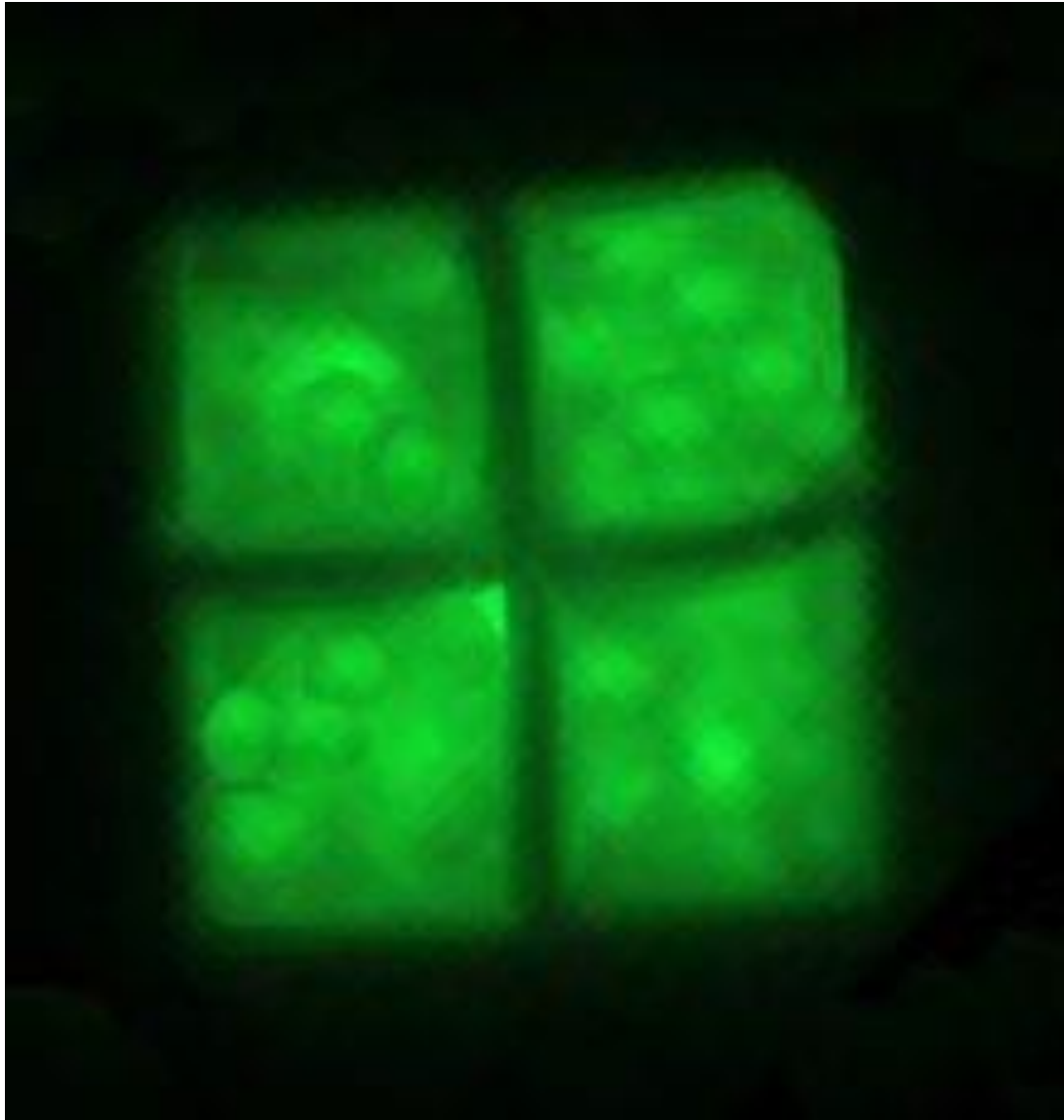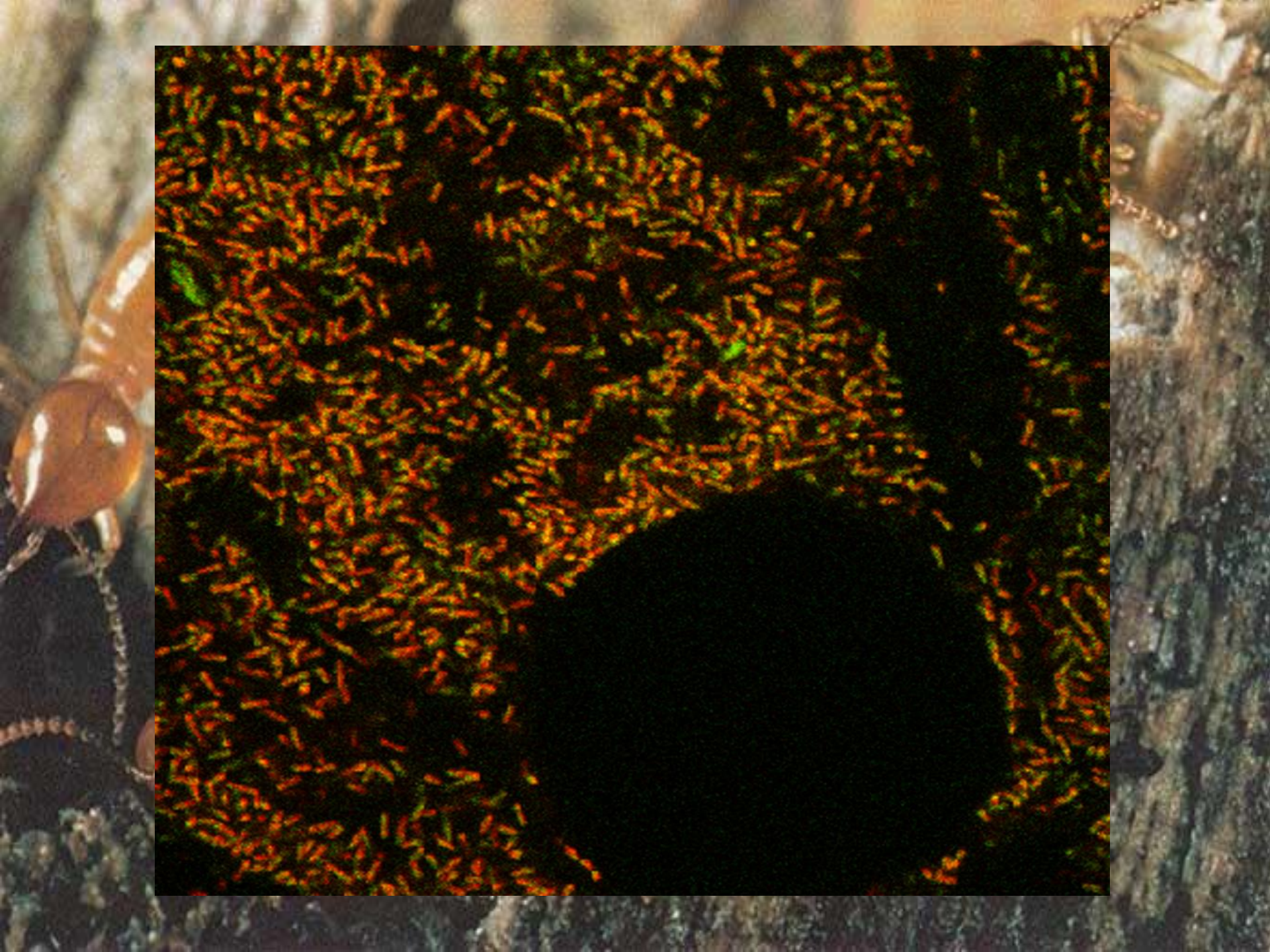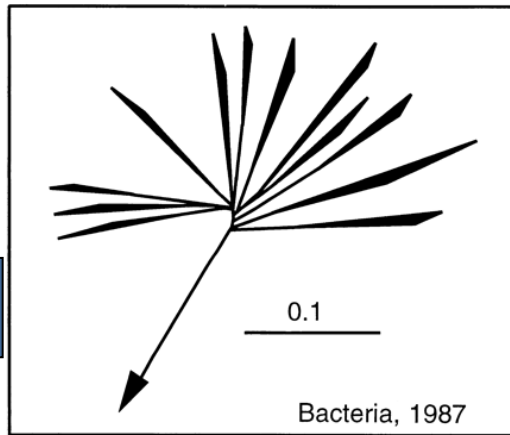# Microbial Systematics

Haloquadratum walsbyi
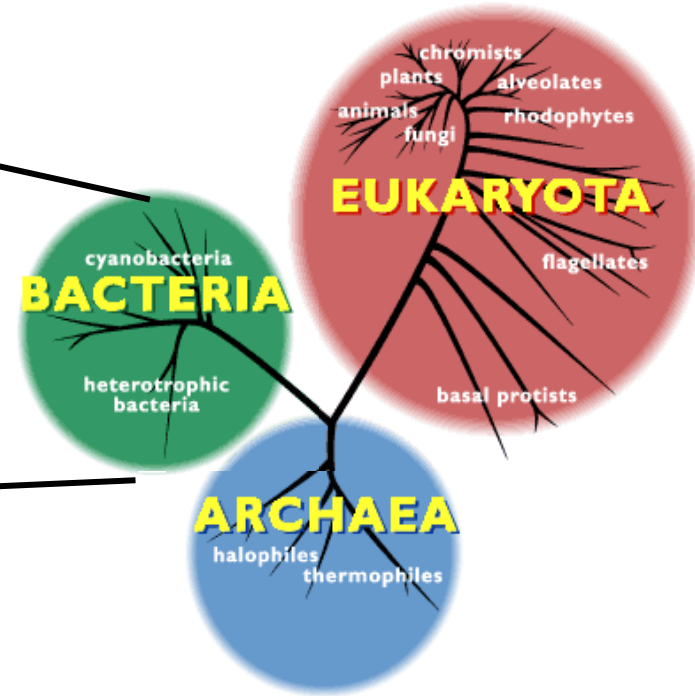
Complexity of Bacteria

1987

10 yrs

1997

0.1

Bacteria, 1987

EUKARYOTA
chromists
plants
animals
fungi
alveolates
rhodophytes
flagellates
basal protists

BACTERIA
cyanobacteria
heterotrophic bacteria

ARCHAEA
halophiles
thermophiles

Bacteria, 1997

Proteobacteria
Leptospira
OP5
OP4
Acidobacterium
Spirochaetes
Chlamydia
Verucomicrobium
Thermus/Deinococcus
Fibrobacter
Bacteroides/Cytophaga
Chlorobiaceae
Planctomycetales
OP3
OP6
Nitrospira
OP1
Flexistipes
Synergistes
Fusobacteria
Cyanobacteria
low GC Gram-positive
Actinomycetales
OP8
OP7
Green non-sulfur
OP10
Thermotogales
Dictyoglomus
OP9
Thermodesulfobacterium
EM19
Aquificales
Archaea, Eucarya
0.1 changes per site

Almost
10 yrs

> 20, 000
species/L

2006

Pace, *Science,* **1997**

Sogin et al., *PNAS,* **2006**

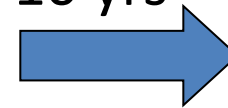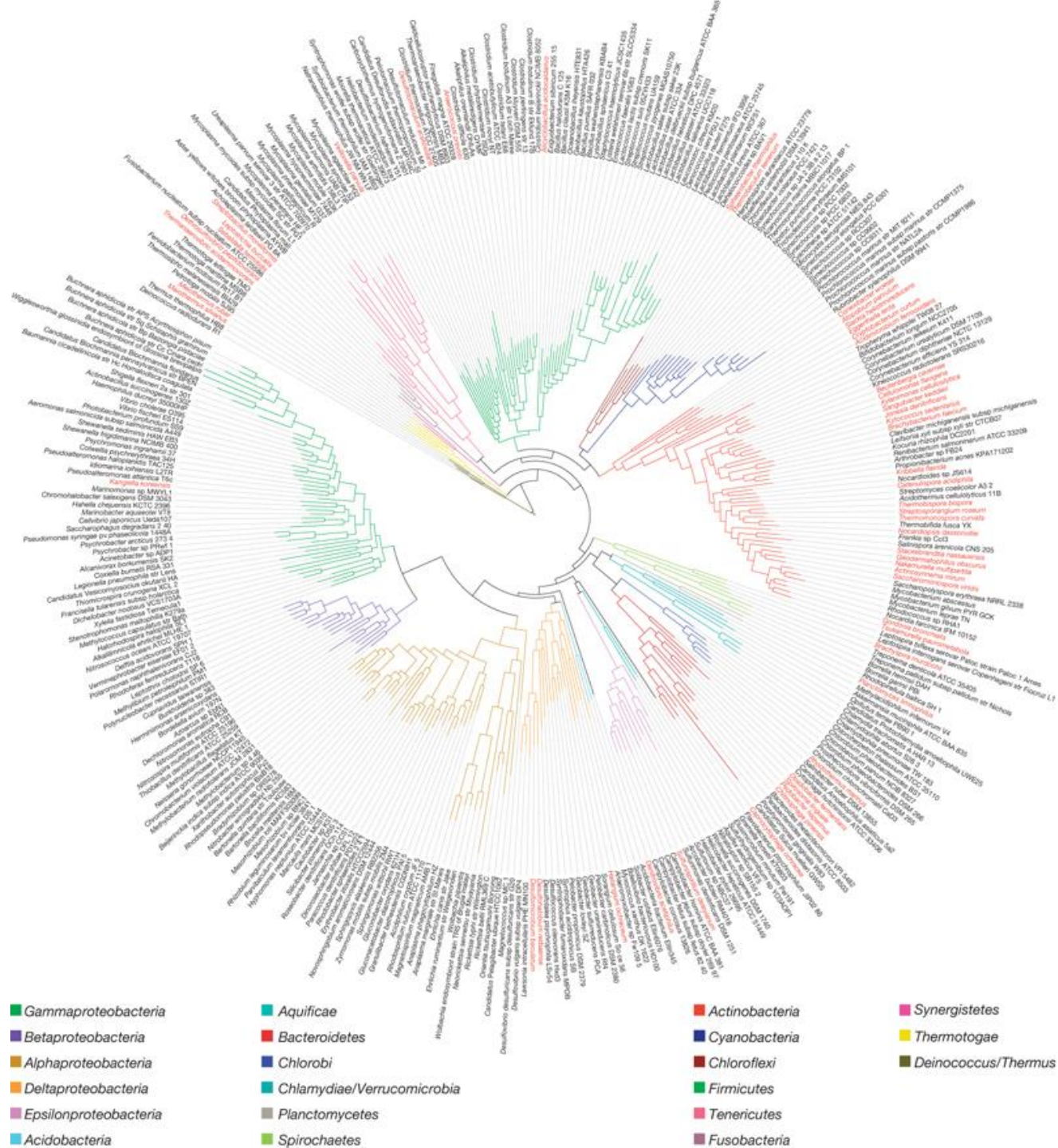|			
■ Gammaproteobacteria	■ Aquificae	■ Actinobacteria	■ Synergistetes
■ Betaproteobacteria	■ Bacteroidetes	■ Cyanobacteria	■ Thermotogae
■ Alphaproteobacteria	■ Chlorobi	■ Chloroflexi	■ Deinococcus/Thermus
■ Deltaproteobacteria	■ Chlamydiae/Verrucomicrobia	■ Firmicutes	
■ Epsilonproteobacteria	■ Planctomycetes	■ Tenericutes	
■ Acidobacteria	■ Spirochaetes	■ Fusobacteria	

Wu et al (2009)

Phylogeny

- Evolutionary ties between organisms by analyzing changes occurring in different organisms during evolution

- Understand relationships between an ancestral sequence and its descendants

- Estimate time of divergence between a group of organisms that share a common ancestor
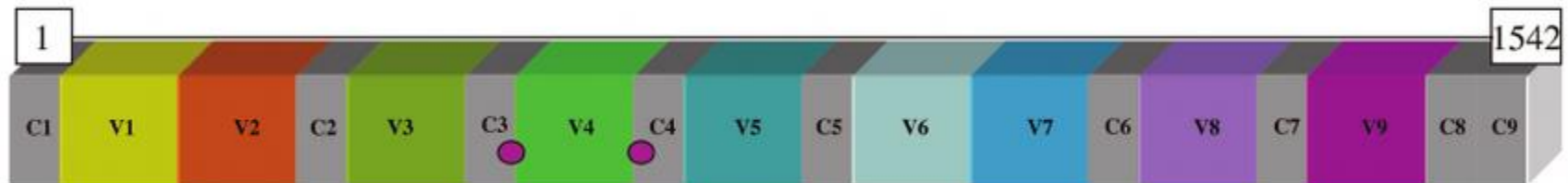
Evolutionary Process

- Mutations
  - Changes in the nucleotide sequence of an organism's genome
  - Occur because of errors in replication, UV radiation, and other factors
  - Adaptative mutations improve fitness of an organism, increasing its survival
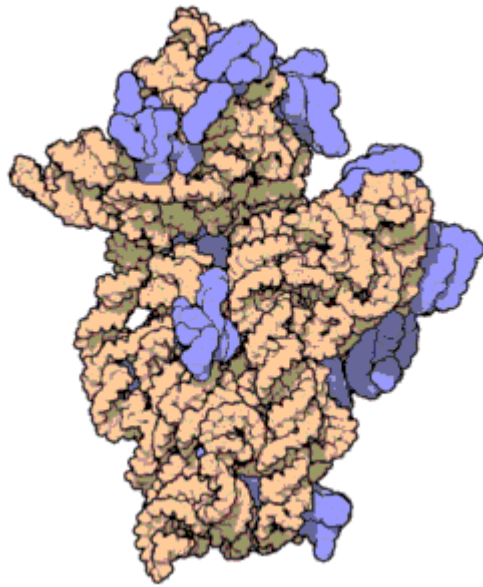- Other genetic changes include gene duplication, horizontal gene transfer, and gene loss

Evolutionary Analysis: Theoretical Aspects

- *Phylogeny*
  - Evolutionary history of a group of organisms
  - Inferred indirectly from nucleotide sequence data

- *Molecular clocks (chronometers)*
  - Certain genes and proteins that are measures of evolutionary change
  - Major assumptions of this approach are that nucleotide changes occur at a constant rate, are generally neutral, and are random

Evolutionary Analysis: Theoretical Aspects

- The most widely used molecular clocks are small subunit ribosomal RNA (SSU rRNA)
  - Found in all domains of life
    - 16S rRNA in prokaryotes and 18S rRNA in eukaryotes
  - Functionally constant
  - Sufficiently conserved (change slowly)
  - random sequence changes are a more accurate measure of time (evolution)
  - Sufficient length
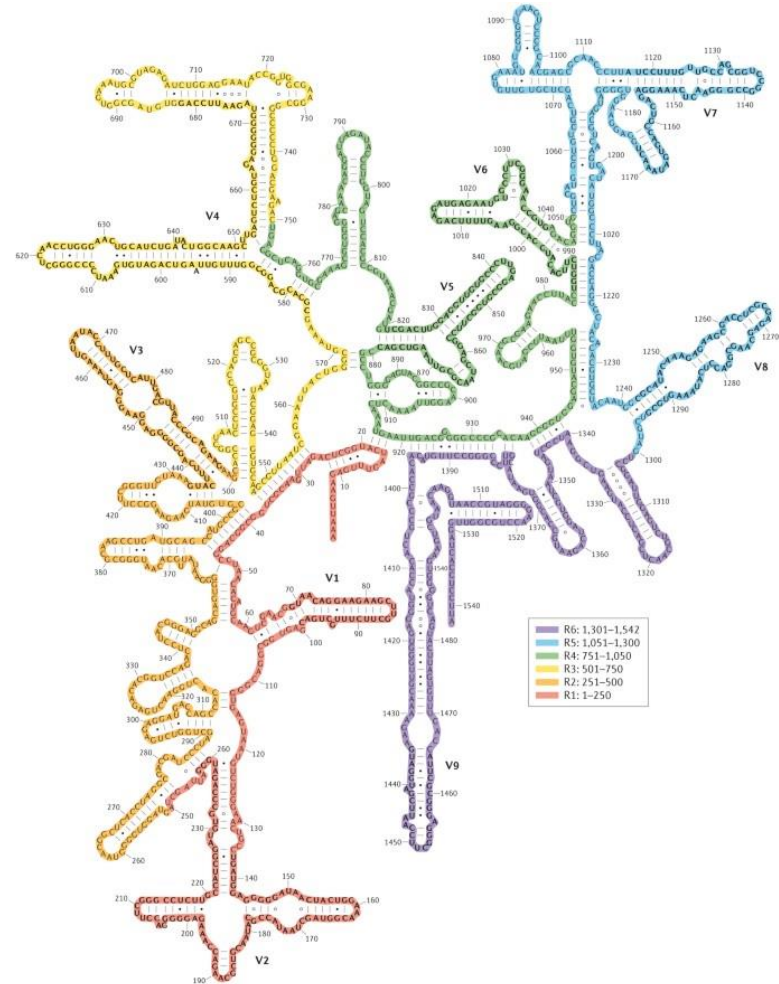 - Multiple copies (*E. coli*- 7 copies of rRNA)

Prokaryotic Ribosome

Large Subunit (LSU)

5S rRNA

23S rRNA

Small Subunit (SSU)

16S rRNA

R6: 1,301–1,542
R5: 1,051–1,300
R4: 751–1,050
R3: 501–750
R2: 251–500
R1: 1–250

Nature Reviews | Microbiology

16S rRNA

- 16S rRNA molecule present in all bacteria
- Broad range primers: amplification of universal regions
- ~66% variability in the first 500 bases
- Total sequence- distinct between related taxa/strains

   - description of new species

97% cut off- bacterial taxon delineation

Sequence Conservation Level

nearly universal ——————

intermediate ——

hypervariable ·············
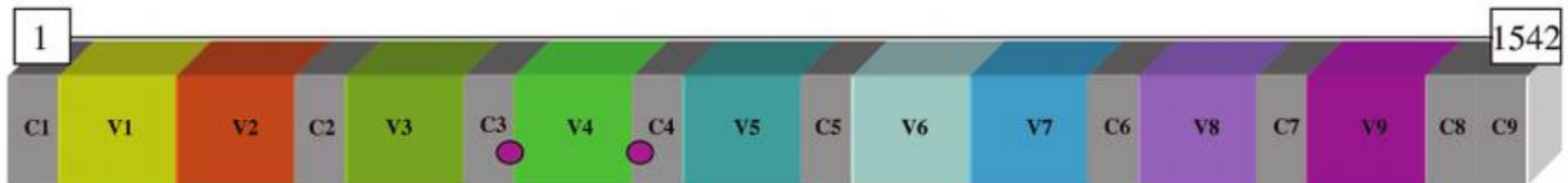
Evolutionary Analysis: Theoretical Aspects

- Carl Woese
    - Pioneered the use of SSU rRNA for phylogenetic studies in 1970s
    - Established the presence of three domains of life:
        - *Bacteria, Archaea,* and *Eukarya*
    - Provided a unified phylogenetic framework for *Bacteria*
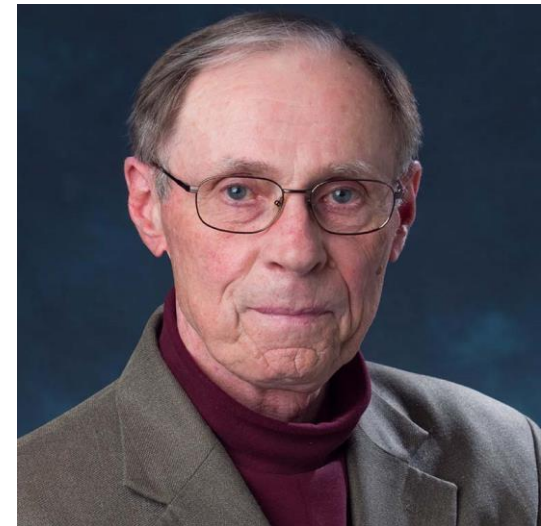
Evolutionary Analysis: Theoretical Aspects

- The Ribosomal Database Project (RDP)
  - A large collection of rRNA sequences
    - Currently contains >3,356,809 sequences
  - Provides a variety of analytical programs

RDP Database

my rdp
login

RDP Taxonomy 18 :: August 14, 2020

RDP Release 11, Update 5 :: September 30, 2016

3,356,809 16S rRNAs :: 125,525 Fungal 28S rRNAs
Find out what's new in RDP Release 11.5 *here*.

Cite RDP's latest tool articles.

RDP provides quality-controlled, aligned and annotated Bacterial and Archaeal 16S rRNA sequences, and Fungal 28S rRNA sequences, and a suite of analysis tools to the scientific community. New to RDP release 11:

- RDP tools have been updated to work with the new fungal 28S rRNA sequence collection.
- A new Fungal 28S Aligner and updated Bacterial and Archaeal 16S Aligner. We optimized the parameters for these secondary-structure based Infernal aligners to provide improved handling for partial sequences.
- Updated RDPipeline offers extended processing and analysis tools to process high-throughput sequencing data, including single-strand and paired-end reads.
- Most of the RDP tools are now available as open source packages for users to incorporate in their local workflow.

ANNOUNCEMENTS

RDP News

01/04/2022 RDP Systems Are Running
RDP and FunGene websites are back online! We experienced a multi-server hardware failure in October that took the sites offline The cause has stil...

10/04/2020 RDP Taxonomy Updated
Now using RDP taxonomy 18. Check the updated release and reinstall any older versions of the rdp classifier to use the new taxonomy.

12/12/2018 RDP and Fungene Pipelines are back online now!
The issues causing long delays in RDP and Fungene Pipelines in the past week have been resolved. Users need to re-submit the jobs for which resul...

12/06/2018 RDP and Fungene Pipeline problems
RDP Pipeline and Fungene Pipeline are currently not working properly due to technical issues. While RDP team is working hard on restoring the servi...

11/14/2018 myRDP and RDP Pipeline back to normal
The issue that caused submitted jobs being delayed in myRDP and RDP Pipeline has been resolved. All service functions are working normally.

06/05/2018 RDP phone system restored
RDP phone service is now back online.

06/04/2018 RDP phone system down
RDP phone system is temporarily out of service!

03/05/2018 RDP web tool problems fixed!

03/05/2018 RDP web tool problems
We apologize for ongoing problems with several RDP web tools. Our team is now working hard to get them fixed!

Hb Hierarchy Browser
Cl Classifier
Pm Probe Match
Fg FunGene

Mg MIxS GoogleSheets
Lc Library Compare
Sm Sequence Match
Rp RDPipeline

Al Aligner
Tb Tree Builder
Os RDP Open Source
Tu Tutorials

SILVA Database

SILVA

Welcome to the SILVA rRNA database project

A comprehensive on-line resource for quality checked and aligned ribosomal RNA sequence data.

SILVA provides comprehensive, quality checked and regularly updated datasets of aligned small (16S/18S, SSU) and large subunit (23S/28S, LSU) ribosomal RNA (rRNA) sequences for all three domains of life (*Bacteria, Archaea* and *Eukarya*).

SILVA are the official databases of the software package **ARB**.

For more background information → Click here

SILVAngs

Check out our service for Next Generation Amplicon data

SILVA Alignment, Classification and Tree (ACT) Service

The SILVA ACT service combines alignment, search and classify as well as reconstruction of trees in a

News

20.12.2022

Merry XMas and a Happy New Year

The SILVA Team wishes you a Merry Christmas & Happy New Year. Many thanks for using SILVA and all your support to improve SILVA and SILVAngs. Looking forward to see you again in 2023.

18.11.2022

de.NBI Quarterly Newsletter

Annual Meeting of the de.NBI Industrial Forum - de.NBI Cloud User Meeting - 2022 - BioHackathon Germany

07.10.2022

SILVA.DSMZ.Permanent

Great news today! SILVA is now part of the integrated data platform DSMZ Digital Diversity. This cooperation will guaranty the long-term sustainability of SILVA. We are now entering a transition phase to migrate SILVA to our new host the Leibniz-Institute DSMZ-German Collection of Microorganisms and Cell Cultures, which is one of the largest biological resource centers worldwide.

07.03.2022

Update on SILVA taxonomy

This news provides an overview on the latest developments regrading the SILVA project and its taxonomy.

Evolutionary Analysis: Analytical Methods

- Comparative rRNA sequencing is a routine procedure that involves the following:

    - Amplification of the region or marker encoding SSU rRNA
    - Sequencing of the amplified region or marker
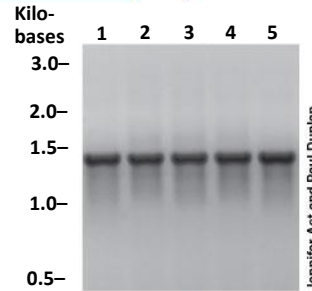   - Analysis of sequence in reference to other sequences
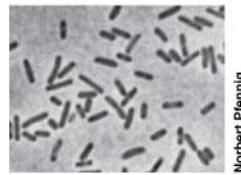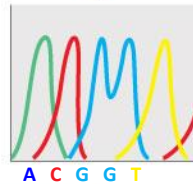
Isolate DNA

16 S gene

Amplify
16S rRNA
by PCR

Run on agarose
gel; check for
correct size

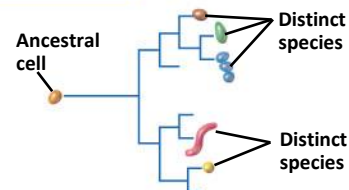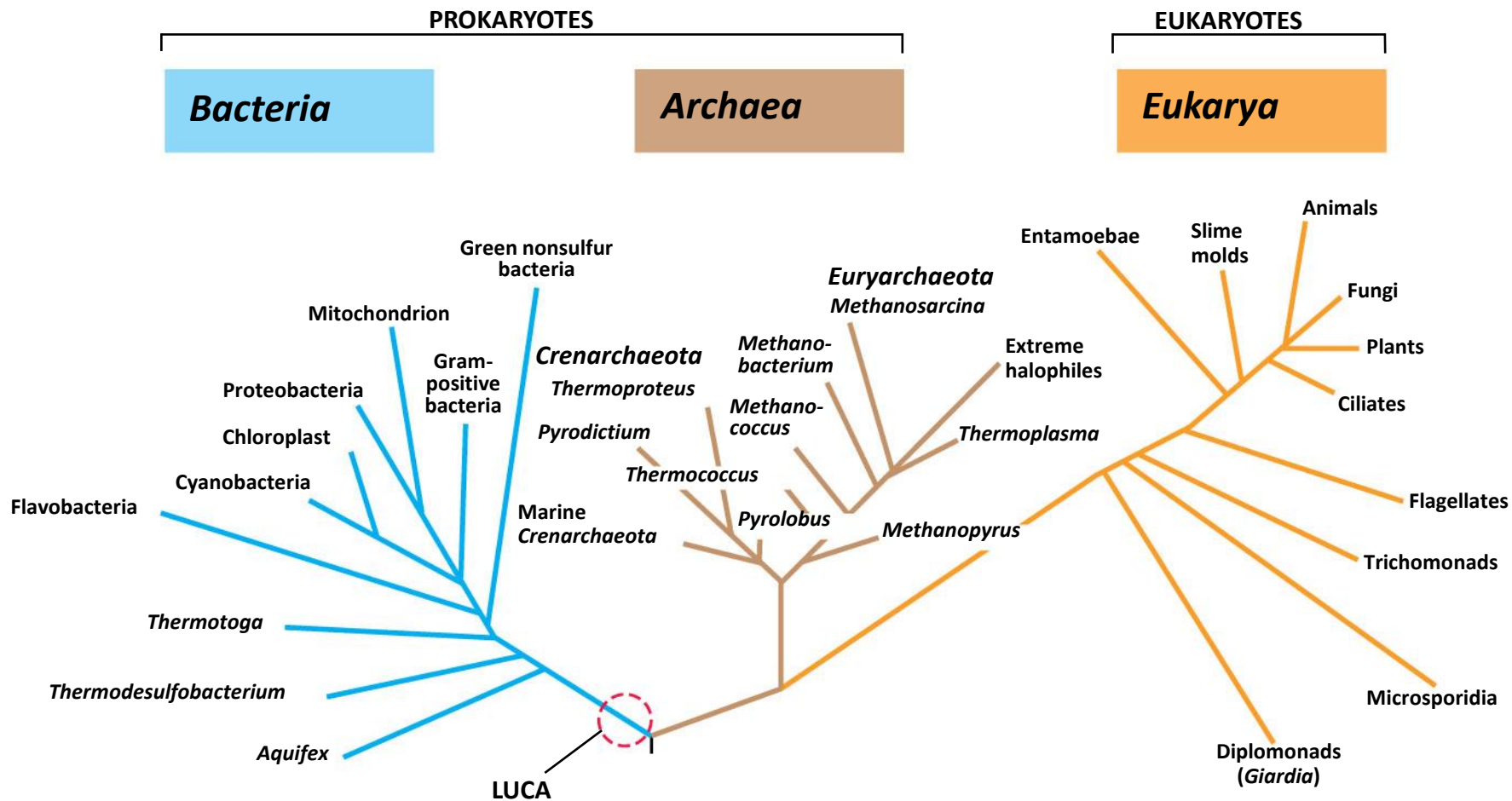| Kilo-bases	1	2	3	4	5
3.0–					
2.0–					
1.5–					
1.0–					
0.5–					

Sequence

A C G G T

Align sequences;
generate tree

Ancestral
cell

Distinct
species

Distinct
species

Microbial Phylogeny

- Domain *Bacteria*
  - Contains at least 80 major evolutionary groups (phyla)
  - Many groups defined from environmental sequences alone—i.e., there are no cultured representatives
  - Many groups are phenotypically diverse—i.e., physiology and phylogeny not necessarily linked

Microbial Phylogeny

- Eukaryotic organelles originated within *Bacteria*
  - Mitochondria arose from *Proteobacteria*
  - Chloroplasts arose from the cyanobacteria
- Domain *Archaea* consists of two major groups:
  - *Crenarchaeota*
  - *Euryarchaeota*
- Each of the three domains of life can be characterized by various phenotypic properties

Genotypic Analysis

- Several methods of genotypic analysis are available:
    - DNA–DNA hybridization
    - DNA profiling
    - Multilocus sequence typing (MLST)
    - GC ratio

Genotypic Analysis

- Multilocus sequence typing (MLST)
  - Method in which several different "housekeeping genes" from an organism are sequenced
  - Has sufficient resolving power to distinguish between very closely related strains

  Multilocus sequence analysis- based on concatenation of sequences representing key genes