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◆ 연구관심분야 :

*Bacillus*균 유전체 해독 및 기능분석

*Bacillus*균 분화제어 및 응용

B. thuringiensis 생물농약 개발

효소생산 *Bacillus* 산업균주 개발

◆ 학력

1976. 3. ~ 1980. 2. 서울대학교 농과대학 농화학과 졸업 (농학사)

1980. 3. ~ 1982. 2. 한국과학기술원 생물공학과 석사학위 취득 (이학석사)

1982. 3. ~ 1987. 2. 한국과학기술원 생물공학과 박사학위 취득 (이학박사)

◆ 주요경력

2002. 2 ~ 현 재 유전체연구센터 미생물유전체연구팀장

1998. 3 ~ 현 재 한국생명공학연구원 책임연구원

1987. 3 ~ 1998. 2 KIST부설 유전공학센터 선임연구원

1996. 2 ~ 1999. 8 미생물분자유전학 RU장

1991. 6 ~ 1992. 8 뉴욕 Public Health Research Institute 에서 연수(Post. Doc.)

◆ 학회 활동 / 수상 / Honors

한국미생물·생명공학회 평의원

한국분자·세포생물생물학회 회원

한국농화학회 회원

한국유전체학회 회원

◆ 연구 실적 요약

• 학술잡지 논문발표 : 39 편

• 학술컨퍼런스 논문발표 : 25 편

• 국제학회 기조연설, 초청강연, 초청세미나 : 5 회

• 특허 : 6 건 (국제특허 1 건 포함)

• 저서/edited books : 1 권

• 연구과제 프로젝트 : 20 건

Genome Sequencing of the Plant-Probiotic Bacterium *Paenibacillus polymyxa* E681

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Haeyoung Jeong,⁴ Soo-Keun Choi,¹ Cheol-Goo Hur,²
Tae Kwang Oh,³ Young Ho Moon,⁴ and Chang Seuk Park⁵

¹ Genome Research Center, KRIBB

² National Center for Genome Information

³ Division of Life Science, KRIBB

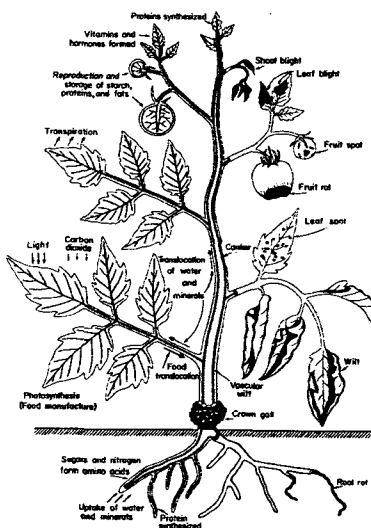
⁴ Genomics Center, GenoTech Corporation

⁵ Gyeongsang National University

Bacteria Inhabiting Plants

Friends

Acetobacter
Azoarcus
Azorhizobium
Azospira
Azospirillum
Azotobacter
Bacillus
Bradyrhizobium
Burkholderia
Enterobacter
Herbaspirillum
Mesorhizobium
Paenibacillus
Pantoea
Pseudomonas
Rhizobium
Sinorhizobium
and many others



Foes

Agrobacterium
Brenneria
Burkholderia
Clavibacter
Erwinia
Pantoea
Pectobacterium
'Phytoplasma'
Pseudomonas
Ralstonia
Rhodococcus
Spiroplasma
Streptomyces
Xanthomonas
Xylella
and some others

[Agrios. 1997. Plant Pathology, 4th ed]

Probiotics in Nutrition

Probiotic [Greek] = for life

Lilly & Stillwell (1965) – substance secreted by one microorganism which stimulates the growth of another; *con.* antibiotic

Parker (1974) – organism or substance which contributes to intestinal microbial balance

Fuller (1989) – a live microbial feed supplement which beneficially affects the host animal by improving its intestinal microbial balance

Schrezenmeir & de Vrese (2001) – a preparation of or a product containing viable, defined microorganisms in sufficient numbers, which alter the microflora (by implantation or colonization) in a compartment of the host and by that exert beneficial health effects on the host

Probiotic Bacteria *Bifidobacterium, Lactobacillus, Sacchomyces, etc.*

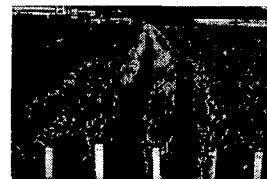
[Teitelbaum & Walker. 2002. Annu Rev Nutr 22:107-138]

Paenibacillus polymyxa, a Plant-Probiotic Bacterium

- [Type species of the genus *Paenibacillus* (Ash et al., 1993)]

- Plant-growth-promoting rhizobacterium (PGPR)

1. Fixes atmospheric nitrogen
2. Produces plant hormones auxin and cytokinin
3. Solubilizes soil phosphorus
4. Enhances soil porosity



[Photo courtesy by Prof. CS Park at GSNU]

- Agent for biological control of plant diseases

1. Antagonizes or suppresses several plant pathogens
2. Induces plants' resistance to biotic and abiotic stress

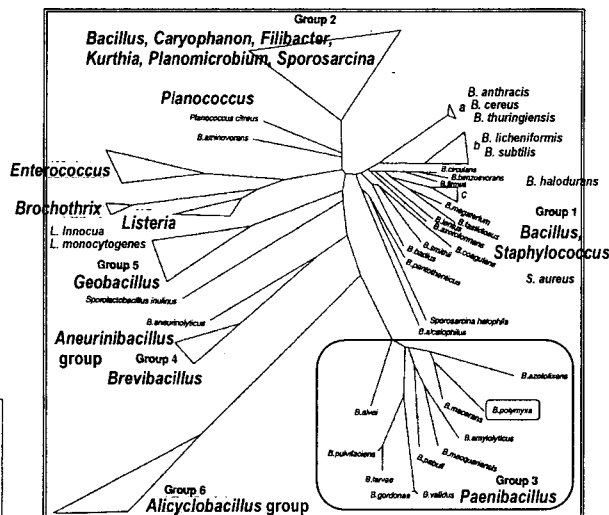
- Bacterium of industrial significance

1. Produces chitinases and many other hydrolytic enzymes
2. Produces a number of antibiotic compounds

The Genus *Paenibacillus*

- Low G+C Gram⁺ bacteria
- Form endospores
- rRNA group 3 bacilli
- *Paeni* + *bacillus* = almost a bacillus
- Includes >30 species (one of the three biggest genera in the *Bacillaceae*)

Species of *Paenibacillus* are often isolated from Korean soil



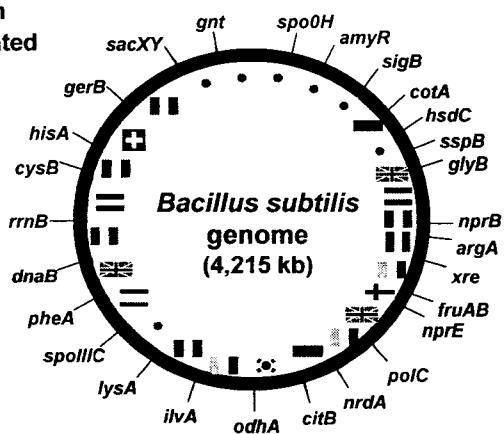
[Ash et al. 1993. *Antonie van Leeuwenhoek* 64: 253-260]

International *Bacillus* Genome Project

The first genome project in which a Korean research team participated

An international consortium involving 25 European, seven Japanese and one Korean laboratories, and two biotechnology companies was established to sequence the *B. subtilis* 168 genome

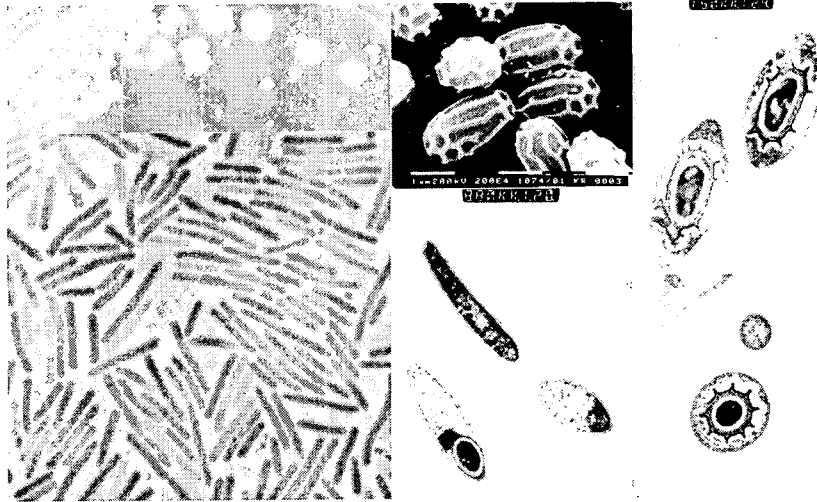
The Korean laboratory sequenced the 53-kb region between the *attSPβ* and *odhA* loci (180°-185°)



[Kunst, F., ... Choi, S.-K., ...Ghim, S.-Y., ... Park, S.-H., ...Shin, B.-S., ... and 146 other authors. 1997. *Nature* 390:249-256]

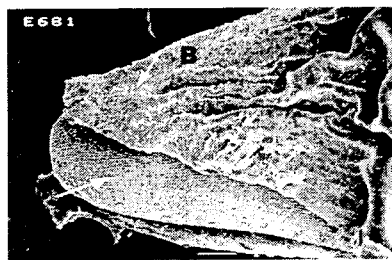
Paenibacillus polymyxa E681

isolated from the rhizosphere of winter barley grown in Chonnam province, Korea

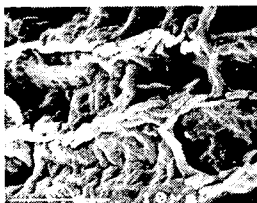


E681 on the Surface of Emerging Root

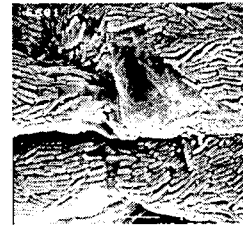
6 hpi



10 hpi

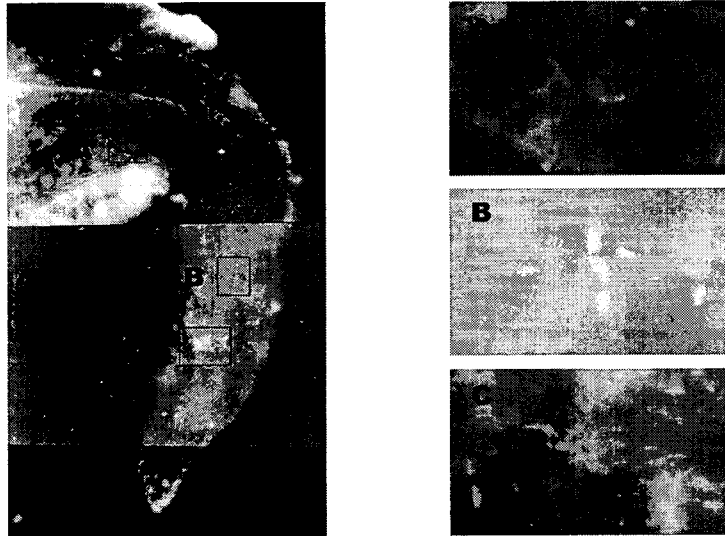


20 hpi



[Photo courtesy by Prof. CS Park at GSNU]

E681 inside the Root Tissue



[Photo courtesy by Prof. CS Park at GSNU]

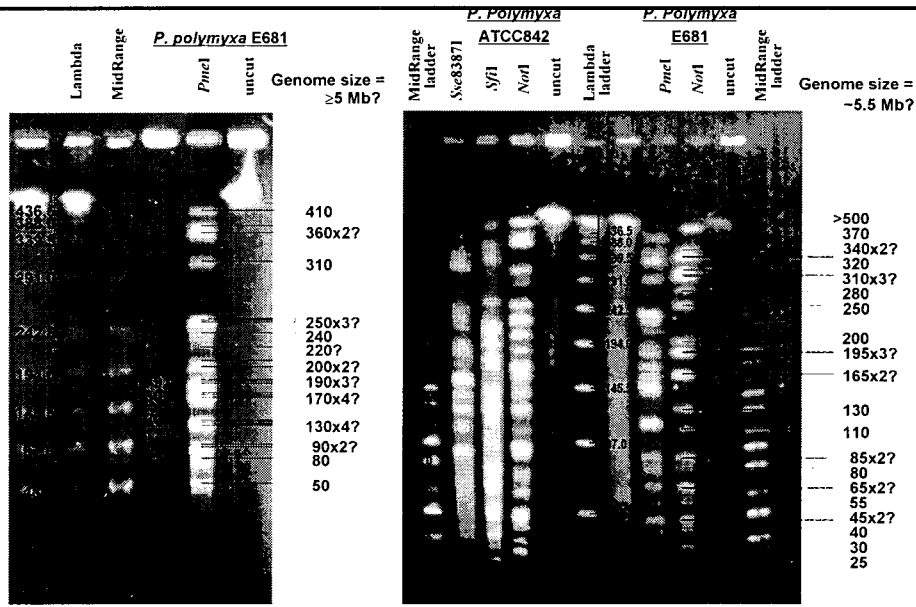
Antibiotic Activity of E681

Organism	Size of Inhibition Zone ¹
<i>Aspergillus spp.</i>	4-5 mm
<i>Botrytis cinerea</i>	>6 mm
<i>Cladosporium fulvum</i>	>6 mm
<i>Colletotricum lagenarium</i>	>6 mm
<i>Fusarium oxysporum</i>	>6 mm
<i>Rhizoctonia solani</i>	>6 mm
<i>Phytophthora capsici</i>	>6 mm
<i>Pythium ultimum</i>	>6 mm
<i>Erwinia carotovora</i>	4-5 mm
<i>Ralstonia solanacearum</i>	4-5 mm
<i>Xanthomonas campestris</i>	4-5 mm

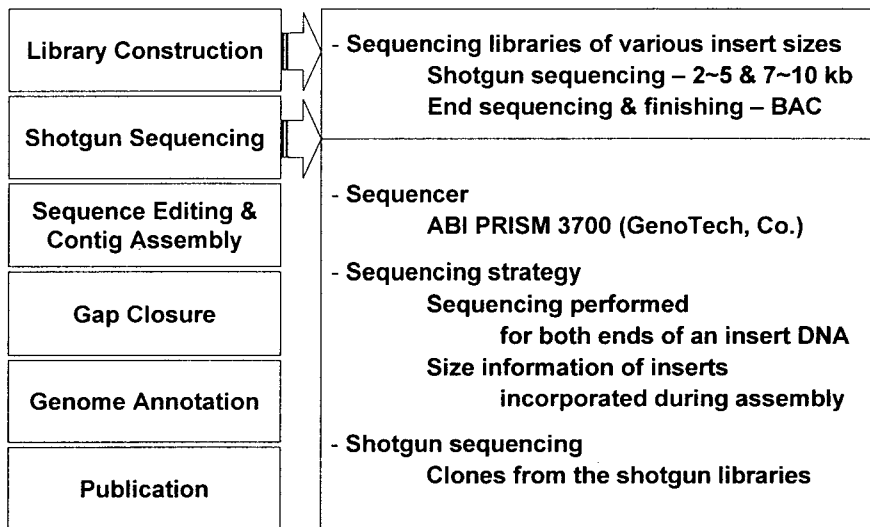
¹ measured after 5 days of co-cultivation

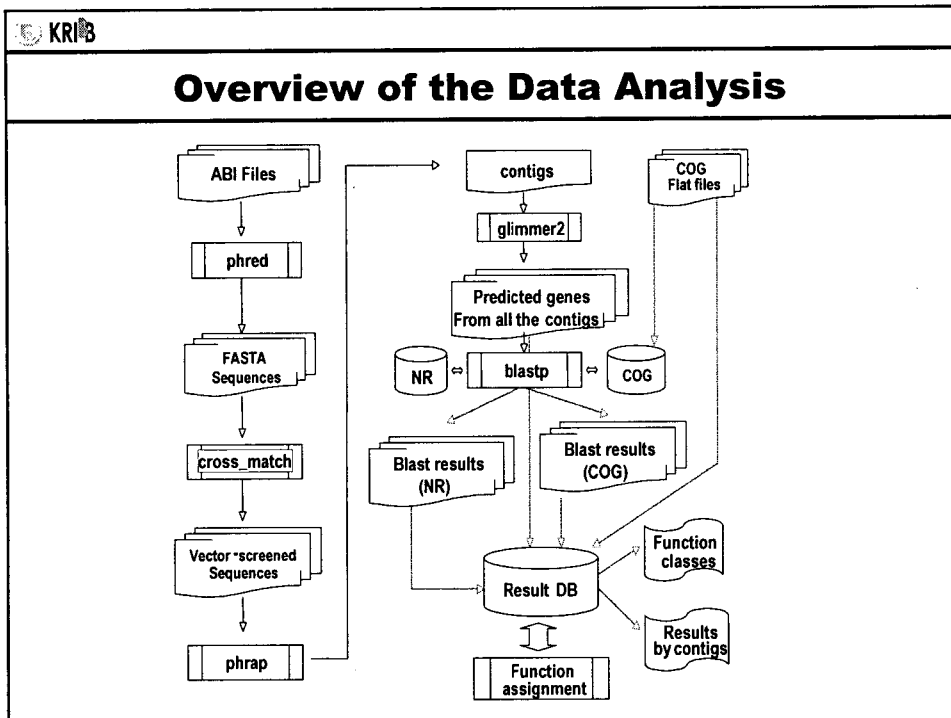
[Ryu. 1998. MS Thesis, GSNU, 110p]

Estimation of the Genome Size of E681



Genomic Libraries & Sequencing Strategy





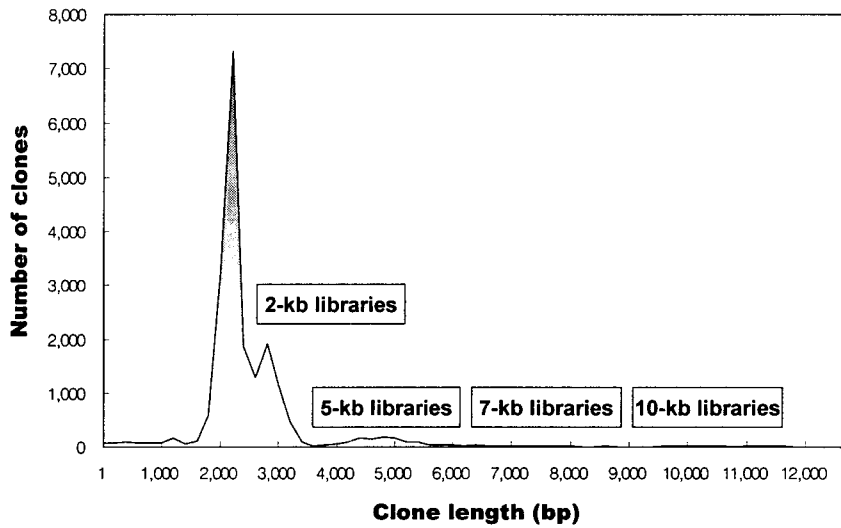
KRI B

Sequencing Libraries and the Number of Reads

Library name	Insert size	Cloning vector	Restriction enzyme	Number of reads
PP01	2 kb	pUC18	<i>Sma</i> I	26,303
PP02	2 kb	pUC18	<i>Sma</i> I	12,384
PP21	2 kb	pUC19	<i>Sma</i> I	14,495
PP21	2 kb	pUC18	<i>Hinc</i> II	
PP31	5 kb	pUC19	<i>Sma</i> I	3,264
PP51	7 kb	pBC KS	<i>Bam</i> HI	1,152
PP71	10 kb	pTB	<i>Sma</i> I	1,152

(as of Feb. 2002)

Sequencing Libraries: Size Distribution of the Inserts



Summary of the Sequencing Results

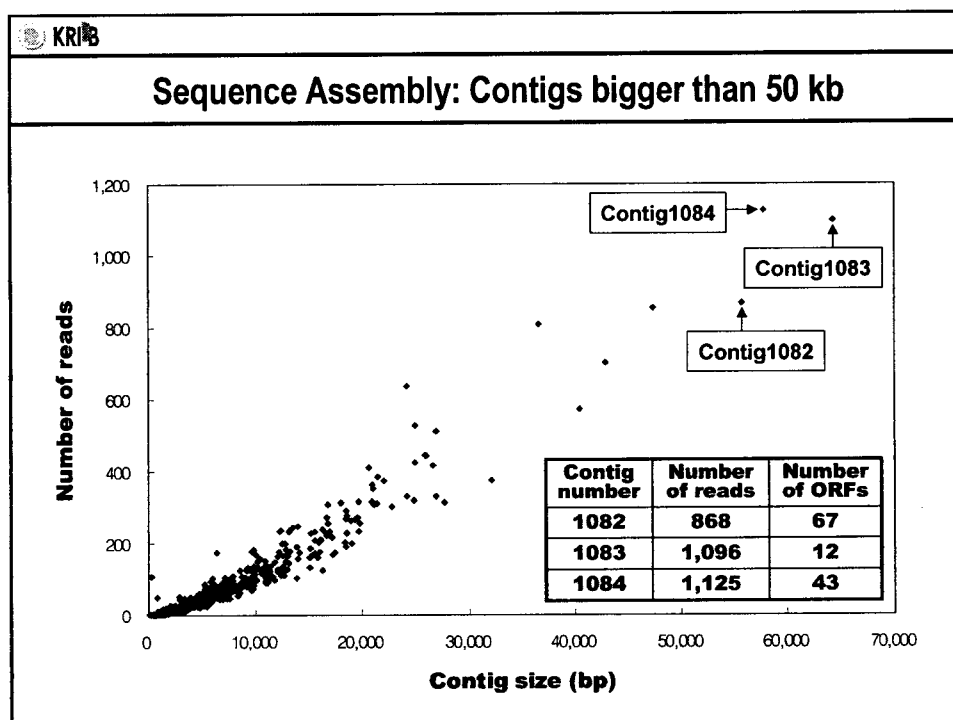
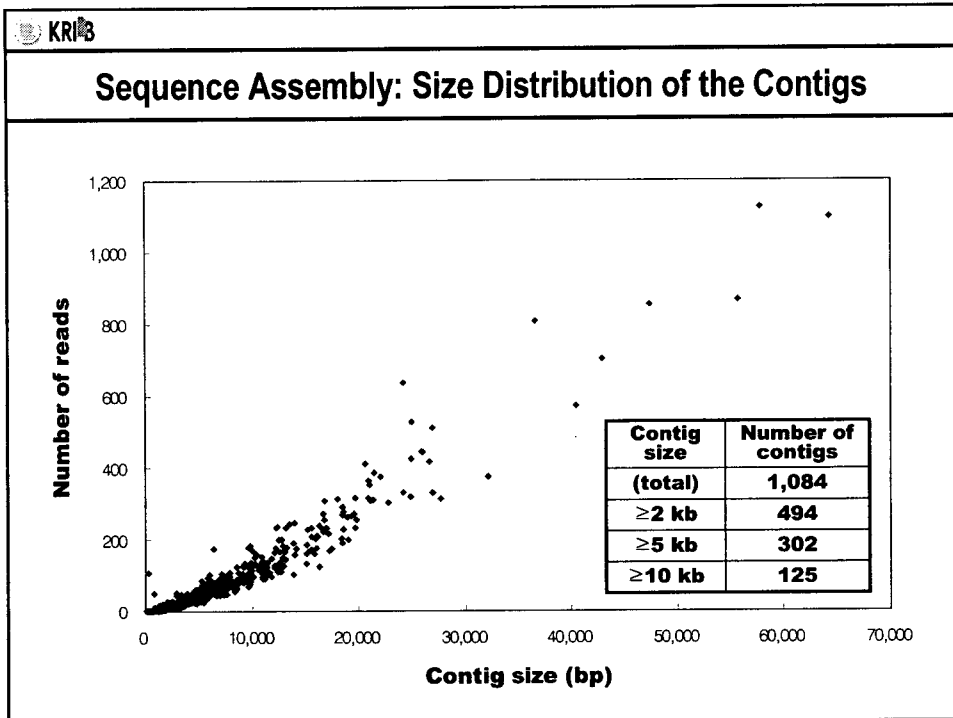
Number of reads	Total read length	Average read length	Trimming condition
58,725	47,548,144 bp	809.7 bp	untrimmed
55,021	31,046,388 bp	564.3 bp	trim_alt /0.050 nonvector >30bp

Number of entries : 55,021

Residue counts : A 8,432,970
 T 8,468,660
 G 7,046,069
 C 7,093,585
 N 5,104
 X 674,710
 Total 31,721,098

Average G+C = 45.55%
 [ATCC842 G+C
 = 44.3% (Tm) or 45.6% (Bd)]

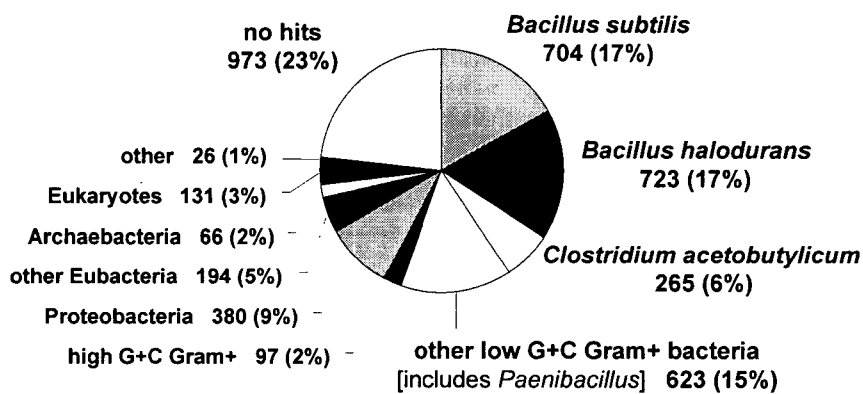
(as of Feb. 2002)



Summary of the Sequence Annotation Results

Category	Number of genes	%
Total number of predicted genes	4,182	100
Functional assignment by COG	2,350	56.2
Homologs in the databases	859	20.5
No functional clues, no homologs	973	23.3

Taxonomic Distribution of Highest BLAST Hits



Functional Assignment based on COG Analysis

Code	Description	E681	COG	E681/COG
J	Translation, ribosomal structure and biogenesis	120	217	55.3%
K	Transcription	319	133	239.8%
L	DNA replication, recombination and repair	149	184	81.0%
D	Cell division and chromosome partitioning	39	32	121.9%
O	Posttranslational modification, protein turnover, chaperones	69	109	63.3%
M	Cell envelope biogenesis, outer membrane	162	155	104.5%
N	Cell motility and secretion	121	133	91.0%
P	Inorganic ion transport and metabolism	225	160	140.6%
T	Signal transduction mechanisms	181	96	188.5%
G	Carbohydrate transport and metabolism	393	170	231.2%
C	Energy production and conversion	158	223	70.9%
E	Amino acid transport and metabolism	373	234	159.4%
F	Nucleotide transport and metabolism	105	85	123.5%
H	Coenzyme metabolism	174	154	113.0%
I	Lipid metabolism	83	75	110.7%
Q	Secondary metabolites biosynthesis, transport and catabolism	164	64	256.3%
R	General function prediction only	487	449	108.5%
S	Function unknown	150	753	19.9%