



M Ű E G Y E T E M 1 7 8 2

BUDAPESTI MŰSZAKI ÉS GAZDASÁGTUDOMÁNYI EGYETEM

Alkalmazott Biotechnológia és Élelmiszertudományi Tanszék

Válogatott fejezetek mikrobiológiából

Dr. Tardy Gábor, Dr. Sveiczler Ákos

Tantárgyprogram

- A baktériumok filogenetikai módszeren nyugvó taxonómiája a Bergey's Manual of Systematic Bacteriology alapján.
 - Elektron transzport lánc működése oxigén és nitrát terminális elektron akceptorokkal
 - Exoelektrogén baktériumok metabolizmusa és felhasználásuk elektromos energia termelésére
 - Mikrobapopulációk és -sejtek növekedése
 - Söripari mikrobiológia – sörrontók és kimutatásuk
 - A klór dioxid titka (*Chlorine Dioxide is a Size-Selective Antimicrobial Agent*)
-



Figure 1-6 Microbiology, 7/e
© Corbis



Figure 1-10 Microbiology, 7/e
National Library of Medicine/SPL/Photo Researchers, Inc.



Figure 9-23 Microbiology, 7/e
Courtesy American Society for Microbiology Archives

DNS hibridizáció

- Extrakció, endonukleázos hasítás
- Melegítés → egyszálú DNS
- Repetítív szekvenciák hibridizációja és kiszűrése
- Maradék szekvenciák jelölése
- Hibridizáltatás saját DNSsel ill. az összehasonlítandó faj DNSével.
- ΔT_m alapján következtetés a homológia fokára

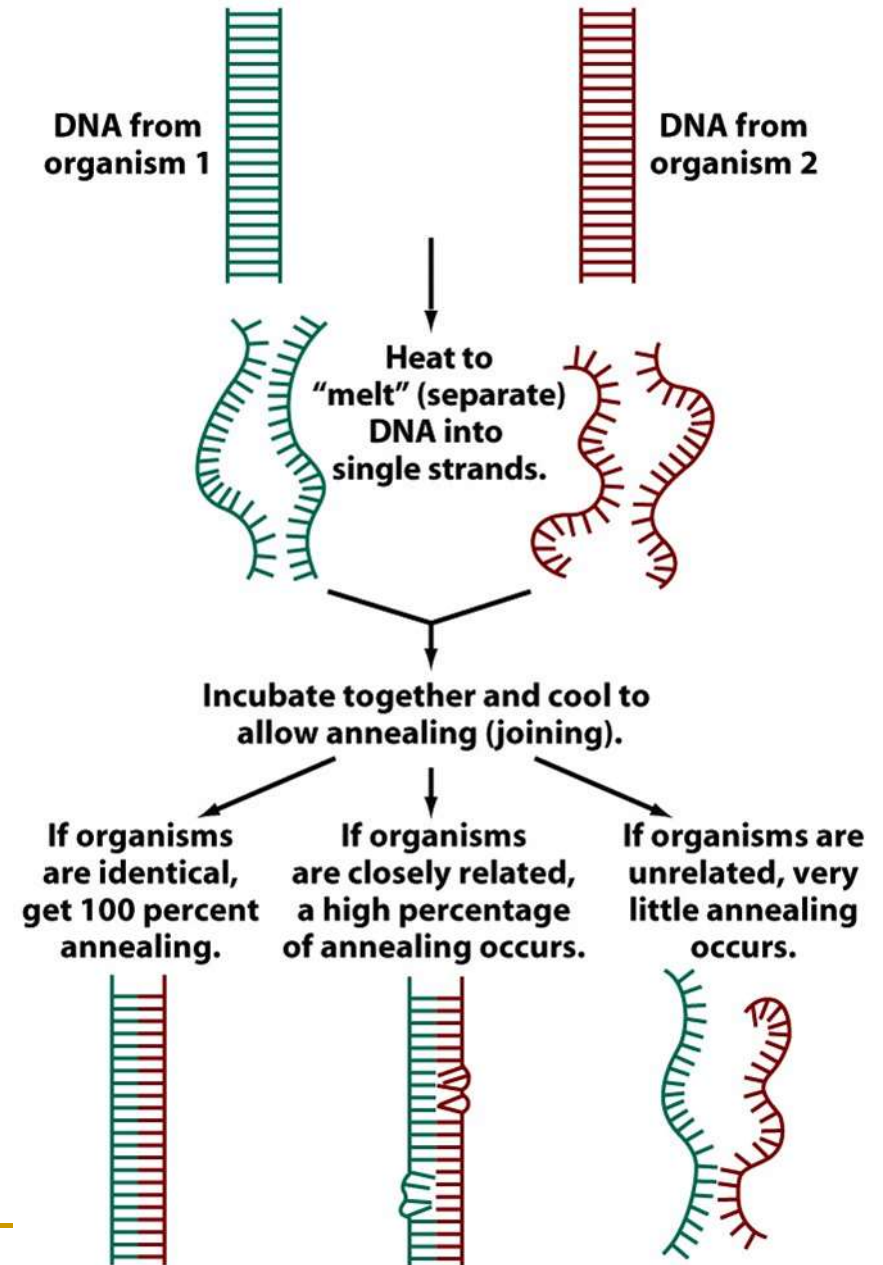
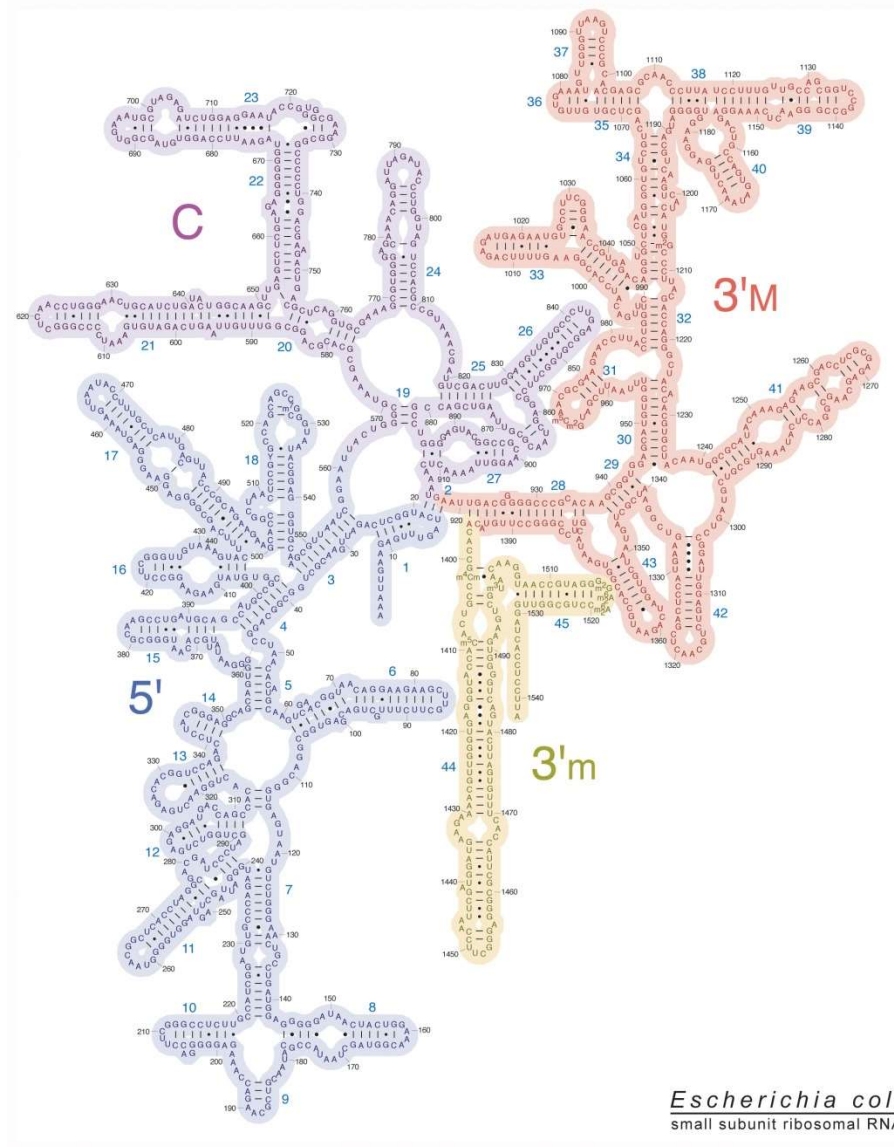


Figure 9-20 Microbiology, 7/e
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16S rRNS



DNS hasonlóság magasabbrendű élőlényekben



98,4%



78%

Az emberhez (Homo sapiens) viszonyítva

Polifázikus taxonómia

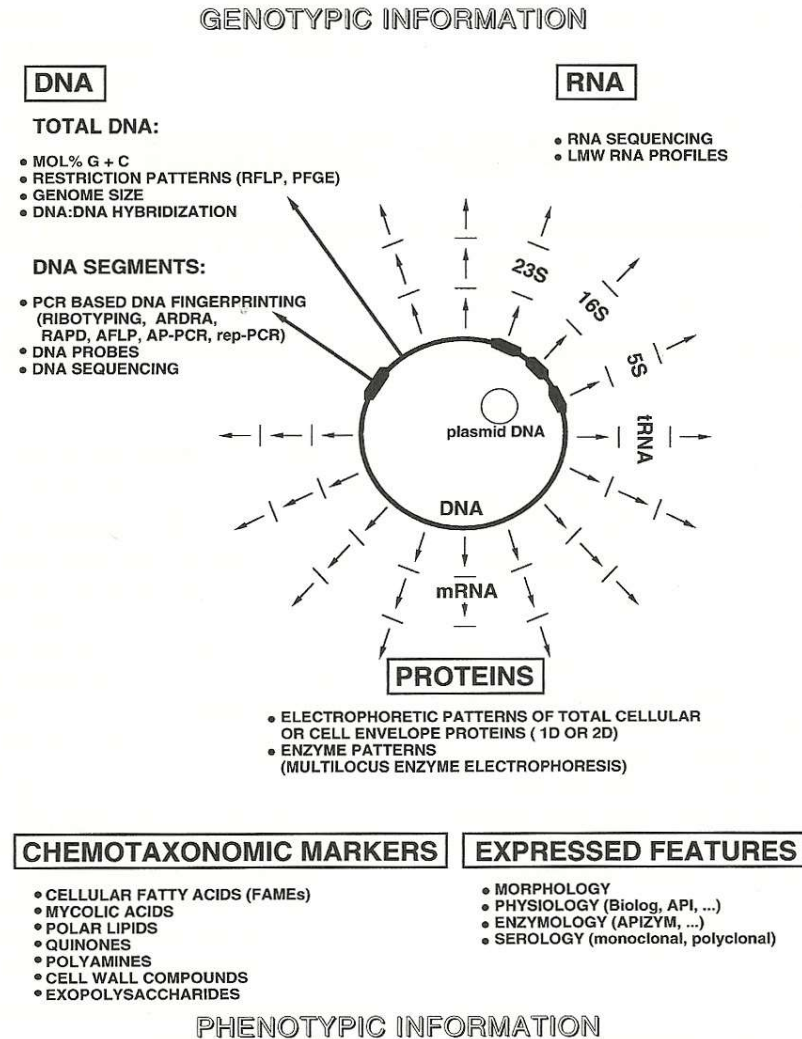
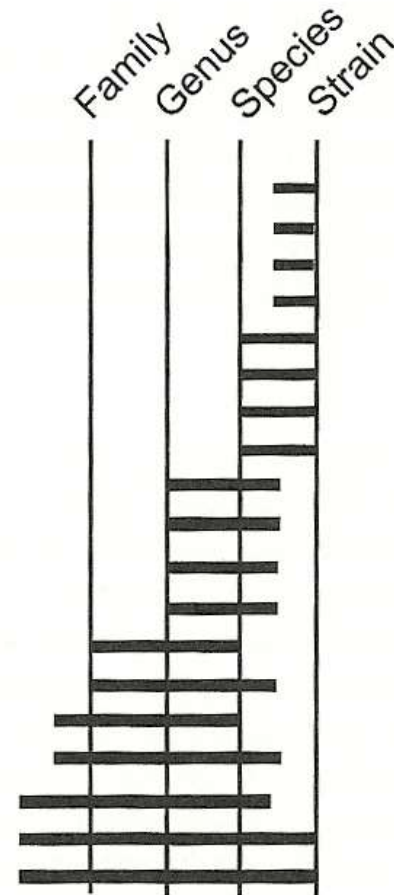


FIGURE 1. Schematic overview of various cellular components and techniques used in polyphasic bacterial taxonomy (adapted from Vandamme et al., 1996a). Abbreviations: AFLP, amplified fragment length polymorphism; AP-PCR, arbitrarily primed PCR; ARDRA, amplified rDNA restriction analysis; FAMEs, fatty acid methyl esters; LMW, low molecular weight; PFGE, pulsed-field gel electrophoresis; RAPD, randomly amplified polymorphic DNA; rep-PCR, repetitive element sequence-based PCR; RFLP, restriction fragment length polymorphism; 1D, 2D, one- and two-dimensional, respectively.

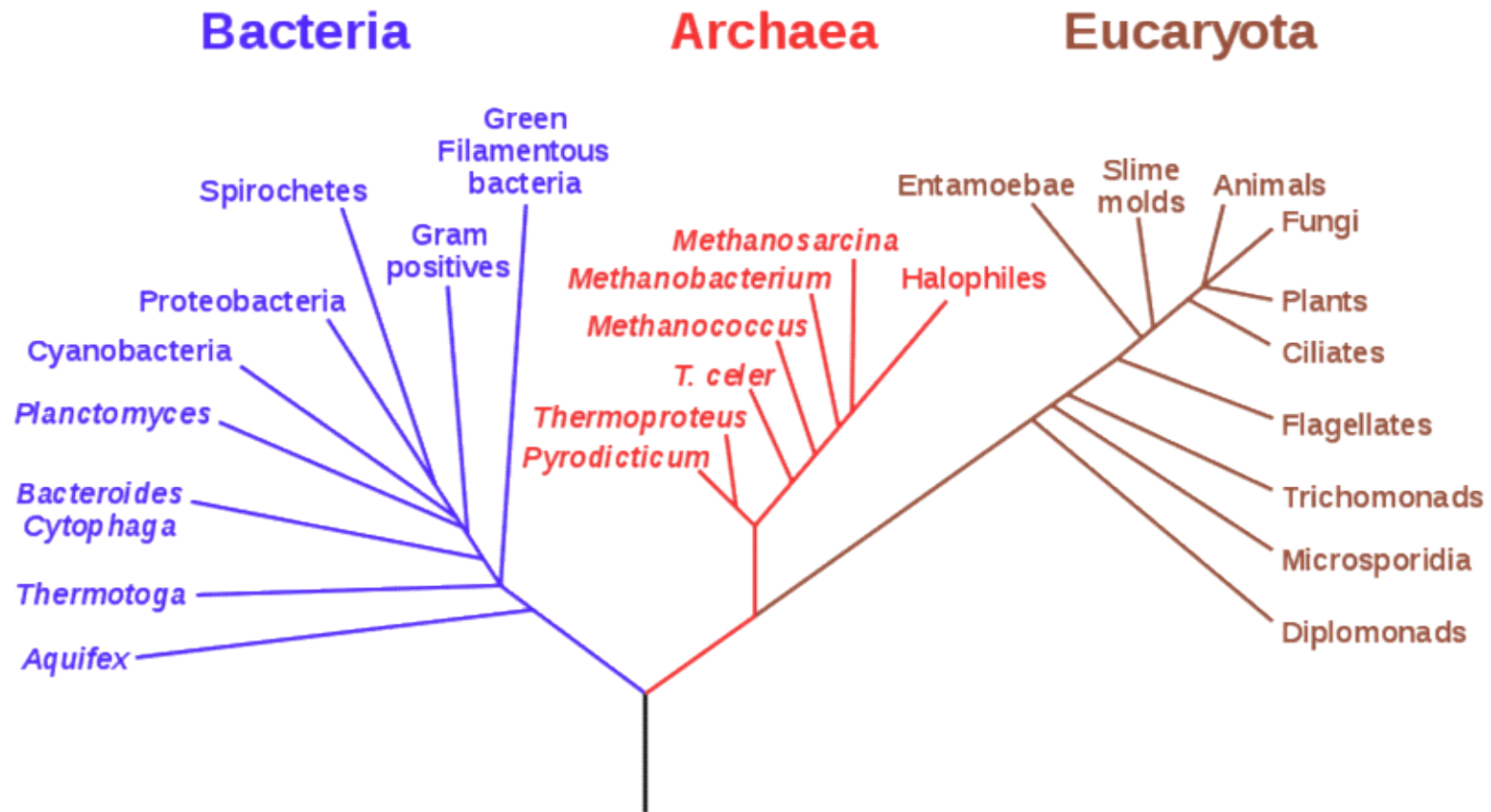
Polifázikus taxonómia

Technique

Restriction fragment length polymorphism (RFLP)
Low frequency restriction fragment analysis (PFGE)
Phage and bacteriocin typing
Serological (monoclonal, polyclonal) techniques
Ribotyping
DNA amplification (AFLP, AP-PCR, rep-PCR, RAPD, ...)
Zymograms (multilocus enzyme polymorphism)
Total cellular protein electrophoretic patterns
DNA-DNA hybridization
Mol% G+C
DNA amplification (ARDRA)
tDNA-PCR
Chemotaxonomic markers (polyamines, quinones, ...)
Cellular fatty acid fingerprinting (FAME)
Cell wall structure
Phenotype (classical, API, Biolog, ...)
rRNA sequencing
DNA probes
DNA sequencing



Filogenetikai törzsfa



A távolságmátrix

TABLE 1. Transformation of measured distances (lower triangle) into phylogenetic distances (upper triangle): applying the Jukes Cantor (Jukes and Cantor, 1969) transformation^a

	<i>Escherichia coli</i>	<i>Klebsiella pneumoniae</i>	<i>Proteus vulgaris</i>	<i>Pseudomonas aeruginosa</i>	<i>Bacillus subtilis</i>	<i>Thermus thermophilus</i>	<i>Geotoga subterranea</i>
<i>Escherichia coli</i>		3.2	7	15.6	26	28.5	35.8
<i>Klebsiella pneumoniae</i>	3.1		7	15.1	25.8	28.2	36.4
<i>Proteus vulgaris</i>	6.7	6.7		17.6	26.6	29.9	37.8
<i>Pseudomonas aeruginosa</i>	14.1	13.7	15.7		23.5	29.2	34.3
<i>Bacillus subtilis</i>	22	21.8	22.4	20.2		27	30.4
<i>Thermus thermophilus</i>	23.7	23.5	24.7	24.2	22.6		32.4
<i>Geotoga subterranea</i>	28.5	28.8	29.7	27.6	25	26.3	

B12

B12

B12

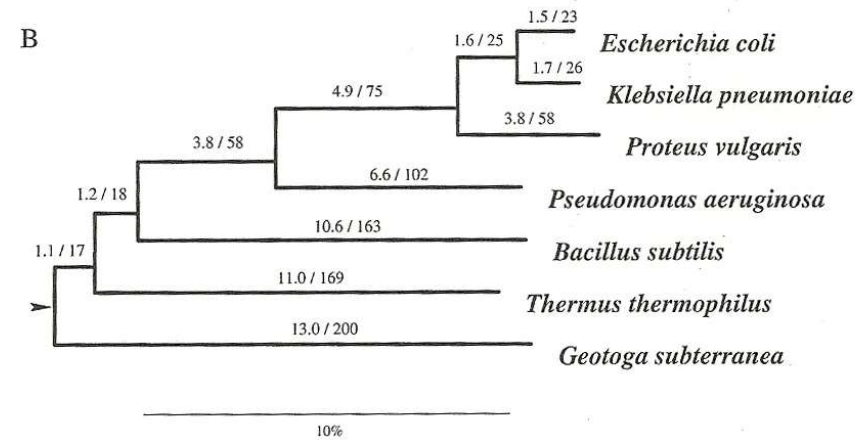
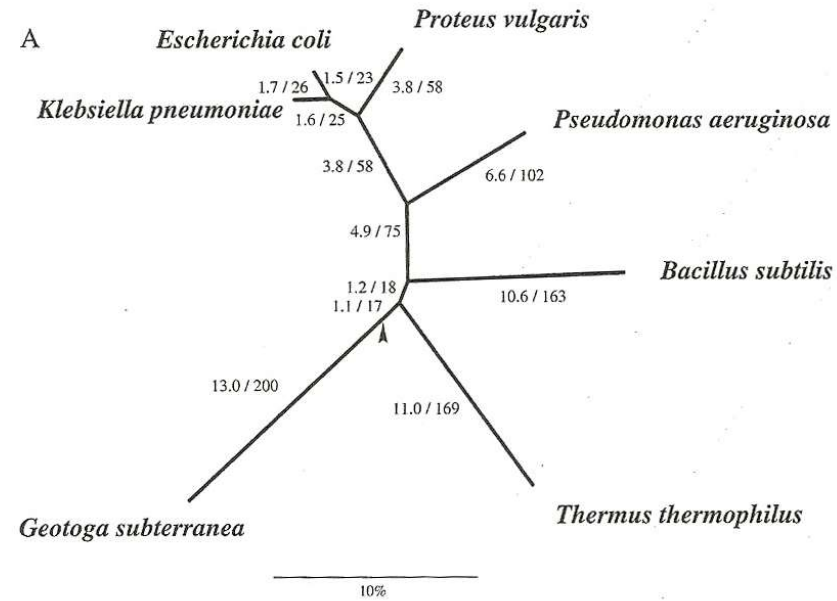
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B13

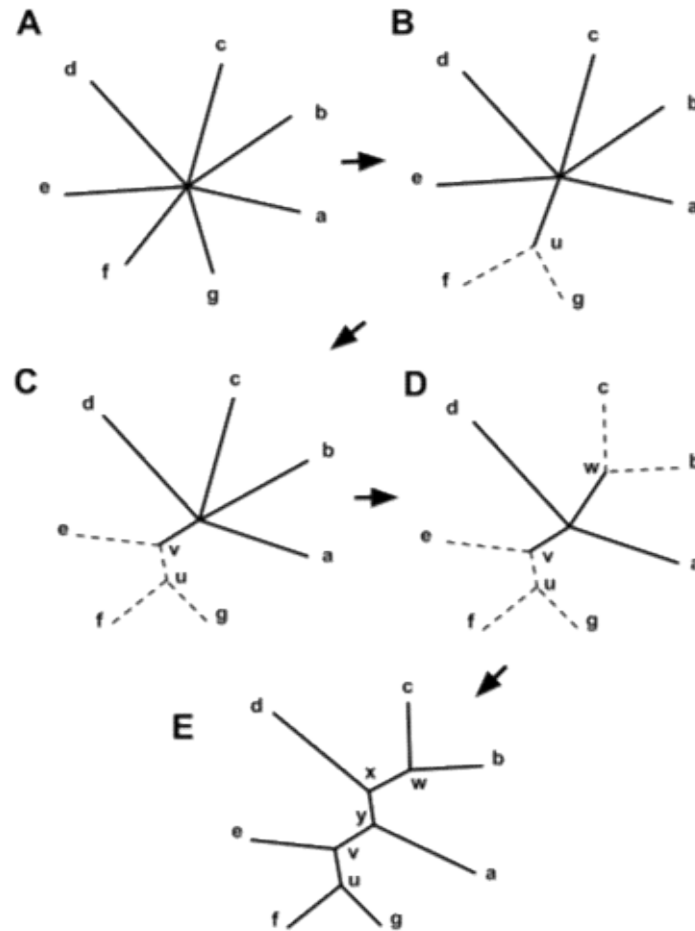
B4

B2

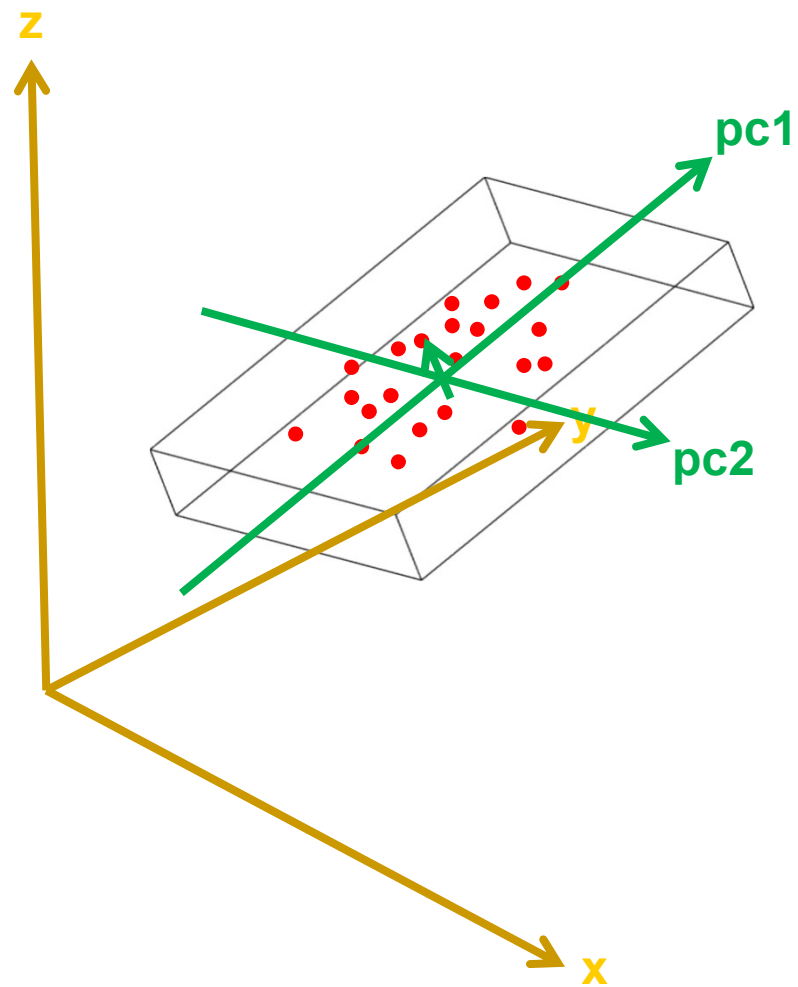
Törzsfa és dendrogram



Neighbor-joining

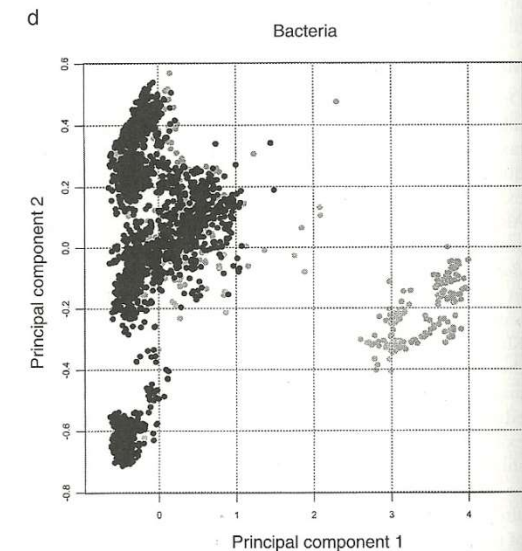
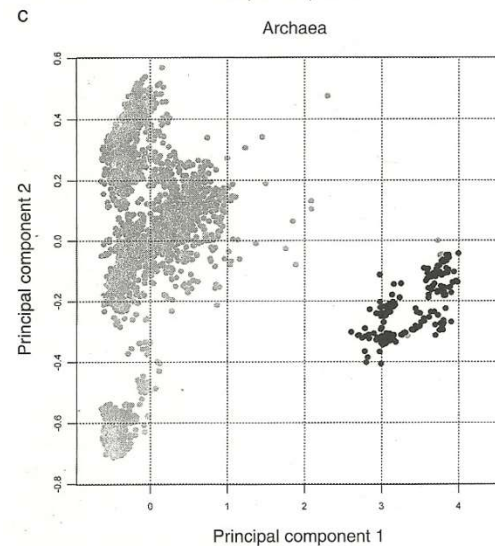
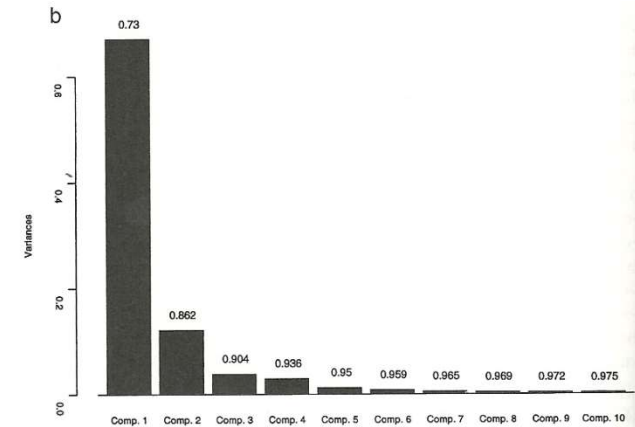
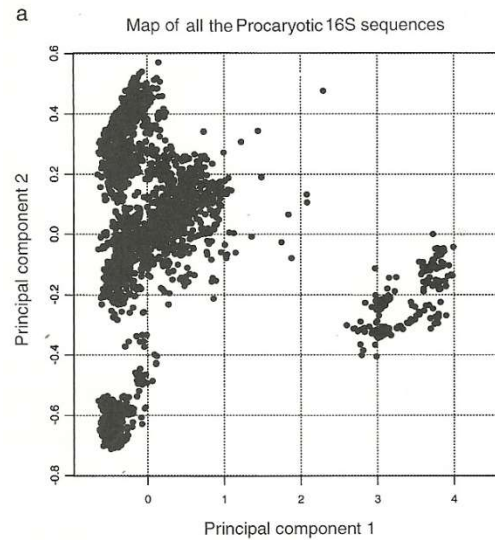


Főkomponens analízis

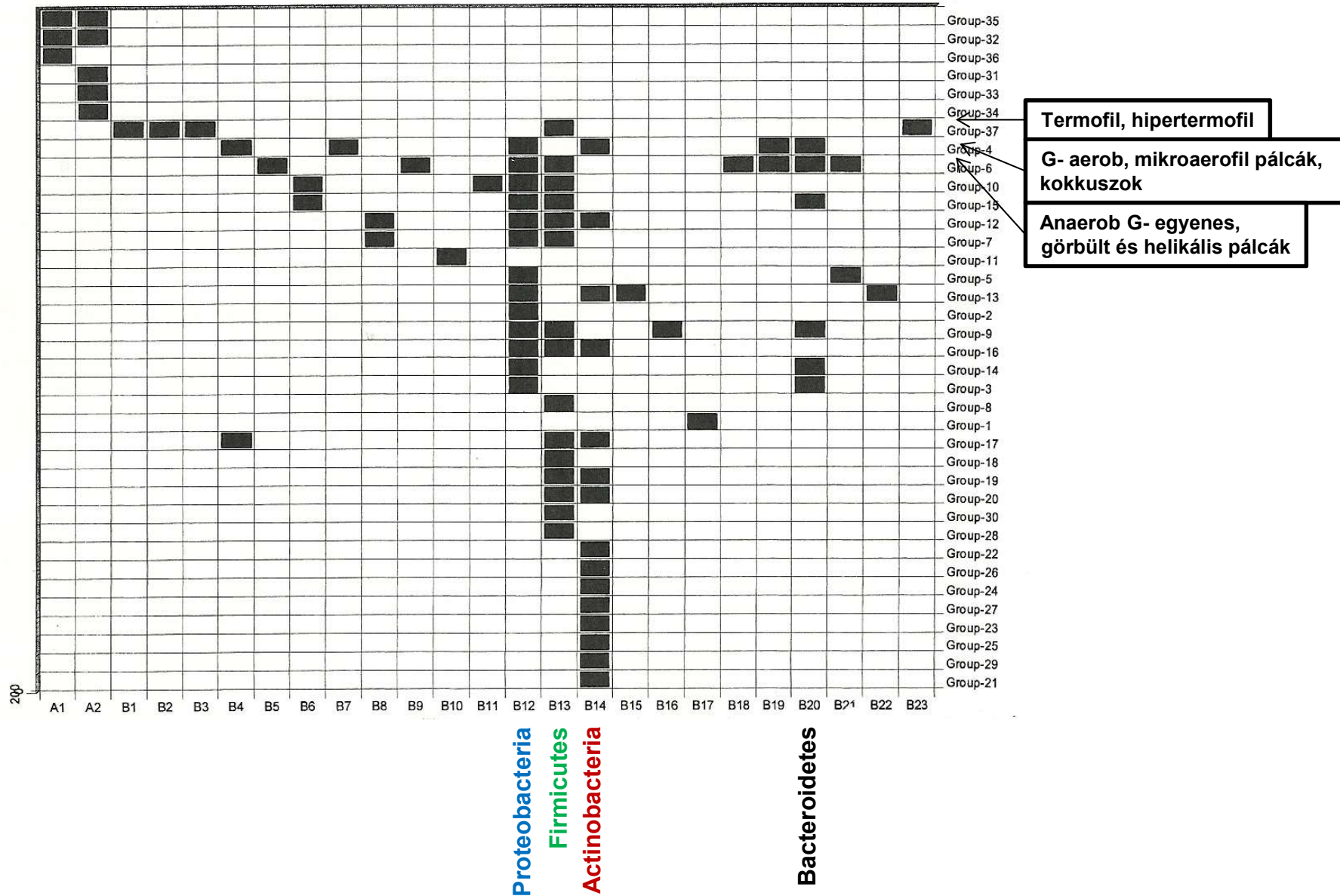


Főkomponens analízis - 16SrDNS

- 4502 minta
- hossz > 1350
- 184 referencia törzs



Fenotípusos csoportok vs. Phylumok



Fenotípusos csoportok vs. Phylumok

FIGURE 2. Occurrence of major phenotypic groups within the 25 prokaryotic phyla. The group number refers to the phenotypic group used in the Ninth Edition of *Bergey's Manual of Determinative Bacteriology* (Holt et al., 1994). Phylum A1-*Crenarchaeota*, A2-*Euryarchaeota*, B1-*Aquificae*, B2-*Thermotogae*, B3-*Thermodesulfobacteria*, B4-*Deinococcus-Thermus*, B5-*Chrysiogenetes*, B6-*Chloroflexi*, B7-*Thermomicrobia*, B8-*Nitrospirae*, B9-*Deferribacteres*, B10-*Cyanobacteria*, B11-*Chlorobi*, B12-*Proteobacteria*, B13-*Firmicutes*, B14-*Actinobacteria*, B15-*Planctomycetes*, B16-*Chlamydiae*, B17-*Spirochaetes*, B18-*Fibrobacteres*, B19-*Acidobacteria*, B20-*Bacteroidetes*, B21-*Fusobacteria*, B22-*Verrucomicrobia*, B23-*Dictyoglomi*. Phenotypic Group 1-Spirochetes, Group 2-Aerobic/microaerophilic, motile, helical/vibrioid Gram-negative *Bacteria*, Group 3-Nonmotile or rarely motile, curved Gram-negative *Bacteria*, Group 4-Gram-negative aerobic/microaerophilic rods and cocci, Group 5-Facultatively anaerobic Gram-negative rods, Group 6-Anaerobic, straight, curved, and helical Gram-negative rods, Group 7-Dissimilatory sulfate- or sulfite-reducing *Bacteria*, Group 8-Anaerobic Gram-negative cocci, Group 9-Symbiotic and parasitic *Bacteria* of vertebrate and invertebrate species, Group 10-Anoxygenic phototrophic *Bacteria*, Group 11-Oxygenic photo-

trophic *Bacteria*, Group 12-Aerobic chemolithotropic *Bacteria* and associated genera, Group 13-Budding and/or appendaged *Bacteria*, Group 14-Sheathed *Bacteria*, Group 15-Nonphotosynthetic, nonfruiting, gliding *Bacteria*, Group 16-Fruiting gliding *Bacteria*: The myxobacteria, Group 17-Gram-positive cocci, Group 18-Endospore-forming Gram-positive rods and cocci, Group 19-Regular, nonsporulating, Gram-positive rods, Group 20-Irregular, nonsporulating, Gram-positive rods, Group 21-Mycobacteria, Group 22-Nocardioform actinomycetes, Group 23-Actinomycetes with multilocular sporangia, Group 24-Actinoplanetes, Group 25-*Streptomyces* and related genera, Group 26-Maduromycetes, Group 27-*Thermomonospora* and related genera, Group 28-*Thermoactinomyces*, Group 29-Other actinomycete genera, Group 30-Mycoplasmas, Group 31-The methanogens, Group 32-Archaeal sulfate reducers, Group 33-Extremely halophilic *Archaea*, Group 34-*Archaea* lacking a cell wall, Group 35-Extremely thermophilic and hyperthermophilic S⁰-metabolizers, Group 36-Hyperthermophilic non-S⁰ metabolizing *Archaea*, Group 37-Thermophilic and hyperthermophilic *Bacteria*.

A prokarióták főbb csoportjai

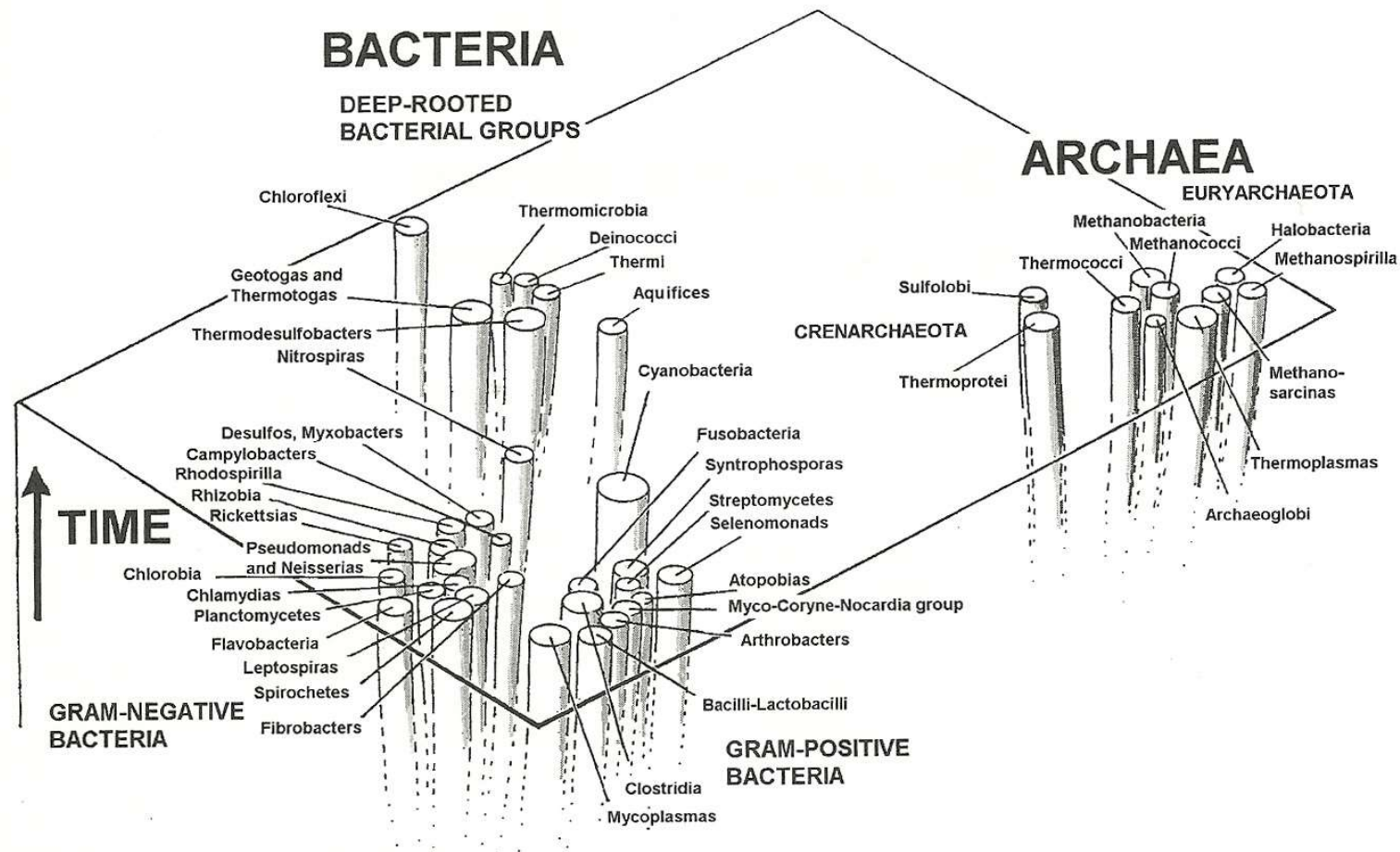
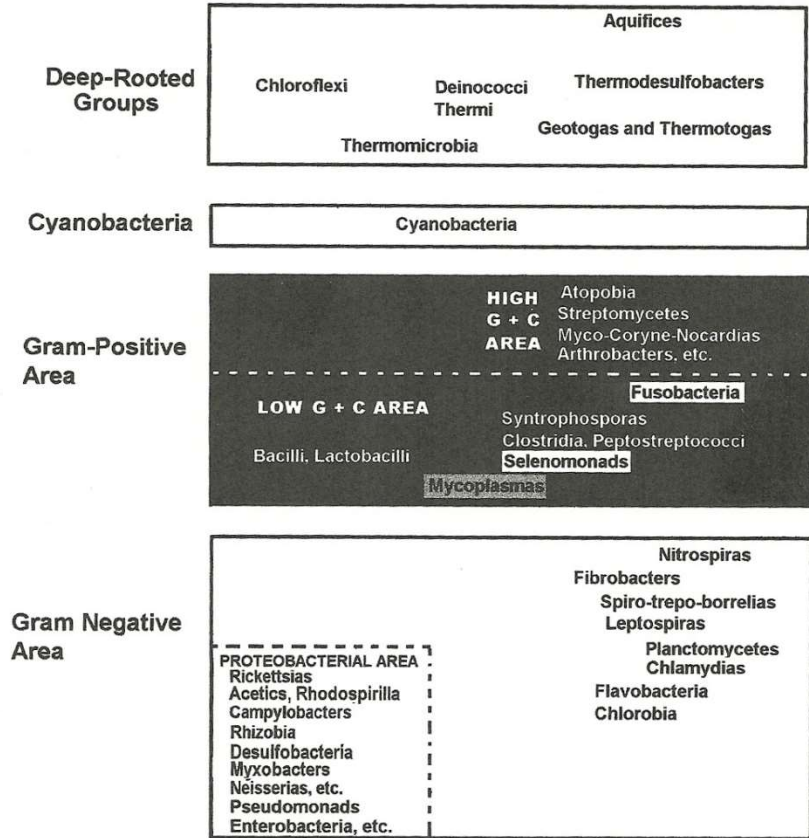


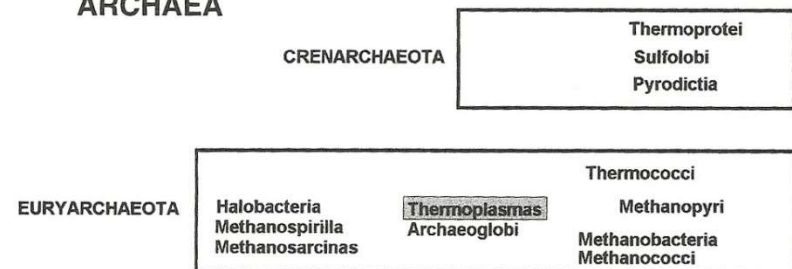
FIGURE 1. The major groups of prokaryotes and their relatedness to one another. The relative size of the oval discs is an approximate indicator of the number of species in each group. The deeper origin of these groups, i.e., their evolution from more primitive forms, is still debatable and therefore is represented only by dashed lines. (Courtesy of Peter H.A. Sneath.)

A prokarióták főbb csoportjai

BACTERIA



ARCHAEA

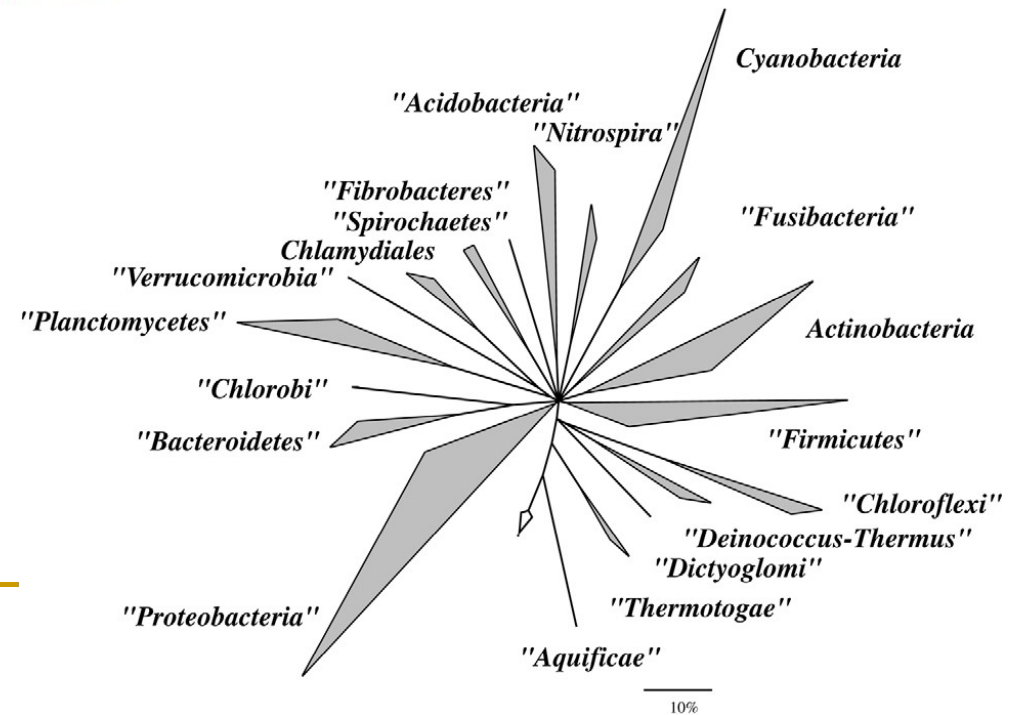
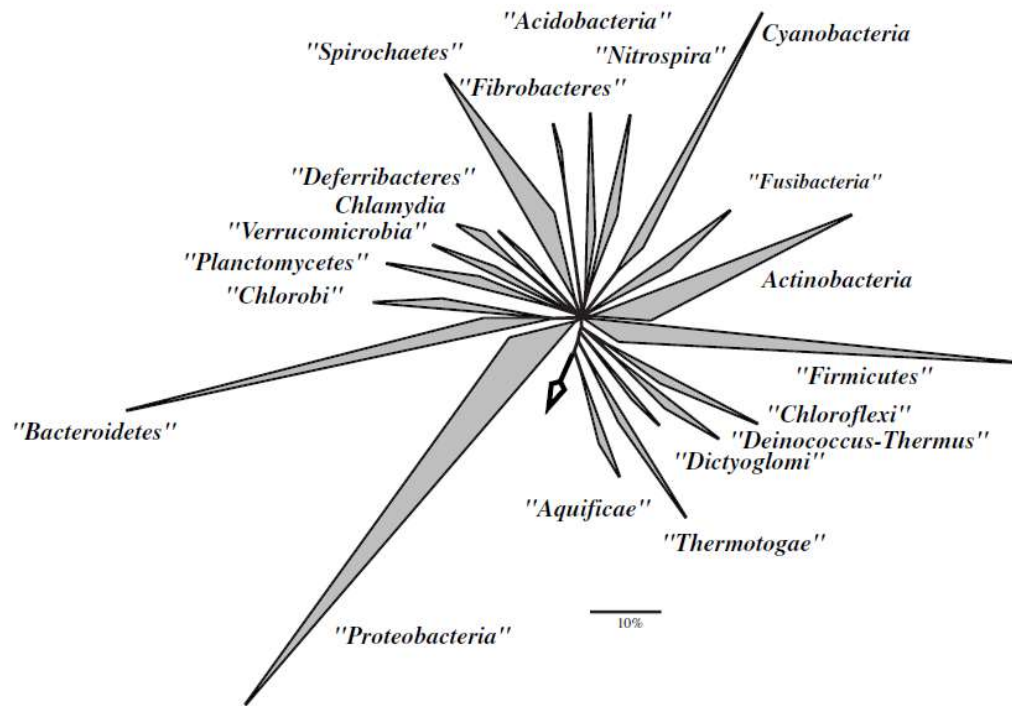


Alternatív filogenetikai markerek

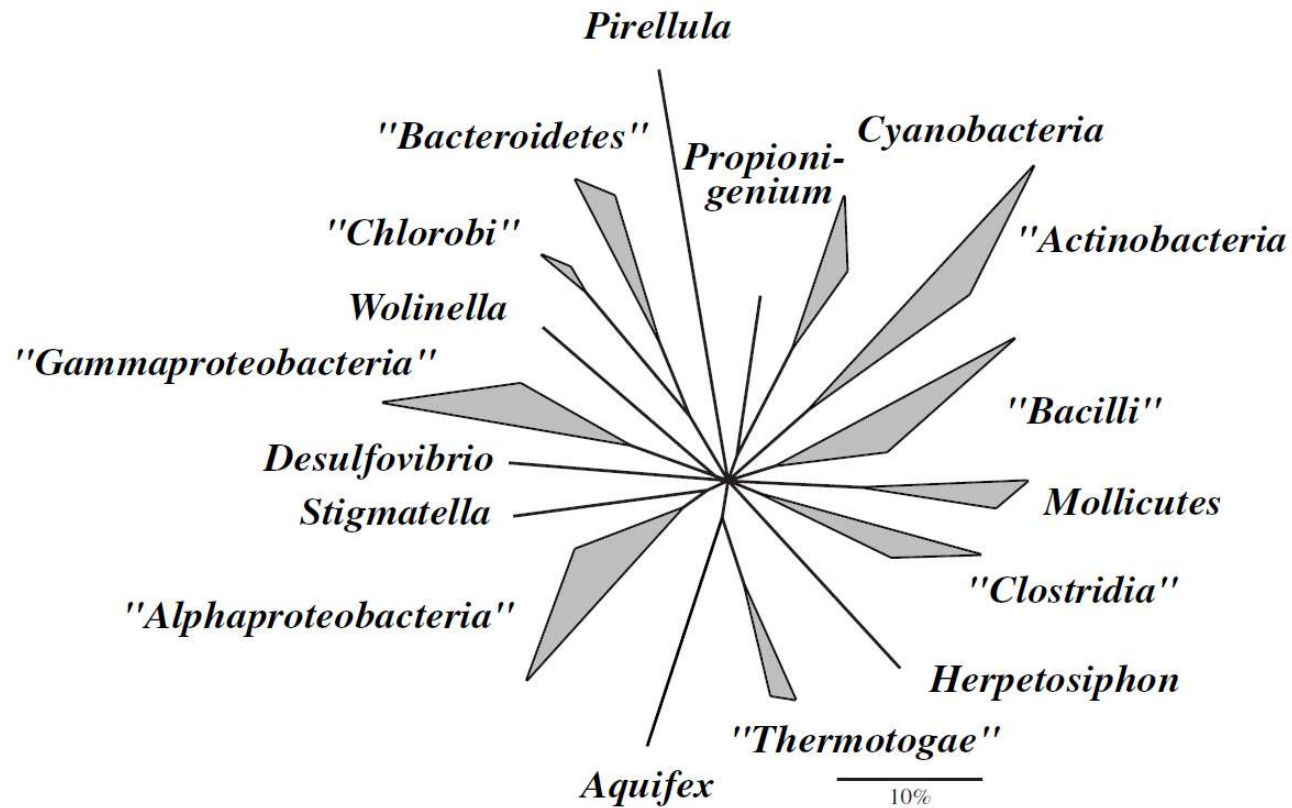
Követelmények:

- Minden vizsgált fajban előforduljon
 - Funkciója konstans maradjon
 - Megfelelő mennyiségű információt szolgáltatasson
 - Legyen róla adatbázis
-
- COGs (Clusters of Orthologous Groups)
 - 16SrRNS, 23SrRNS, DNS függő RNS polimeráz, elongációs faktor, protonpumpa
-

16SrRNS vs. 23SrRNS - törzsfa



Protonpumpa - törzsfa



A1. Crenarchaeota (1o3r)

- Jellemzően termofil, hipertermofil acidofil kén oxidálók
 - Morfológiailag változatosak
 - Sulfolobus (nemzetség)
 - obligát aerob
 - kemolitotróf – elemi kén oxidálás
 - kemoorganotróf anyagcsere is
 - termofil, acidofil
-

A1. Crenarchaeota (1o3r)

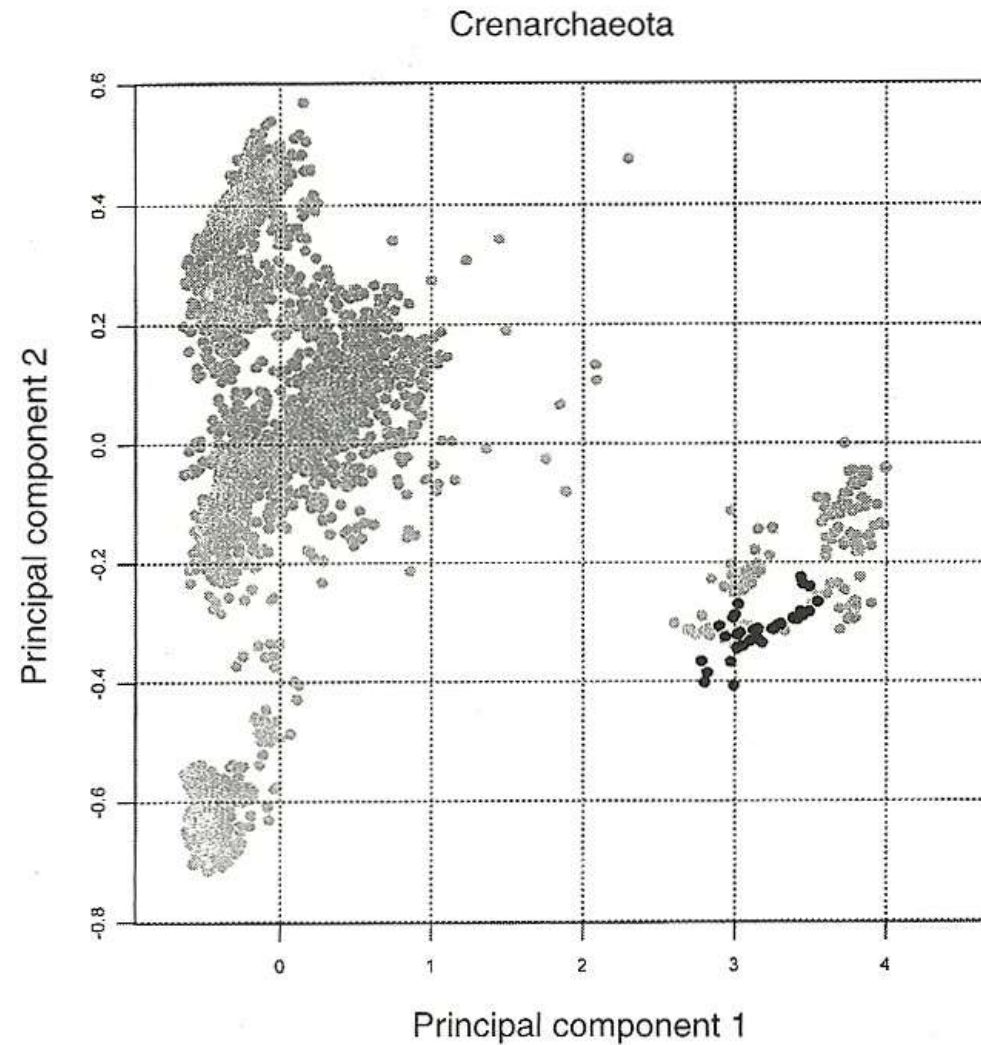


FIGURE 3. Location of Phylum *Crenarchaeota* within the map of the procaryotes.

A2. Euryarchaeota (7o)

- 5 nagyobb fiziológiai csoport
 - Metanogén ősbaktériumok
 - Szulfátreduáló ősbaktériumok
 - Halofil ősbaktériumok
 - Sejtfal nélküli ősbaktériumok
 - Termoacidofil ősbaktériumok
-

A2. Euryarchaeota (7o)

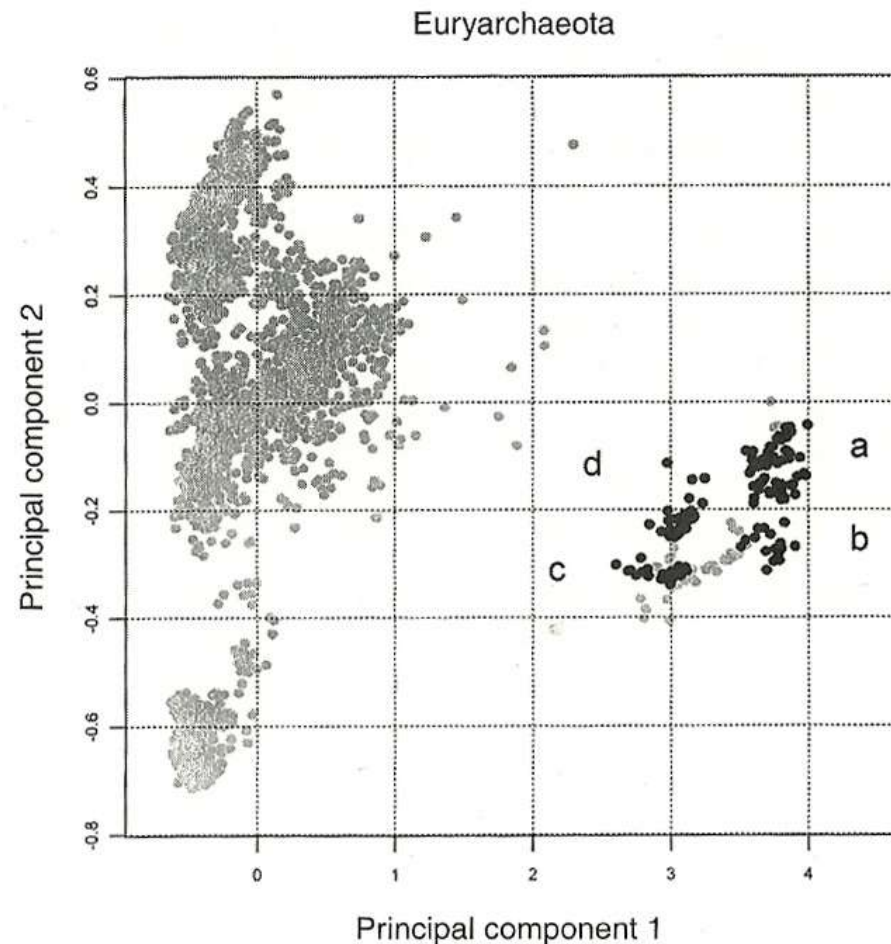


FIGURE 4. Location of Phylum *Euryarchaeota* within the map of the procaryotes. Region a contains the *Halobacteriales*, *Thermoplasmatales*, and *Methanomicrobiales*. Region b contains the *Methanosarcinales*. Region c contains the *Thermococci*, *Archaeoglobi*, *Methanopyri*, and *Methanothermaceae*. Region d contains the *Methanobacteriaceae* and some members of the *Methanococcaceae*, which appears to be polyphyletic.

B1. Aquificae (101r)

- A valódi baktériumok legkorábban elágazó (deeply branching csoportja)
 - G- spórátlan pálca
 - Hydrogenobacter „durranógáz baktériumok”
-

B1. Aquificae (1o1r)

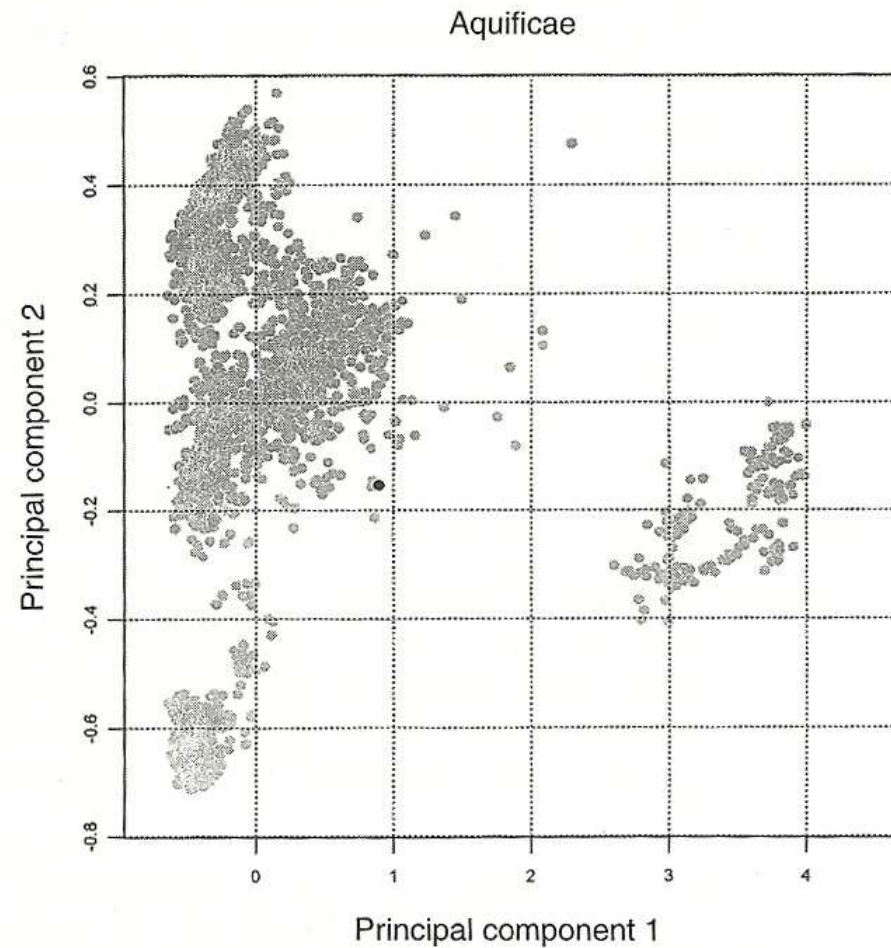


FIGURE 5. Location of Phylum *Aquificae* within the map of the procar-
yotes.

B4. Deinococcus-Thermus (1o2r)

- Aquificia-hez hasonlóan korán divergáló csoport
 - Thermus – G- aerob pálca
 - Deinococcus – G+ kokkusz
-

B6. Chloroflexi (1o2r)

- G- fonálképző baktériumok
 - Nincs lipopoliszacharid dús külső membrán
 - Csúszó mozgás

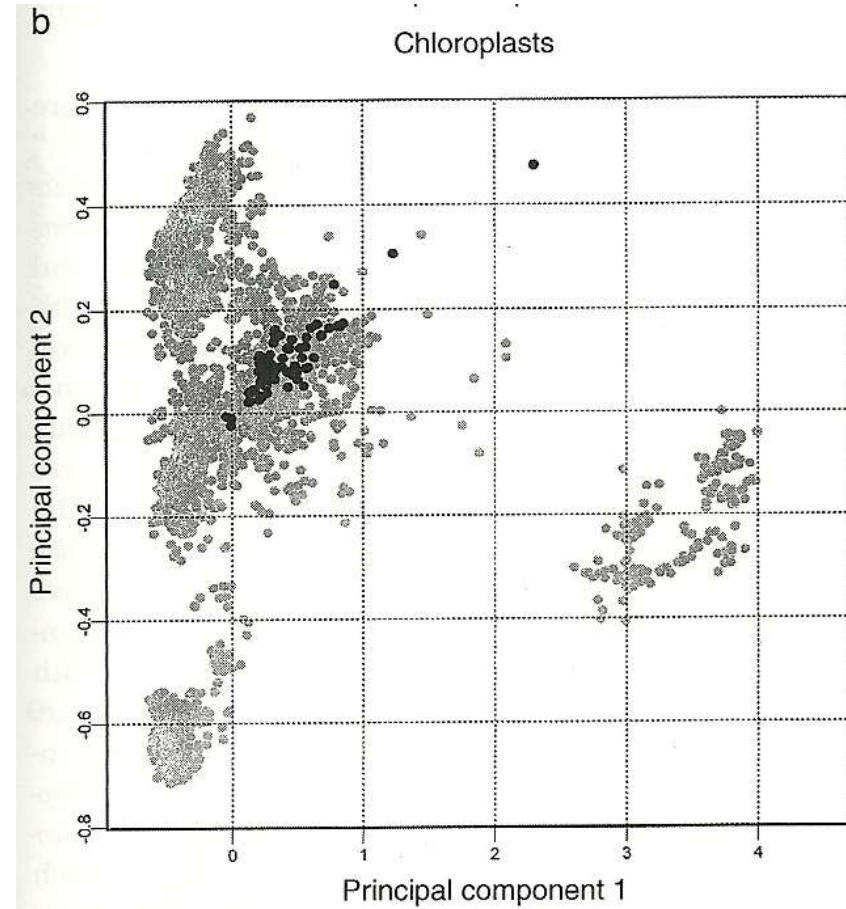
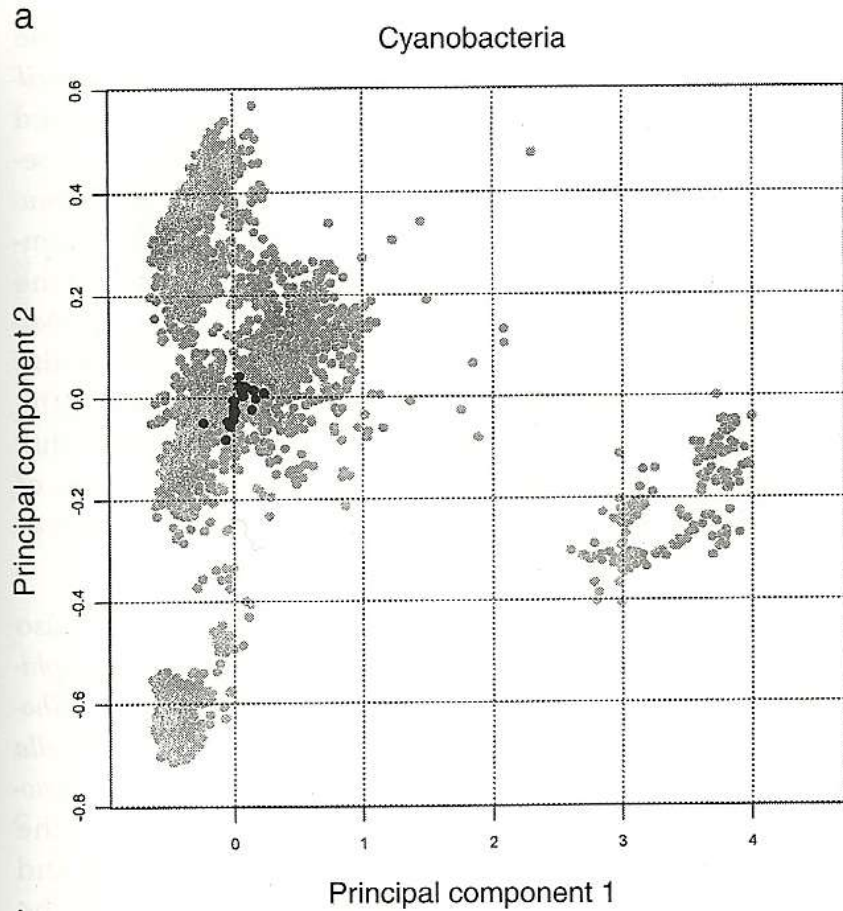
 - Chloroflexales – zöld nemkén
(van bakterioklorofill és karotenoid is)

 - Herpetosiphonales
(csak karotenoid van)
-

B10. Cyanobacteria (10⁵asz)

- A nomenklatura inkább a botanikában szokásos módszert követi, mint a bakteriológiát
 - G- egysejtes, telepes, fonalas fajok komplex morfológiával és élelciklussal
 - Minden faj képes fotoautotrófiára
-

B10. Cyanobacteria (105asz)



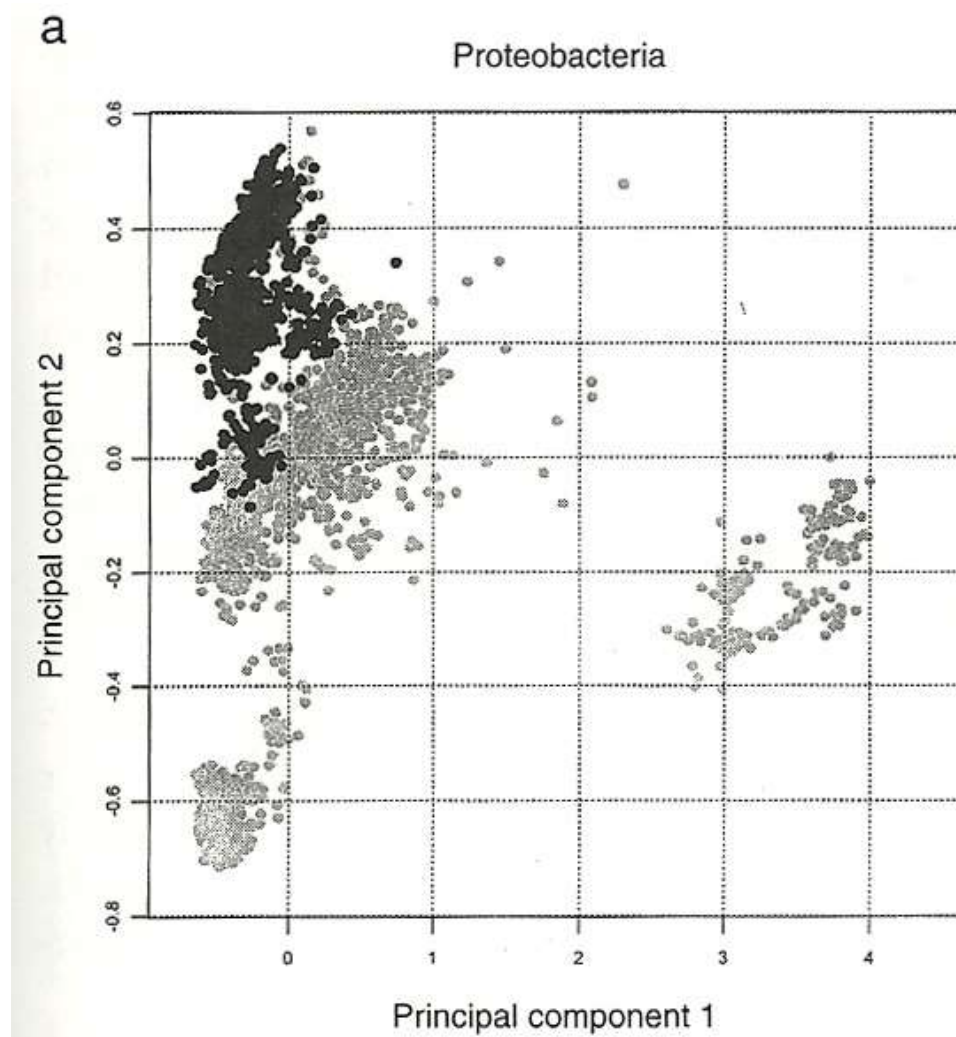
B11. Chlorobi (1o1r)

- Tipikusan anaerob, fotoautotróf
 - „Zöld kénbaktériumok” (Gram negatívok)
 - Sejten kívülre választják ki az elemi ként
-

B12. Proteobacteria (6o>30r)

- Több, mint 1300 faj, közel 400 nemzetség
 - Legnagyobb filogenetikus koherens csoport
 - G- baktériumok
 - Az összes metabolizmus típus megtalálható benne
-

B12. Proteobacteria (6o>30r)

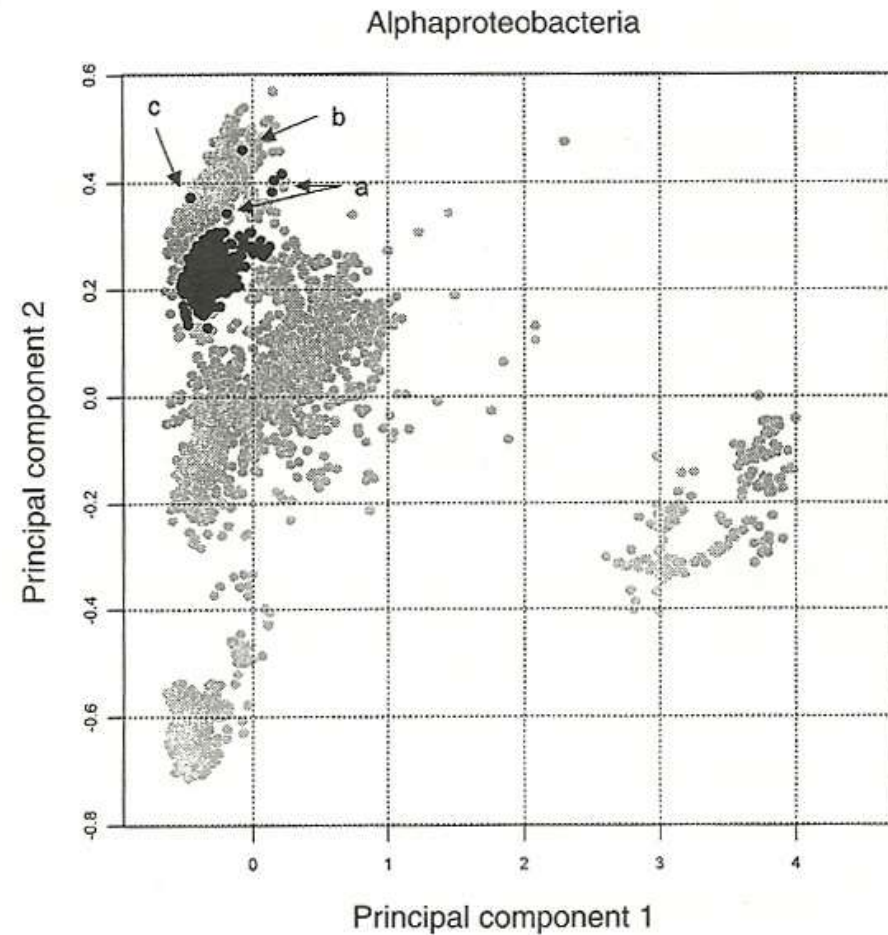


B12.1 Alphaproteobacteria

Fontosabb rendek:

- Rhodospirillales
- Rhizobiales
- Rickettsiales
- Caulobacterales

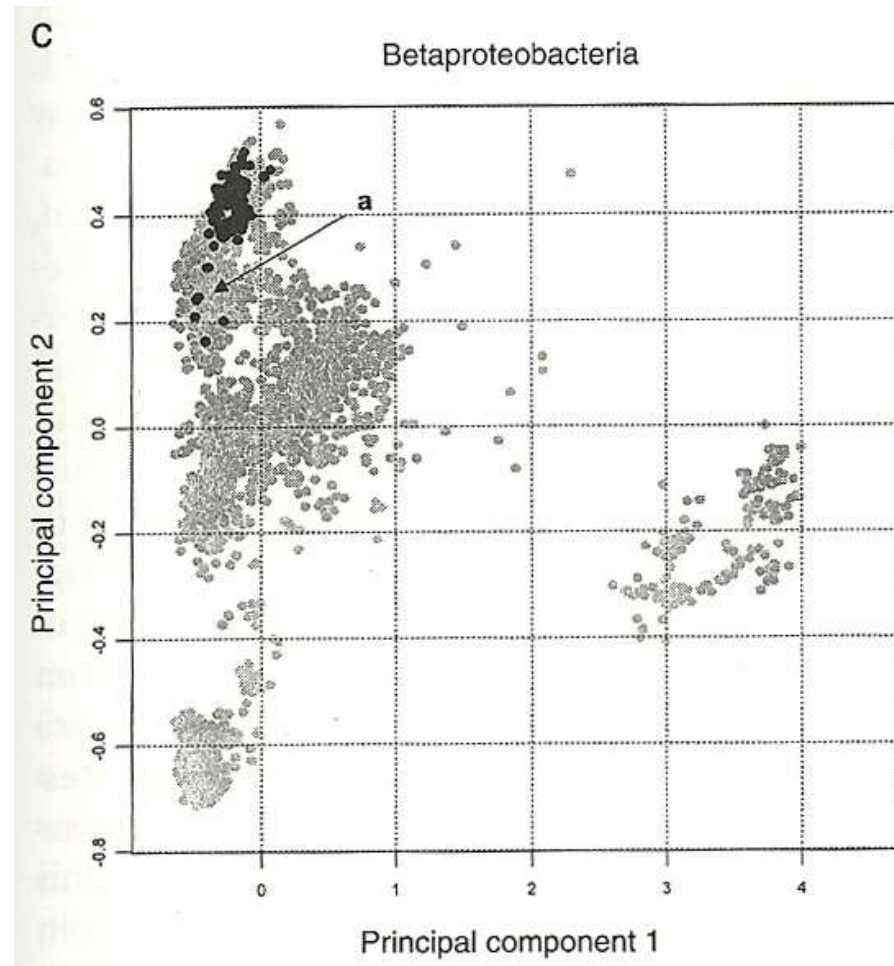
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B12.2 Betaproteobacteria

Fontosabb rendek:

- Neisseriales
- Nitrosomonadales

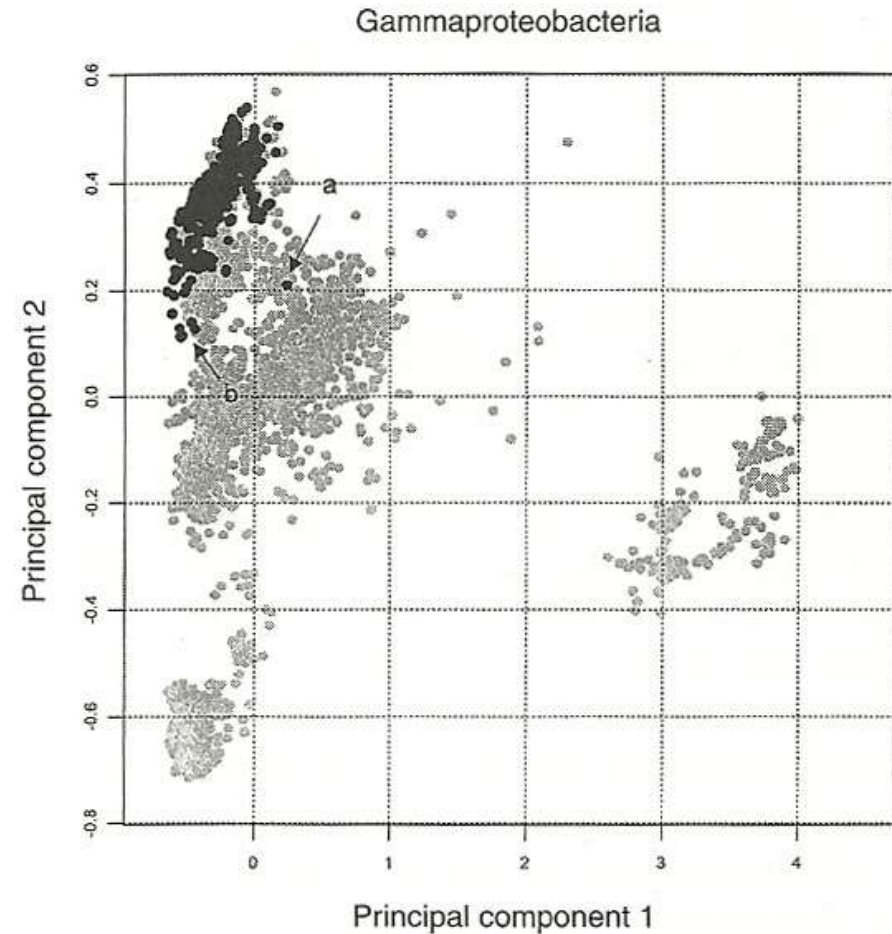


B12.3 Gammaproteobacteria

Fontosabb rendek:

- Pseudomonadales
- Xanthomonadales
- Legionellales
- Chromatiales
- Enterobacteriales

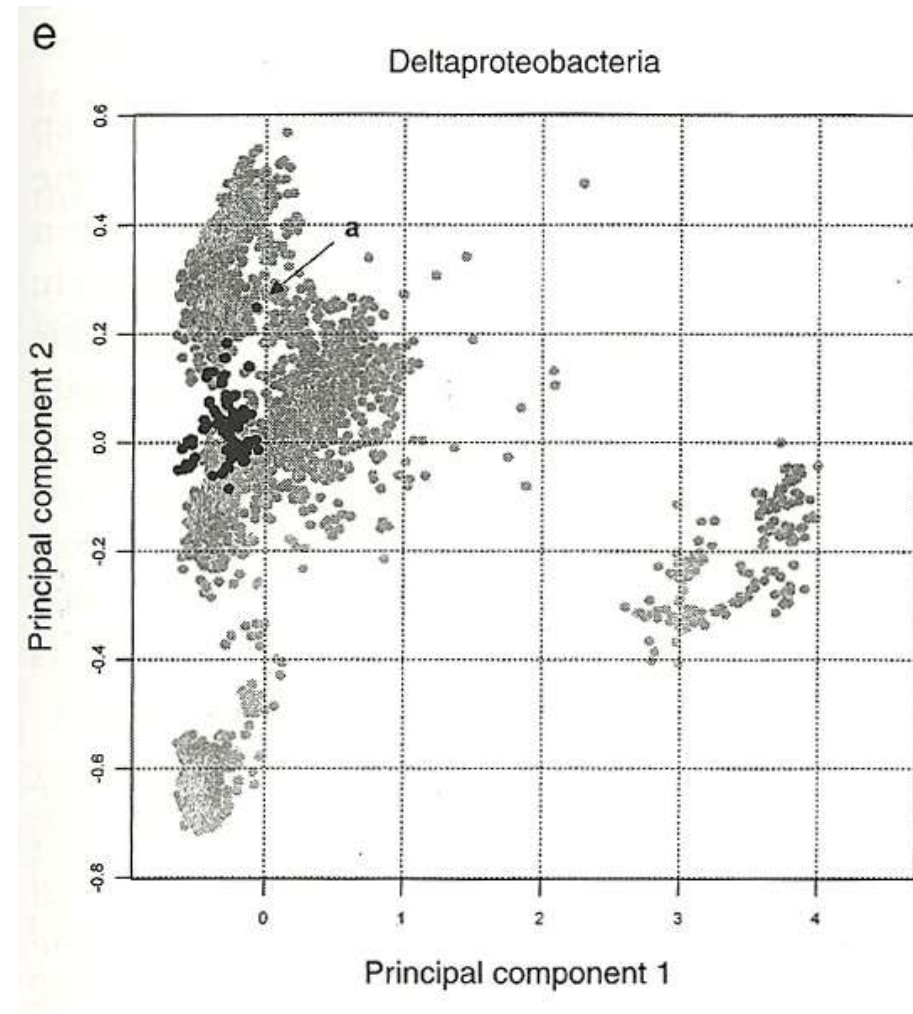
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B12.4 Deltaproteobacteria

Fontosabb rendek:

- Desulfovibrionales
- Bdellovibrionales

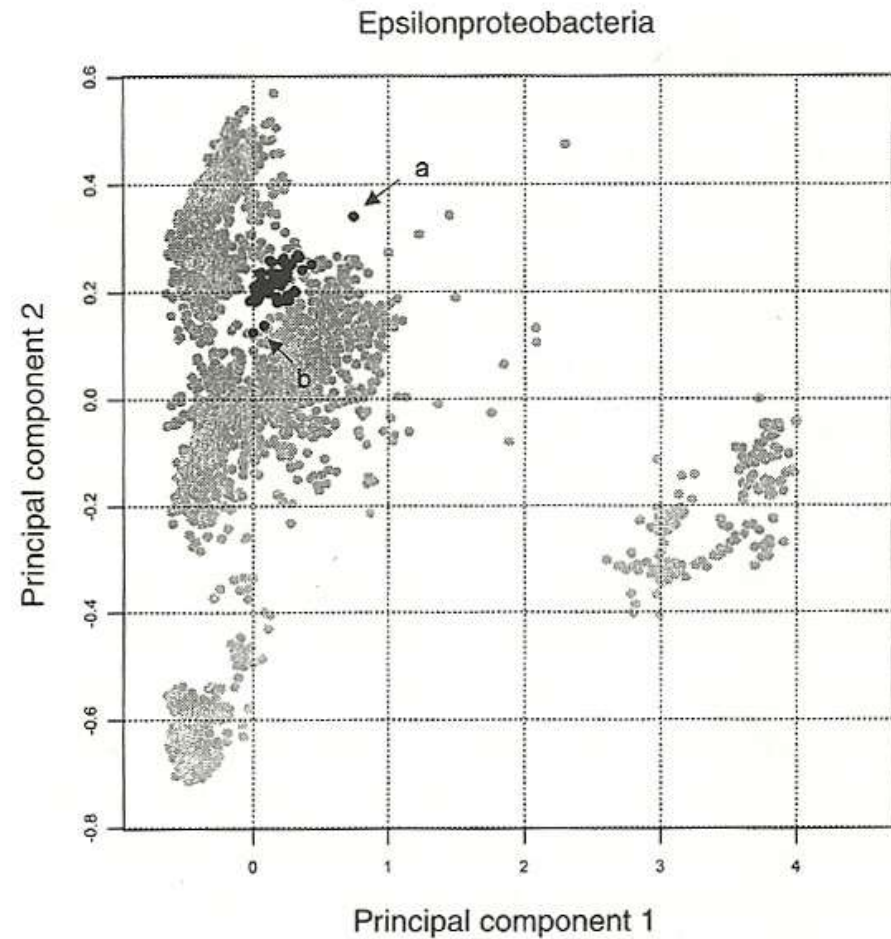


B12.5 Epsilonproteobacteria

Fontosabb rendek:

- Campylobacterales

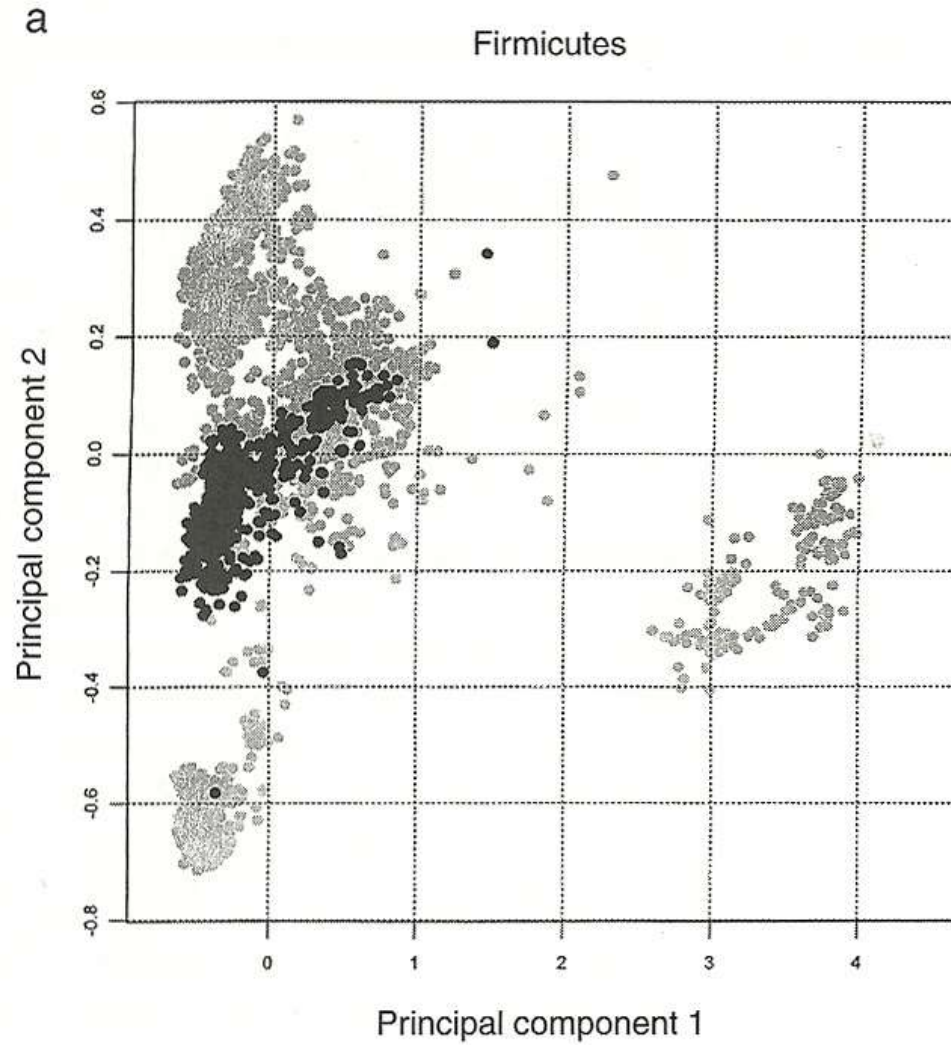
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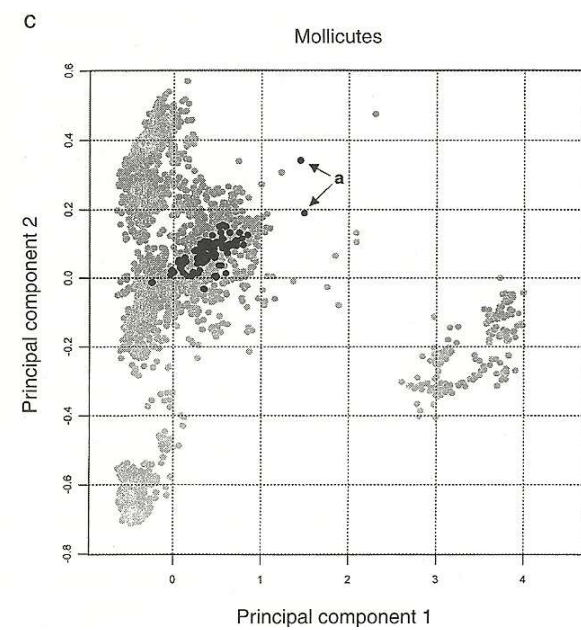
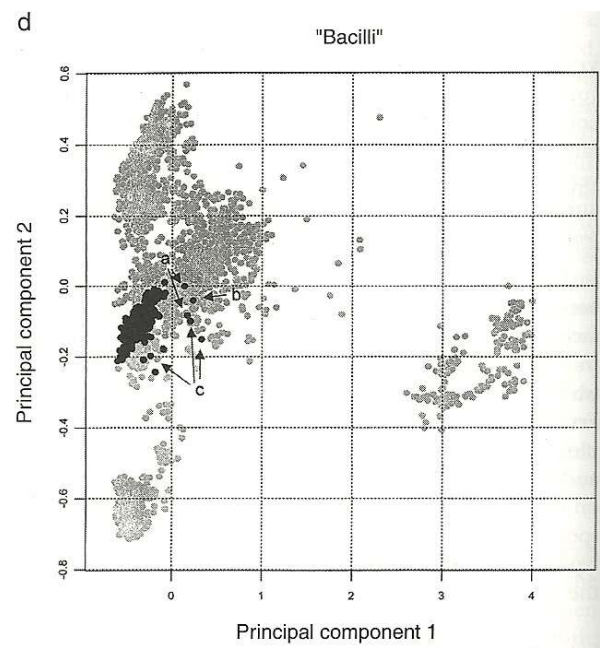
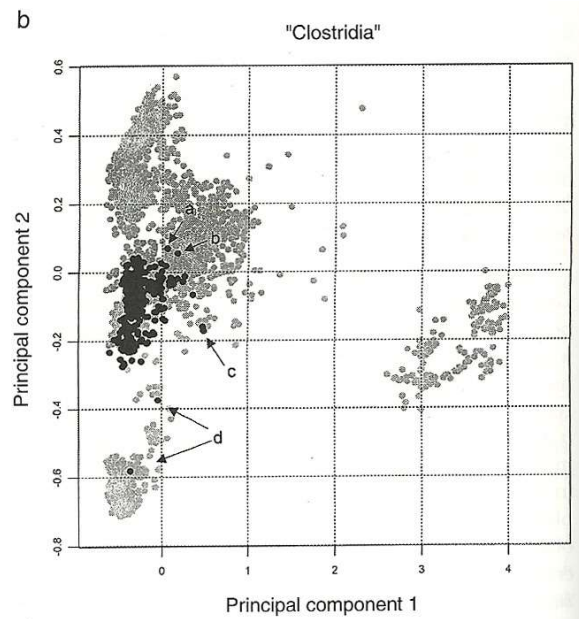
B13. Firmicutes (3o8r)

- Korábbi divízió nevét kapta
 - Alacsony G+C arányú G+ baktériumok
 - Fenotípusosan igen változatos nemzetségek
-

B13. Firmicutes (3o8r)



B13. Firmicutes (3o8r)



B14. Actinobacteria (2014ao)

- Magas G+C arányú G+ baktériumok
 - Jelentős részük micélium/hifa képző
 - Talajbaktériumok
 - Antibiotikum termelésben jelentősek
-

B14. Actinobacteria (2014ao)

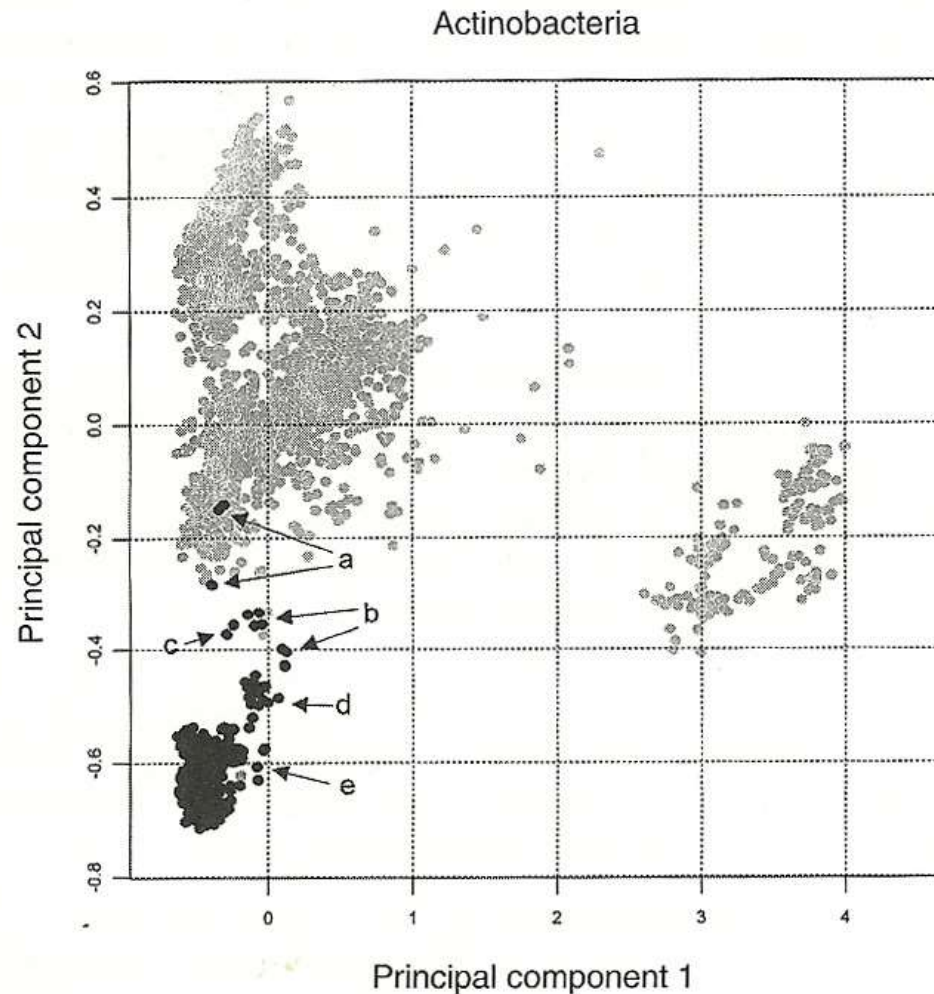


FIGURE 17. Location of Phylum *Actinobacteria* within the map of the procaryotes. Outliers are members of the orders *Rubrobacterales* (a), *Coriobacterales* (b), *Acidimicrobiales* (c), and *Bifidobacteriales* (d). Those at position (e) are atypical members of the genus *Actinomyces*.

B16. Chlamidiae (1o1r)

- Obligát intracelluláris paraziták
 - Emlősök és madarak sejtjeinek membrán határolt vakuólumaiban szaporodnak
 - Sejtfaluk nem tartalmaz muraminsavat
-

B16. Chlamydiae (101r)

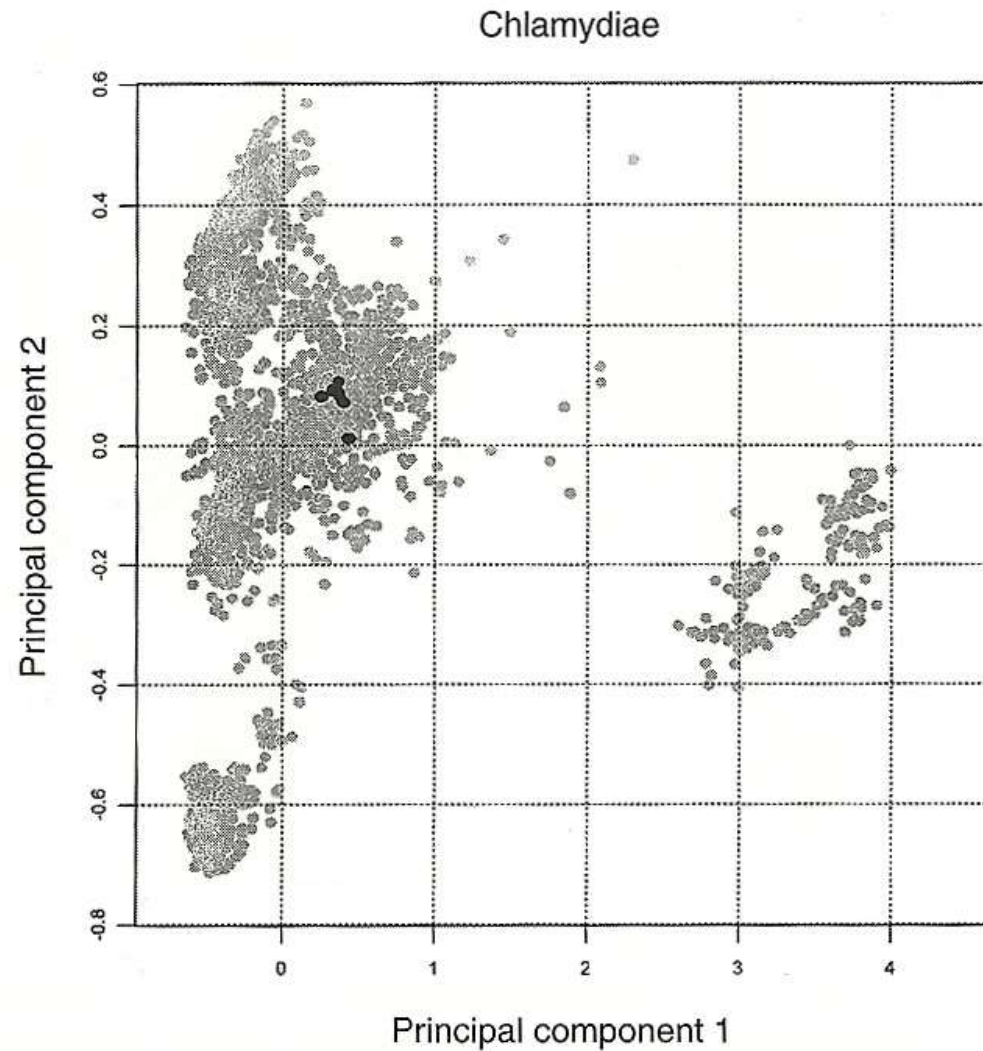


FIGURE 19. Location of Phylum *Chlamydiae* within the map of the prokaryotes. Members of the family *Simkaniaceae* lie outside the main cluster.

B17. Spirochaetes (101r)

- Gram negatív, kemoheterotróf
 - Helikális
 - Flexibilis sejtek, endoflagellummal
-

B17. Spirochaetes (1o1r)

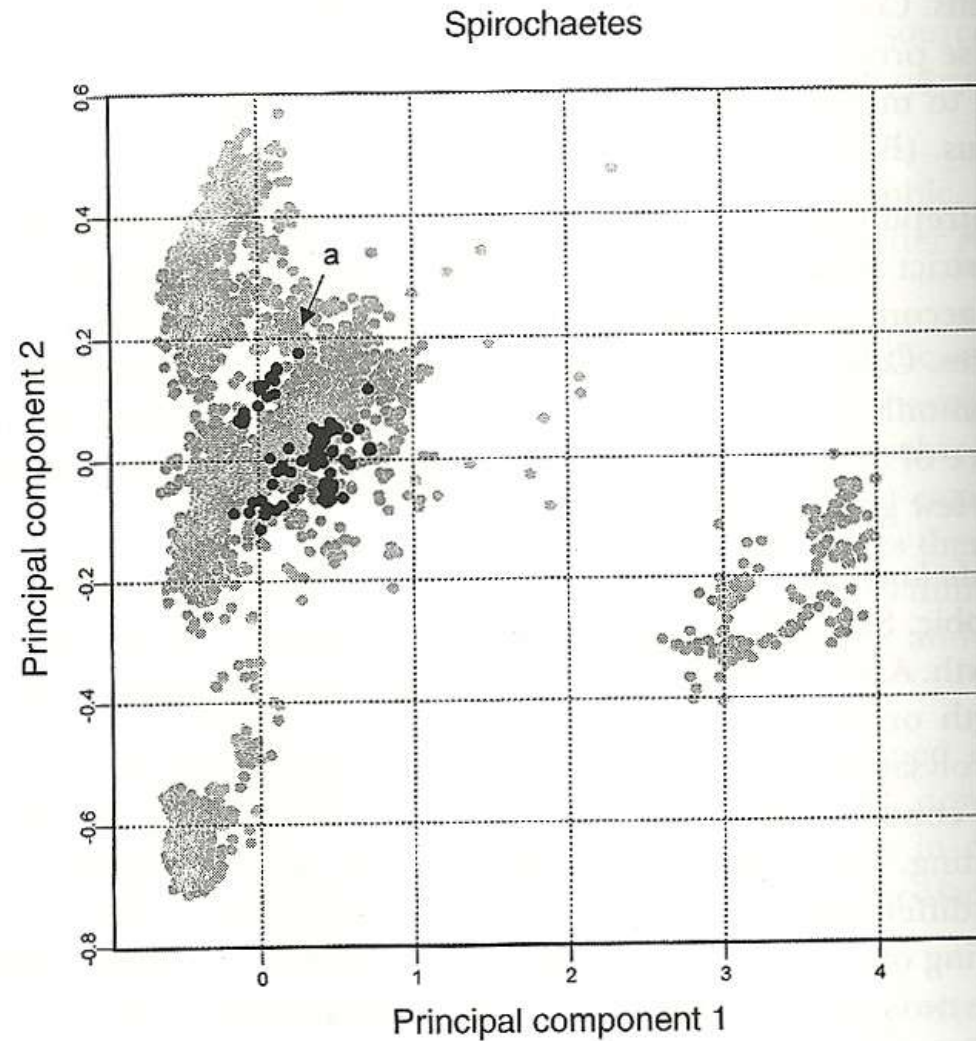


FIGURE 20. Location of Phylum *Spirochaetes* within the map of the prokaryotes. The upper cluster at position (a) consists of the family *Leptospiraceae*.

B20. Bacteroidetes (3o3r)

- Chlorobi phylummal közös gyökér
 - Fenotípusosan igen változatos
-

B20. Bacteroidetes (1o1r)

