bacteriology (2nd ed. 2004)**,
Bacillus acidocalderius	*Acyclobacillus acidocalderius*
Bacillus agri	*Brevibacillus agri*
Bacillus alginolyticus	*Paenibacillus alginolyticus*
Bacillus amylolyticus	*Paenibacillus amylolyticus*
Bacillus alvei	*Paenibacillus alvei*
Bacillus azotofixans	*Paenibacillus azotofixans*

Bacillus brevis	*Brevibacillus brevis*
Bacillus globisporus	*Sporosarcina globisporus*
Bacillus larvae	*Paenibacillus larvae*
Bacillus laterosporus	*Brevibacillus laterosporus*
Bacillus lentimorbus	*Paenibacillus lentimorbus*
Bacillus macerans	*Paenibacillus macerans*
Bacillus pasteurii	*Sporosarcina pasteurii*
Bacillus polymyxa	*Paenibacillus polymyxa*
Bacillus popilliae	*Paenibacillus popilliae*
Bacillus psychrophilus	*Sporosarcina psychrophilia*
Bacillus stearothermophilus	*Geobacillus stearothermophilus*
Bacillus thermodenitrificans	*Geobacillus thermodenitrificans*

chapter continued

Refresh | Next Page