CODATA06
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Dichotomy of major bacterial phyla inferred from gene arrangement comparisons

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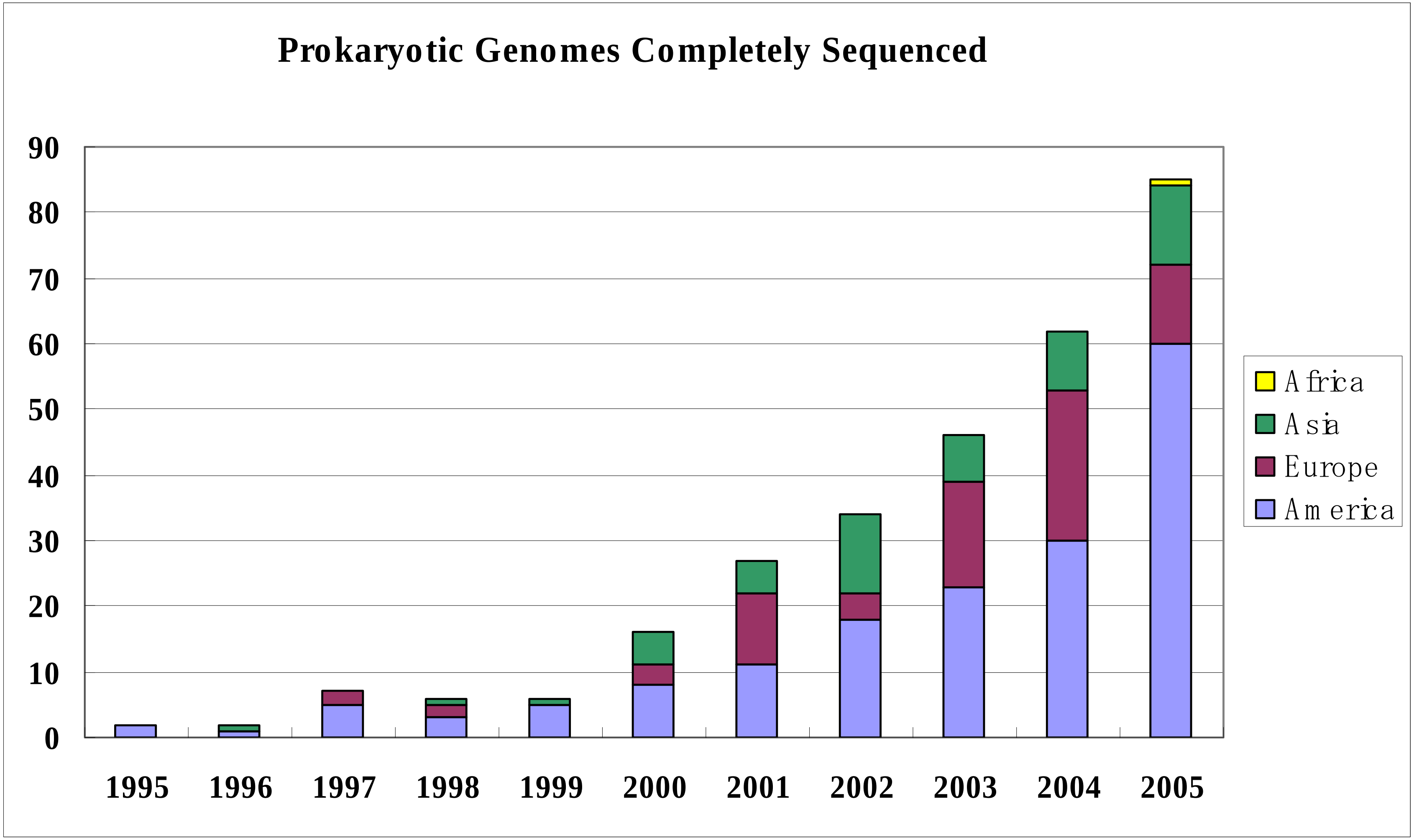

Prokaryotic Genomes Completely Sequenced
90
80
70
60
50
40
30
20
10
0
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
Africa
Asia
Europe
America

		1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	
America													
	USA	2	1	5	3	5	7	11	16	21	28	57	156
	Brazil						1		2	2	2	3	10
Europe													
	France			1				8	1	4	5	3	22
	Germany			1			1		1	4	8	6	21
	UK				1		2	2	1	5	4	2	17
	Sweden				1						4		5
	Denmark							1				1	2
	Spain									2			2
	Italy										1		1
	The Netherlands									1			1
	Switzerland								1				1
	Austria										1		1
Africa													
	South Africa											1	1
Asia													
	Japan		1		1	1	5	5	8	5	6	5	37
	China								3	1	1	4	9
	Korea								1		2	2	5
	Taiwan									1		1	2
	sum	2	2	7	6	6	16	27	34	46	62	85	293

Genome Diversity

Size:

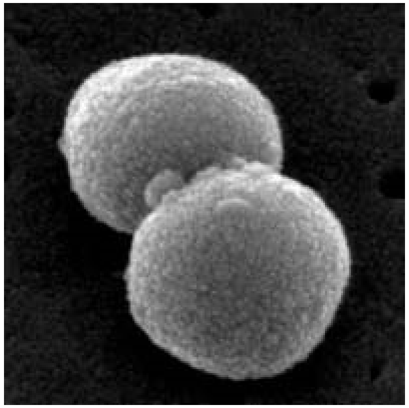
Mycococcus xanthus	9,139,763 bp
Mycoplasma genitalium	580,076 bp

A+T content:

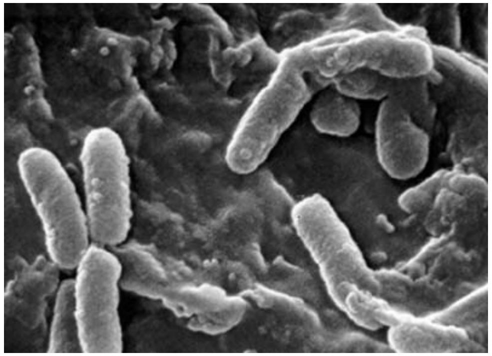
Mycoplasma capricolum	76.2%
Anaeromycobacter dehalogenans	25.1%

Bacterial Shapes

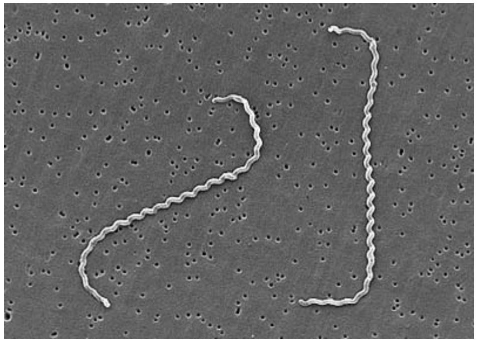
1. The coccus



2. The rod or bacillus



3. The spiral



4. Others

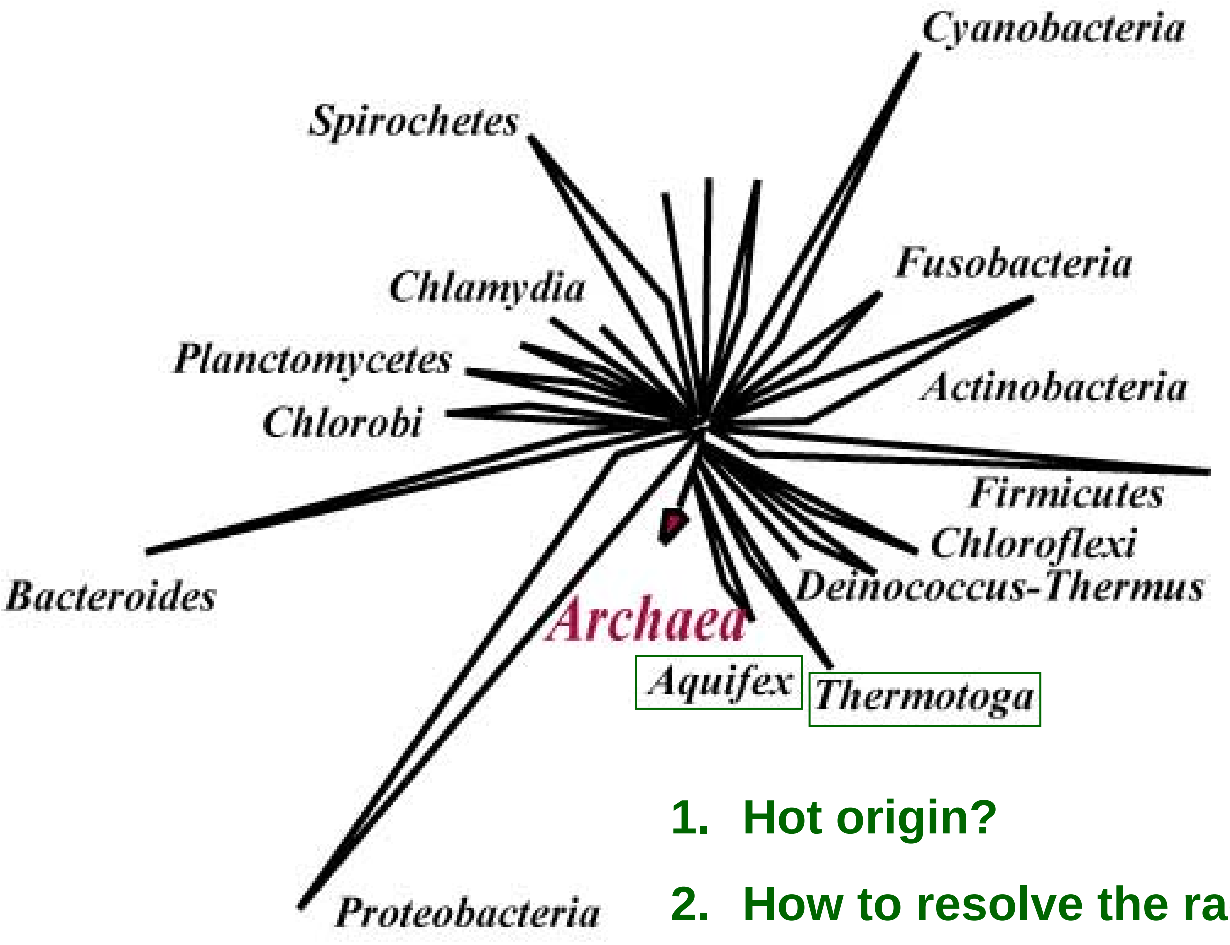
filamentous,

sheathed,

stalked,

etc.

Bacterial Major Phyla based on 16S rRNA Sequences



16S rRNA の比較から作られた系統樹
(Modified from Ludwicg and Klenk, 2001)

1. Hot origin?
2. How to resolve the radiation?

Phylogenomics

1. Amino acid (base) substitutions

(a) Supertree – Combine Multiple Gene Phylogenies

(b) Supermatrix - Concatenation of Multiple Sequences

2. Evolutionary rare changes

(a) Gene-contents methods – Presence/absence of orthologous genes

(b) Genome rearrangements – Entire gene orders

(c) Signature sequence analysis – Insertion/deletion in alignments

(d) Specific gene arrangements – Gene transpositions

Computer search for two arrangements

a-x-b/ c-d in genomes 1 and 2

a-b/ c-x-d in other genomes 3 and 4

1 Transposition of Gtcc

Firmicutes ***Actinobacteria*** ***Thermotoga*** ***Chloroflexi*** ***Deinococcus/Thermus*** ***Fusobacteria***	**Ptgg-Gtcc-Rtct-Hgtg**	***Proteobacteria*** ***Aquifex*** ***Planctomycetes*** ***Spirochetes*** ***Bacteroides*** ***Chlorobi***	**Ygta-Gtcc-Tggt/ Ptgg---Rtct—Hgt**

2 Transposition of *nusB*

Firmicutes ***Actinobacteria*** ***Thermotoga*** ***Deinococcus/Thermus*** ***Fusobacteria***	***efp-(accB-accC)- nusB -folD***	***Proteobacteria*** ***Aquifex*** ***Spirochetes***	***ribC-xthA-ribH- nusB***

3 Transpostion of *yvyD*

Firmicutes ***Actinobacteria*** ***Thermotoga*** ***Chloroflexi***	***comFC- yvyD -secA***	***Proteobacteria*** ***Planctomycetes*** ***Spirochetes***	***rpoN- yvyD -ptsN-fruB***

4 Transposition of *lepA*

Firmicutes ***Actinobacteria*** ***Chloroflexi***	***S20- lepA -hemN***	***Proteobacteria*** ***Cyanobacteria*** ***Chlorobi***	***degQ- lepA -lepB***

Divisions of the major bacterial phyla into Gram-positive bacteria Group (I) and Proteobacteria Group (II)

Phylum	Gtcc	*nusB* (COG0781)	*yvyD* (COG1544)	*lepA* (COG0481)	*rpoC* insert
Gram-positive bacteria	I	I	I	I	-
Thermotoga	I	I	I		-
Chloroflexi	I		I	I	-
Deinococcus-Thermus	I	I			-
Fusobacteria	I	I			+
Proteobacteria	II	II	II	II	+
Aquifex	II	II			+
Planctomycetes	II		II		+
Spirochetes		II	II		+
Bacteroides	II				+
Chlorobi				II	+
Cyanobacteria				II	another insert*
Chlamydia					+

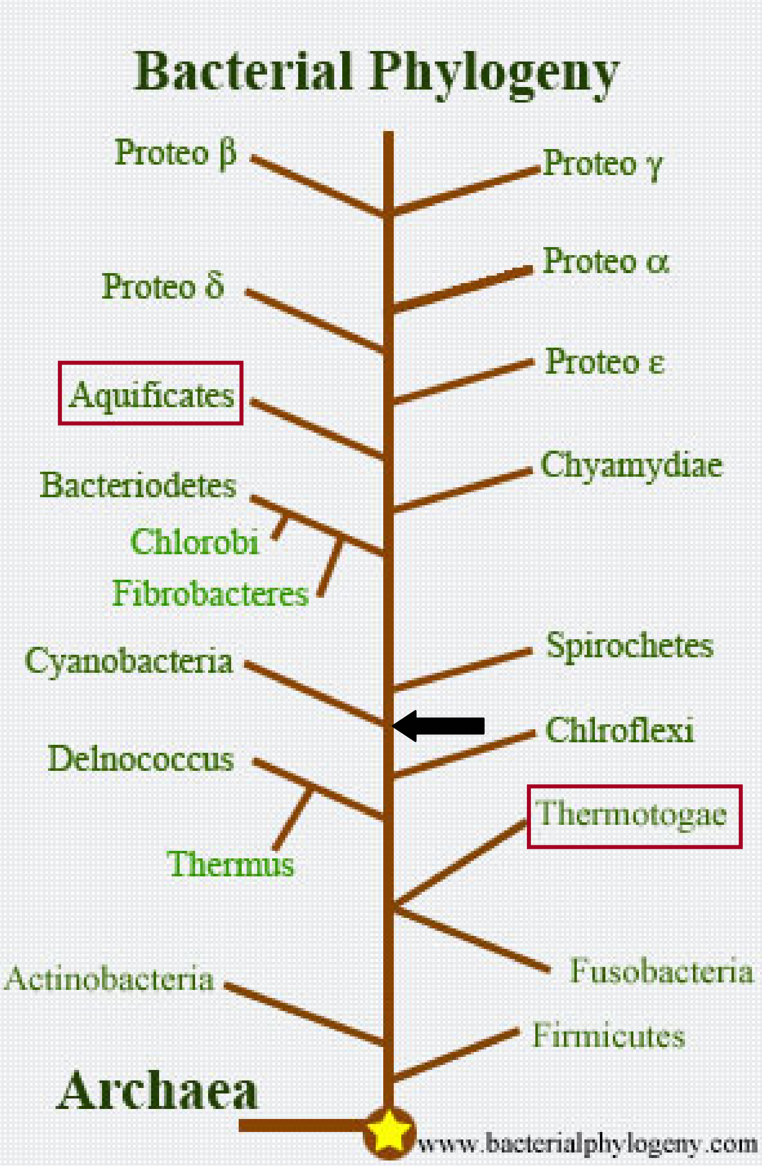
Group Ⅰ

Firmicutes
Actinobacteria
Thermotoga
Chloroflexi
Deinococcus/Thermus
Fusobacteria

Group Ⅱ

Proteobacteria
Aquifex
Planctomycetes
Spirochetes
Bacteroides
Chlorobi

Indel analysis, Gupta RS (2006)



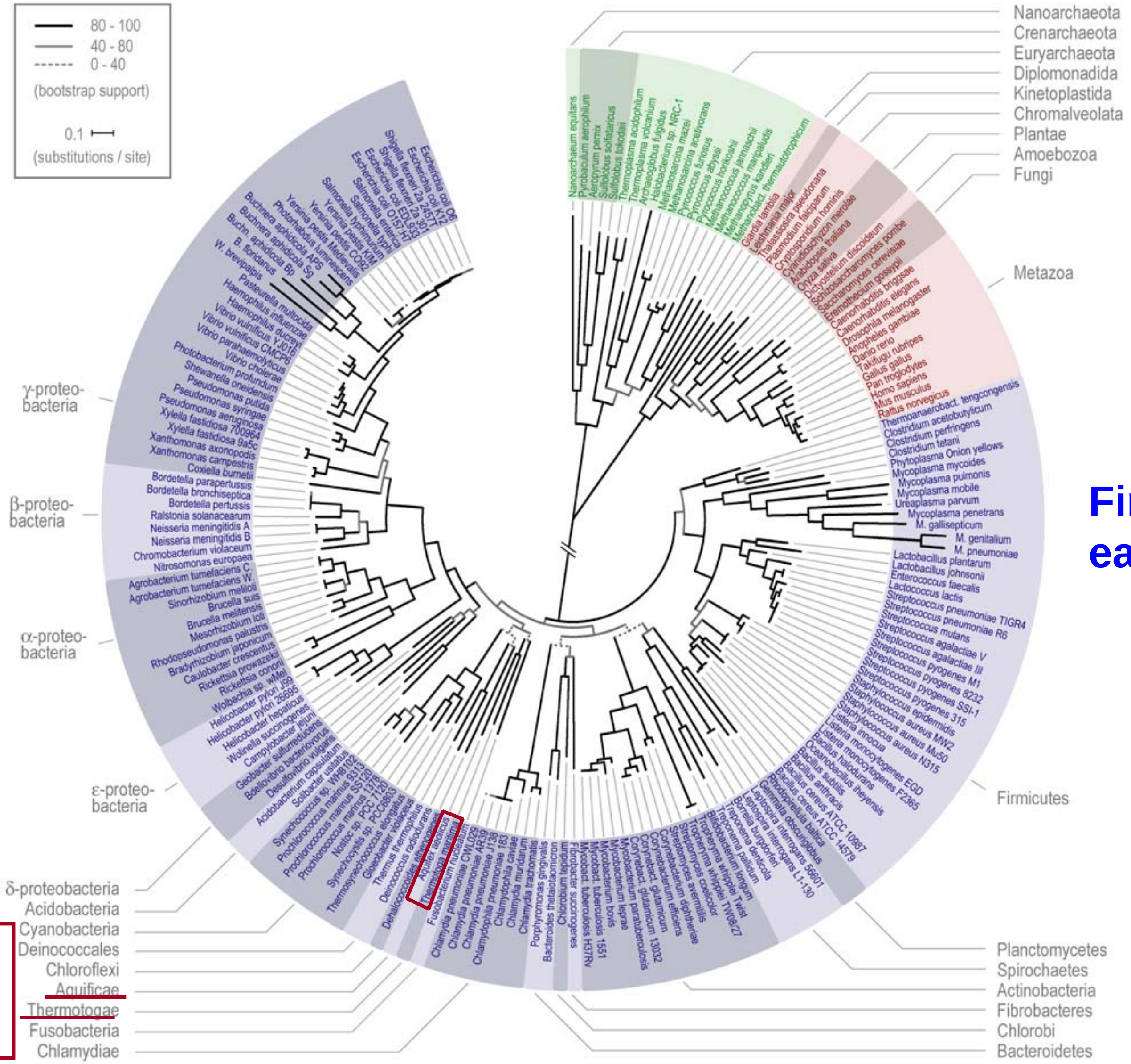
Group II

Proteobacteria
Aquifex
Planctomycetes
Spirochetes
Bacteroides
Chlorobi

Group I

Firmicutes
Actinobacteria
Thermotoga
Chloroflexi
Deinococcus/Thermus
Fusobacteria

Concatenation of 31 proteins, Ciccarelli, et al., Science (2006) **311**,1283



Firmicutes, early

Aquifex

Thermotoga