Hungarian Molecular Life Sciences - Eger - 2015

The results of Whole-Genome Analyses (WGA) force changes in Prokaryote systematics and result new concepts in ecology

Károly MÁRIALIGETI[1], Tamás FELFÖLDI[1], András TÁNCSICS[2]

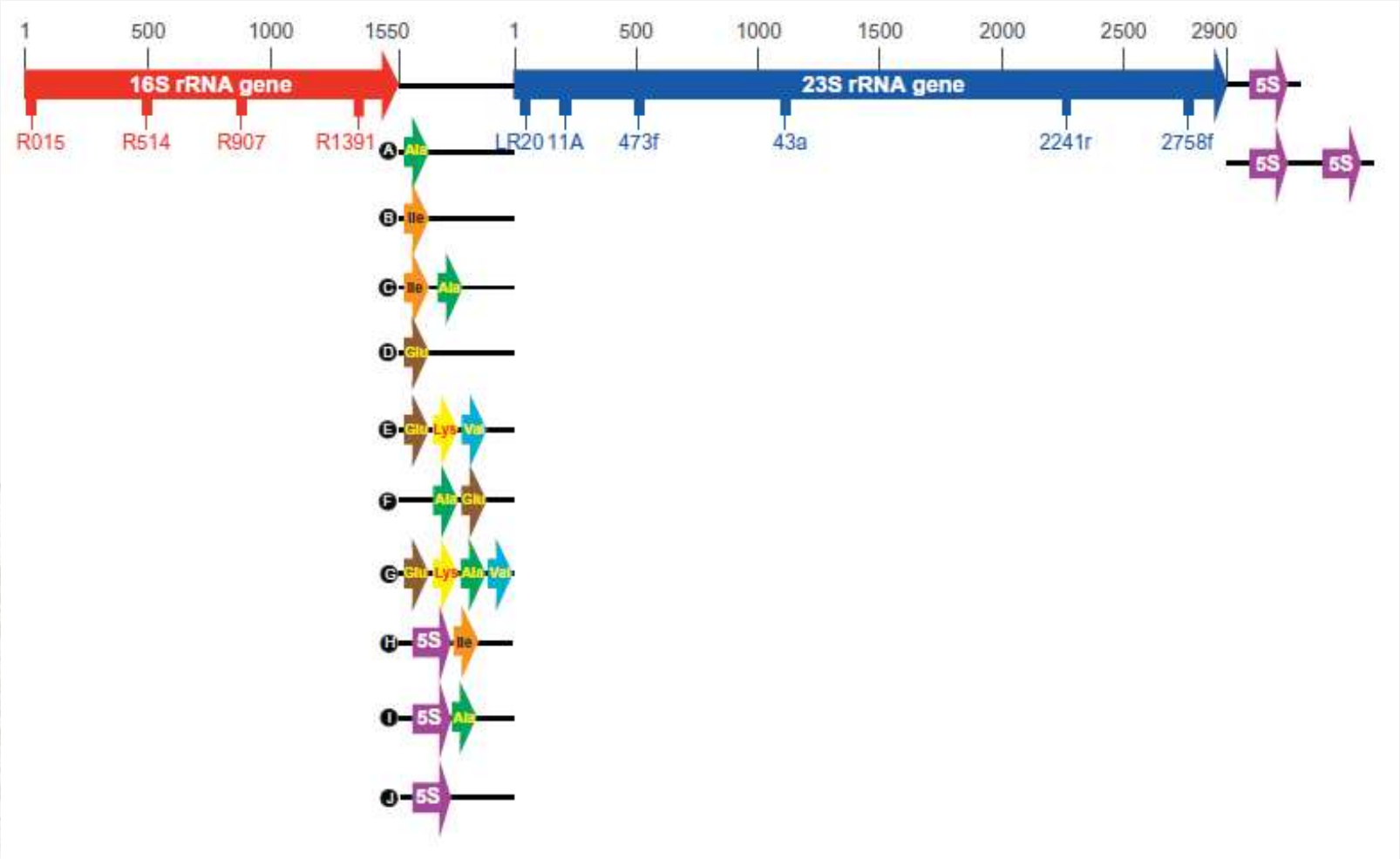
[1]Eötvös Loránd University, Department of MicrObiology, Budapest, [2]Regional University Center of Excellence in Environmental Industry, Szent István University, Gödöllő, Hungary

HUNGARIAN MOLECULAR LIFE SCIENCES - EGER - 2015

THE RESULTS OF WHOLE-GENOME ANALYSES (WGA) FORCE CHANGES IN PROKARYOTE SYSTEMATICS AND RESULT NEW CONCEPTS IN ECOLOGY

KÁROLY MÁRIALIGETI[1], TAMÁS FELFÖLDI[1], ANDRÁS TÁNCSICS[2]

[1]EÖTVÖS LORÁND UNIVERSITY, DEPARTMENT OF MICROBIOLOGY, BUDAPEST, [2]REGIONAL UNIVERSITY CENTER OF EXCELLENCE IN ENVIRONMENTAL INDUSTRY, SZENT ISTVÁN UNIVERSITY, GÖDÖLLŐ, HUNGARY



THAT TIME: SSU RRNA

WOESE AND FOX, 1977.

„THE CHARACTERS WHICH NATURALISTS CONSIDER AS SHOWING TRUE AFFINITY BETWEEN ANY TWO OR MORE SPECIES, ARE THOSE WHICH HAVE BEEN INHERITED FROM A COMMON PARENT”

DARWIN, 1859

EVOLUTION, PHYLOGENY

AD HOC COMMITTEE OF THE JUDICAL COMMISSION OF THE ICSB (INTERNATIONAL COMMITTEE ON THE SYSTEMATICS OF BACTERIA) (1976):

FIRST DRAFT. APPROVED LIST OF BACTERIAL NAMES.

INT. J. SYST. BACTERIOL., 26, 563-599.

SYSTEMATICS, TAXONOMY

SAMPLE

(PHYSICAL, CHEMICAL, ETC. CHARACTERIZATION OF THE SAMPLE)

↓

ENRICHMENT ON MEDIA

(GUILD SELECTION)

↓

ISOLATION

↓

PURE CULTURE

↓

STRAIN CHARACTERIZATION

1.

STRAIN

↓

TYPE STRAIN

↓

STRAIN / CULTURE COLLECTION (ATCC)

2. VALID DESCRIPTION OF A NEW SPECIES: EFFECTIVE PUBLICATION OF THE STANDARD DESCRIPTION IN THE INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY (IJSEM) (FORMERLY INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY - IJSB). SPECIES DESCRIPTION IN AN OTHER JORNAL MUST BE VALIDATED IN IJSEM (VALIDATION LISTS).

SPECIES

THE NATURAL, BIOLOGICAL SPECIES CONCEPTION:

„TWO COMMUNITIES HAVE TO BE REGARDED AS TWO SPECIES IF THEY DO NOT EXCHANGE GENES. THE INHIBITION OF GENE FLOW CAN RESULT FROM GEOGRAPHICAL/SPATIAL/TEMPORAL ISOLATION OF TWO COMMUNITIES THAT SHARE A COMMON ANCESTRY. OTHER GENETICALLY CONTROLLED MEANS TO ACHIEVE ISOLATION CAN BE: BEHAVIOURAL, ANATOMICAL, PHYSIOLOGICAL."

MAYR, 1963; GIBBONS, 1996; MORELL, 1996 ETC.

„A SPECIES FORMS A POPULATION WHOSE MEMBERS ARE ABLE TO INTERBREED FREELY UNDER NATURAL CONDITIONS."

WILSON, 1992

SPECIES

AMONG PROKARYOTES A CONSENSUS SPECIES DEFINITION:

„A BACTERIAL SPECIES MAY BE REGARDED AS A COLLECTION OF STRAINS THAT SHARE MANY FEATURES IN COMMON AND DIFFER CONSIDERABLY FROM OTHER STRAINS. … ONE STRAIN … IS DESIGNATED AS THE TYPE STRAIN … THE PERMANENT EXAMPLE OF THE SPECIES, … REFERENCE SPECIEMEN"

STALEY, AND KRIEG, 1984

A BACTERIAL SPECIES IS „A CATEGORY THAT CIRCUMSCRIBES A (PREFERABLY) GENOMICALLY COHERENT GROUP OF INDIVIDUAL ISOLATES/STRAINS SHARING A HIGH DEGREE OF SIMILARITY IN (MANY) INDEPENDENT FEATURES, COMPARATIVELY TESTED UNDER HIGHLY STANDARDISED CONDITIONS"

STACKEBRANDT ET AL., 2002

TWO STRAINS REPRESENT THE SAME SPECIES WHEN THEY SHARE

> 70% DNA-DNA HYBRIDISATION RELATEDNESS (HOMOLOGY),

AND

> 97% 16 S RDNA GENE SIMILARITY.

STACKEBRANDT AND GOEBEL, 1994

STRAIN

A STRAIN IS (PREFEREABLY) A PURE CULTURE DENOTED BY THREE ESSENTIAL CHARACTERS:

- STRAIN DESIGNATION (NUMBER);
- KNOWN ORIGIN;
- MAINTENANCE BY CONTINUOUS SUBCULTURING.

A SPECIES IS "... A FICTION, A MENTAL CONSTRUCT WITHOUT OBJECTIVE EXISTENCE".

HALDANE, 1949

"THE ULTIMATE SCIENTIFIC GOAL OF BIOLOGICAL CLASSIFICATION CANNOT BE ACHIEVED IN THE CASE OF BACTERIA."

VAN NIEL AND STANIER, 1936-1962

„THERE WILL NEVER BE A DEFINITIVE CLASSIFICATION OF BACTERIA..."

VANDAMME ET AL., 1996

„THE COMPLETE DEOXYRIBONUCLEIC ACID (DNA) SEQUENCE WOULD BE THE REFERENCE STANDARD TO DETERMINE PHYLOGENY AND THAT PHYLOGENY SHOULD DETERMINE TAXONOMY”

WAYNE ET AL., 1987

SAMPLE

(PHYSICAL, CHEMICAL, ETC. CHARACTERIZATION OF THE SAMPLE)

↓

EXTRACTION OF NUCLEIC ACIDS

(METHOD DEPENDENT SELECTIVITY)

↓

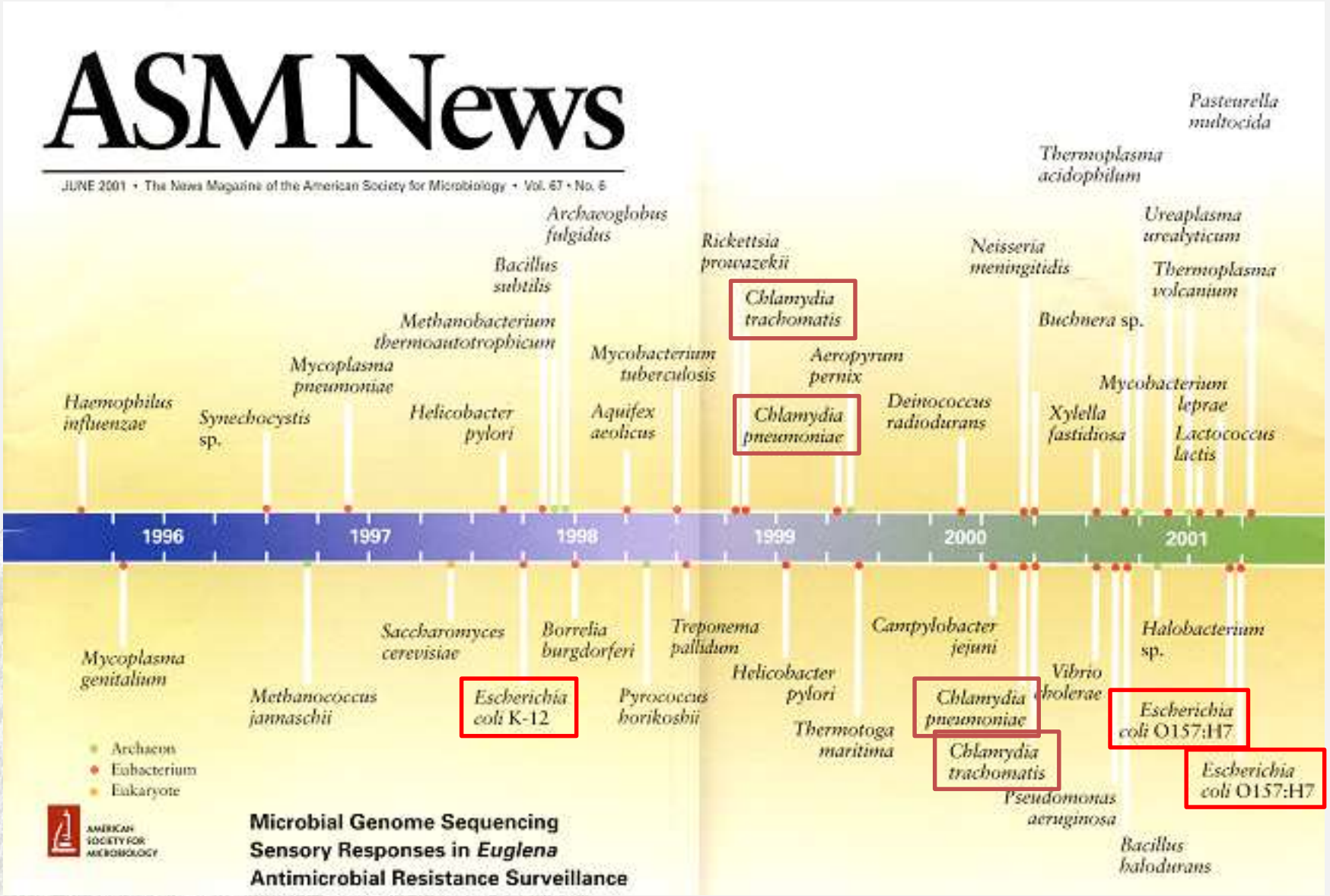
CONSENSUS PCR

↓

CLONE LIBRARY (CLONAL PCR)

↓

CLONE SEQUENCE (WGA, METAGENOME, ETC.)


ASM News
JUNE 2001 • The News Magazine of the American Society for Microbiology • Vol. 67 • No. 6
Haemophilus influenzae
Synechocystis sp.
Mycoplasma pneumoniae
Methanobacterium thermoautotrophicum
Helicobacter pylori
Bacillus subtilis
Archaeoglobus fulgidus
Aquifex aeolicus
Mycobacterium tuberculosis
Rickettsia prowazekii
Chlamydia trachomatis
Chlamydia pneumoniae
Aeropyrum pernix
Deinococcus radiodurans
Neisseria meningitidis
Thermoplasma acidophilum
Buchnera sp.
Xylella fastidiosa
Pasteurella multocida
Ureaplasma urealyticum
Thermoplasma volcanium
Mycobacterium leprae
Lactococcus lactis
1996
1997
1998
1999
2000
2001
Mycoplasma genitalium
Methanococcus jannaschii
Saccharomyces cerevisiae
Escherichia coli K-12
Borrelia burgdorferi
Treponema pallidum
Pyrococcus horikoshii
Helicobacter pylori
Thermotoga maritima
Campylobacter jejuni
Chlamydia pneumoniae
Chlamydia trachomatis
Pseudomonas aeruginosa
Vibrio cholerae
Halobacterium sp.
Escherichia coli O157:H7
Escherichia coli O157:H7
Bacillus halodurans
Archaeon
Eubacterium
Eukaryote
AMERICAN SOCIETY FOR MICROBIOLOGY
Microbial Genome Sequencing
Sensory Responses in Euglena
Antimicrobial Resistance Surveillance

Fájl Szerkesztés Nézet Előzmények Könyvjelzők Eszközök Súgó

MEP Home | Microbial Earth - Prototype

www.microbial-earth.org/cgi-bin/index.cgi

Keresés

About the Microbial Earth Project

The Microbial Earth project is an international effort to generate a comprehensive catalog from genome sequences of all the archaeal and bacterial type strains. The name of the project comes from the recognition that Earth is a predominantly a microbial planet, and by effect in order to understand life on our planet, we need to understand how microbial life works. » more

If you want to support this project **Adopt a Type Strain**

News & Updates

- December 2012
  Presentation of the MEP at the Biodesert International Conference in Tunesia
- November 2012
  Launching of the MEP web site

Type Strains Map

Statistics

Type Strains of Archaea and Bacteria: 10911

- Finished: 1650
- Draft: 113
- With Genome Projects: 1567
- Without Genome Project: 7581

Project Status

Complete: 1650

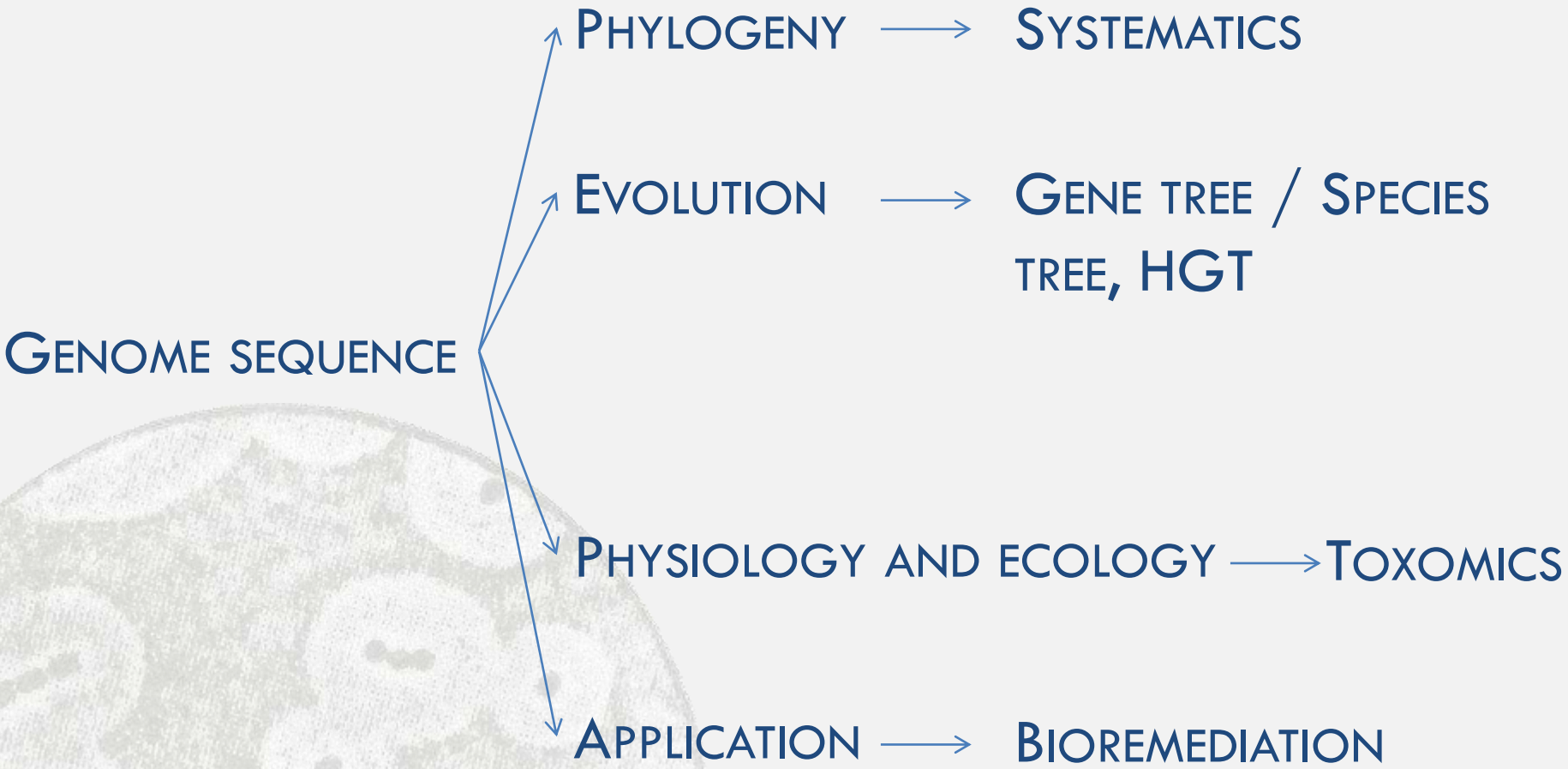
In progress: 1680

Proposed: 7581

Start HU 12:24

Domain	Species with:			
	Validly published name	16S rRNA gene sequence (type strain)	Genome sequence (any strain)	Genome sequence (type strain)
Bacteria	10 546	10 420	2518	1567
Archaea	398	397	176	158
Total (prokaryotes)	10 944	10 817	2694	1725
Percentage	100 %	98.8 %	24.6 %	15.8 %

Márialigeti et al. – Hungarian Molecular Life Sciences – Eger – 2015


Phylogeny → Systematics
Evolution → Gene tree / Species tree, HGT
Genome sequence
Physiology and ecology → Toxomics
Application → Bioremediation

Comparing genomes…

Difficulties:

- Large differences in genome size (0.14 - 0,58-13.7 Mbp)
- Genes are different (few universal genes)
- Genes are at different positions within the genomes
- Horizontal gene tranfer blurs phylogenetic relationships
- Evolution of the same gene may be different comparing different taxa
- No generally accepted scheme (NO STANDARD METHOD)

Overall genome relatedness indices (OGRI)

Average nucleotide identity (ANI)

- a mean of identity values between multiple sets of orthologous regions shared by two genomes
- artificially cutting the query genome sequence into fragments of 1020 bp, simulating the DNA fragmentation at DDH
- ANI values correlate well with DDH values
- based on ANI, species threshold for 16S rDNA comp. is 98.65%

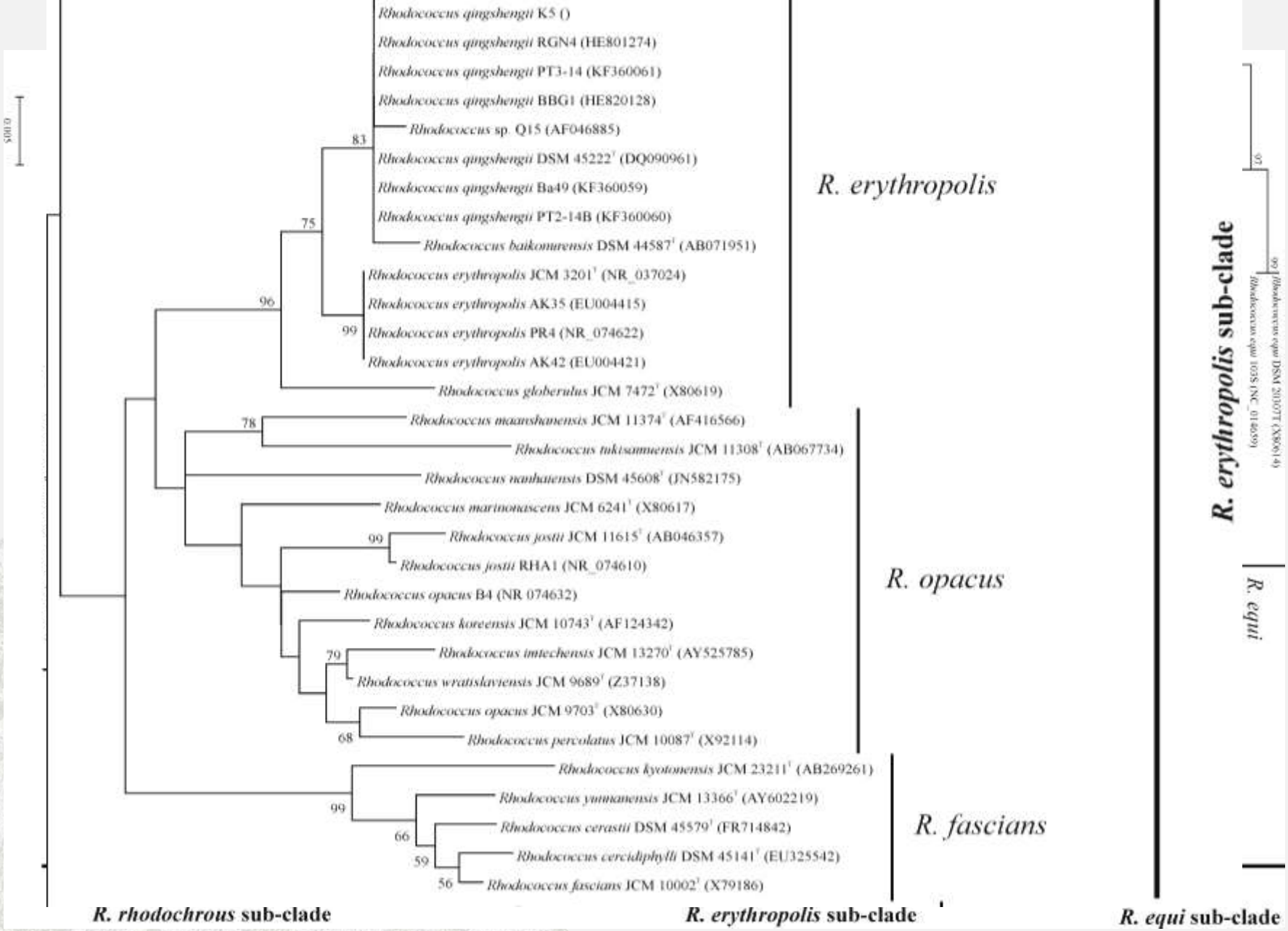
Tetranucleotide frequency

comparison of the frequencies of all 256 possible tetranucleotide (A, T, G, C) combinations

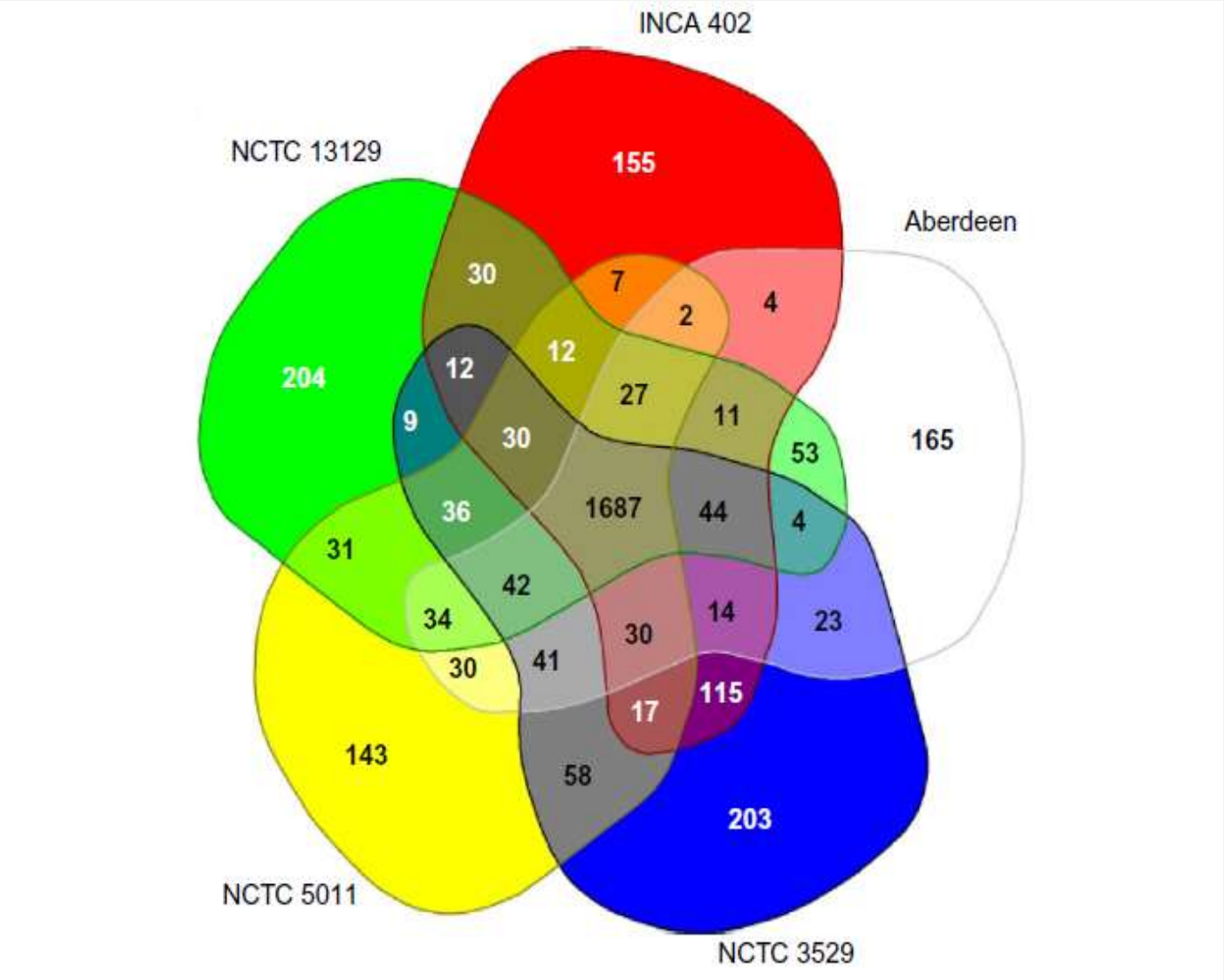
Genome BLAST distance phylogeny (GBDP)

two genome sequences are aligned and compared

Márialigeti et al. – Hungarian Molecular Life Sciences – Eger – 2015



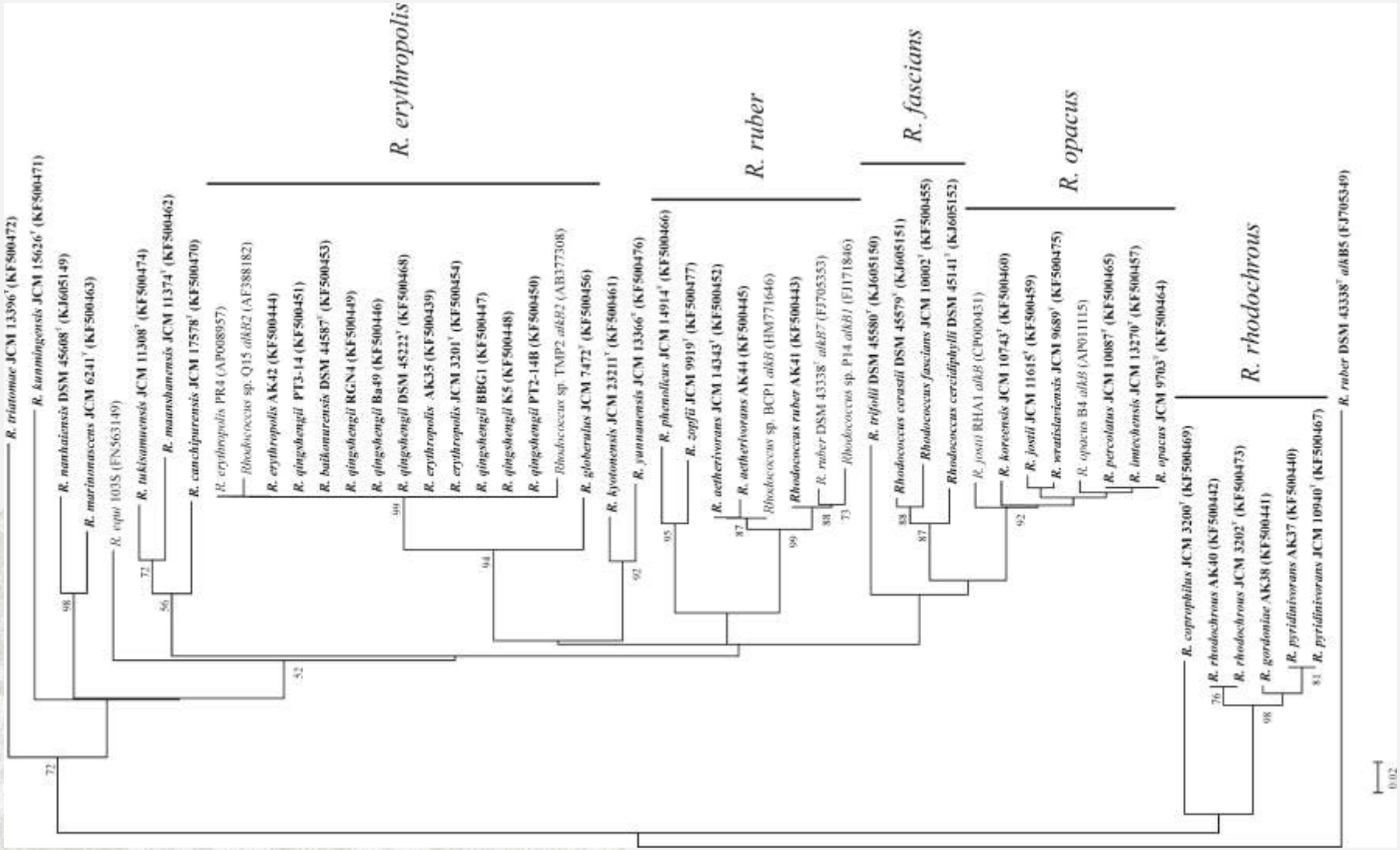
16S rRNS gene



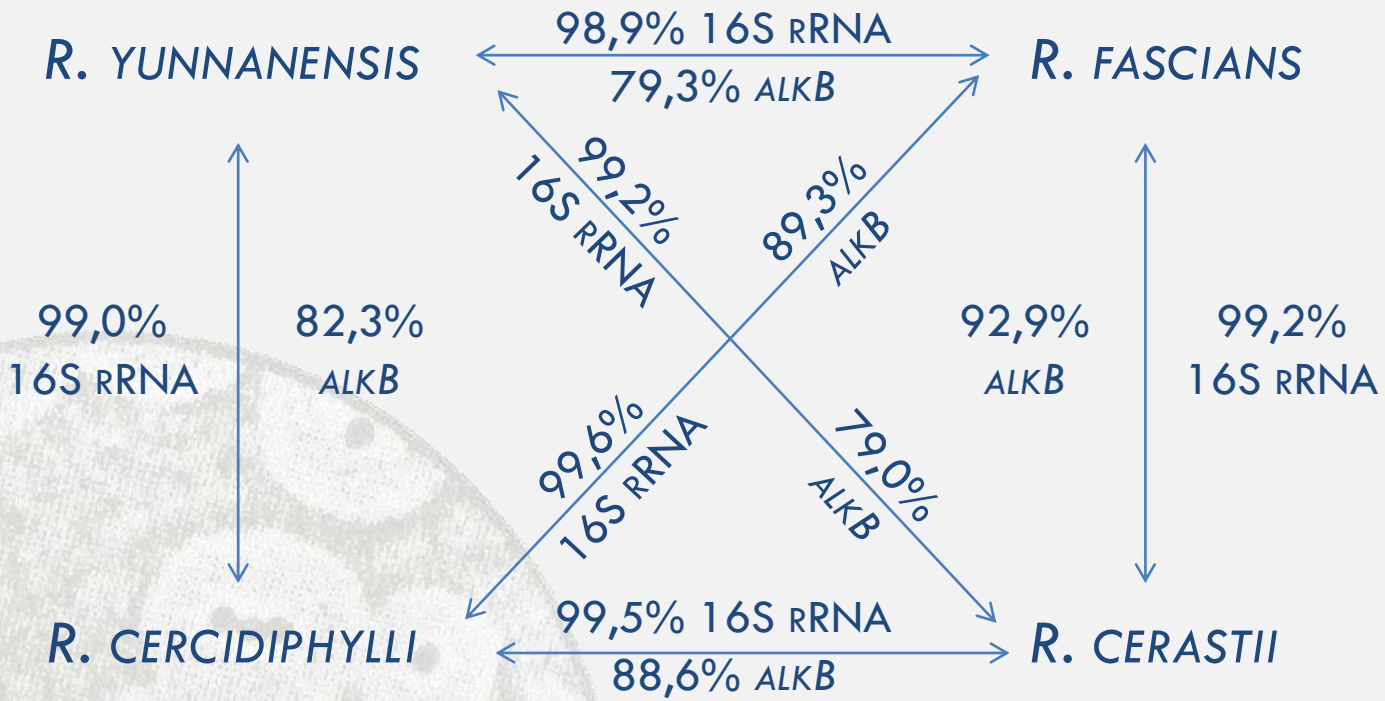
WENN DIAGRAMM:

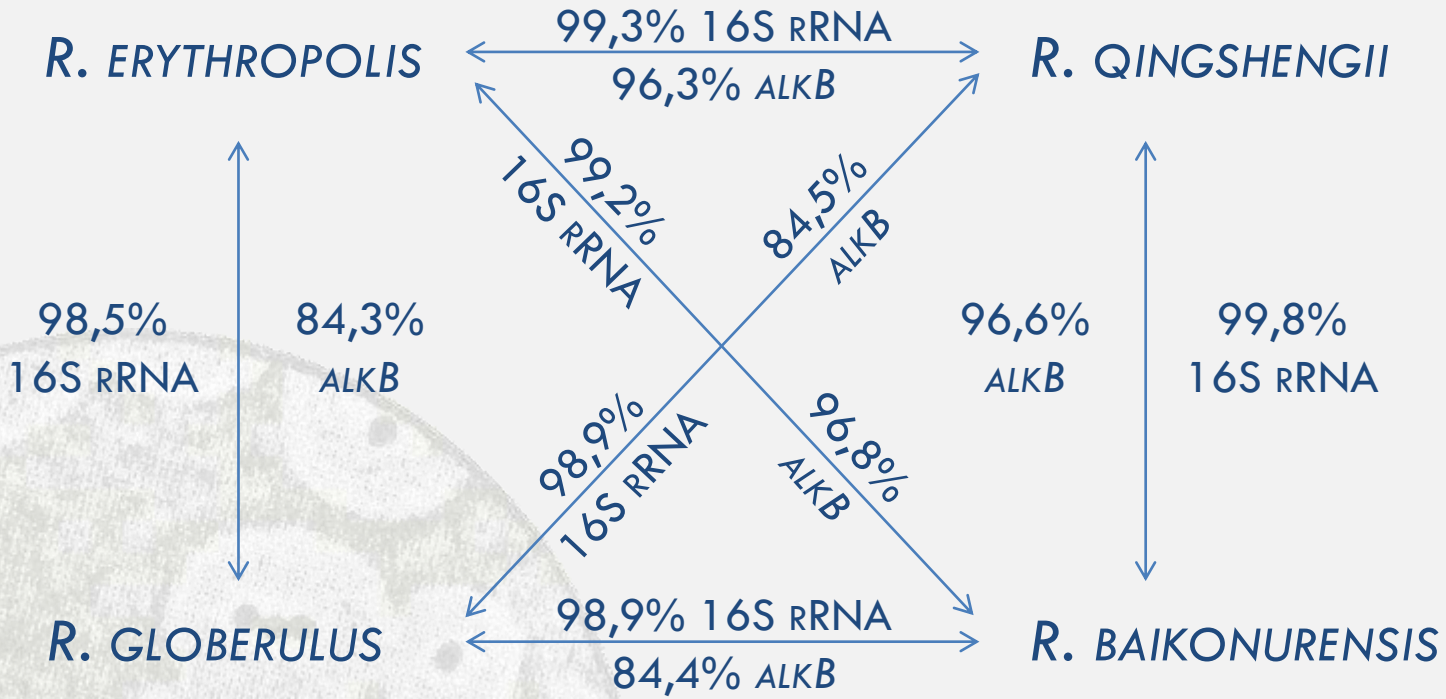
PAN GENOME: 3264 GENES; CORE GENOME: 1687 GENES; DISPENSABLE GENOME: 1577 GENES

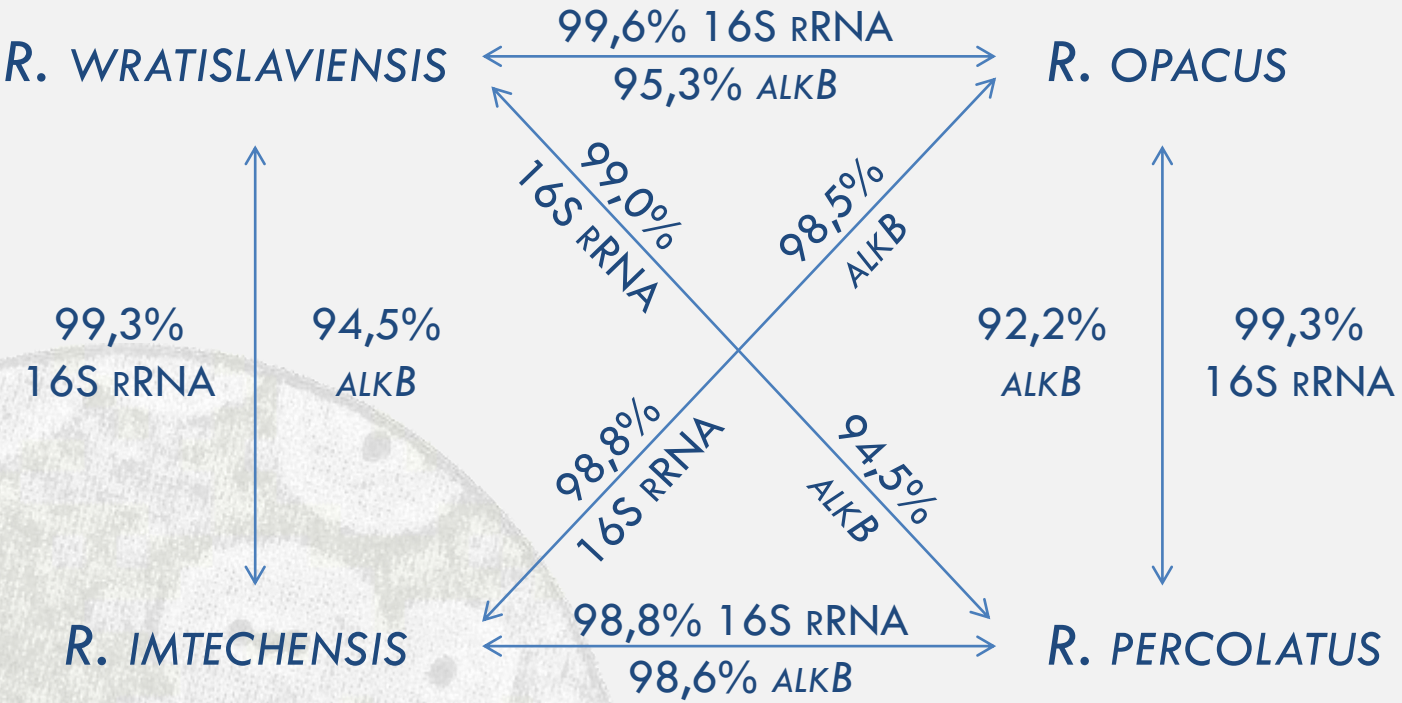
Márialigeti et al. – Hungarian Molecular Life Sciences – Eger – 2015



ALKB PROTEINE


R. YUNNANENSIS
98,9% 16S rRNA
79,3% alkB
R. FASCIANS
99,2% 16S rRNA
89,3% alkB
99,0% 16S rRNA
82,3% alkB
92,9% alkB
99,2% 16S rRNA
99,6% 16S rRNA
79,0% alkB
R. CERCIDIPHYLLI
99,5% 16S rRNA
88,6% alkB
R. CERASTII


R. ERYTHROPOLIS
99,3% 16S rRNA
96,3% alkB
R. QINGSHENGII
99,2% 16S rRNA
84,5% alkB
98,5% 16S rRNA
84,3% alkB
96,6% alkB
99,8% 16S rRNA
98,9% 16S rRNA
96,8% alkB
R. GLOBERULUS
98,9% 16S rRNA
84,4% alkB
R. BAIKONURENSIS



Márialigeti et al. – Hungarian Molecular Life Sciences – Eger – 2015

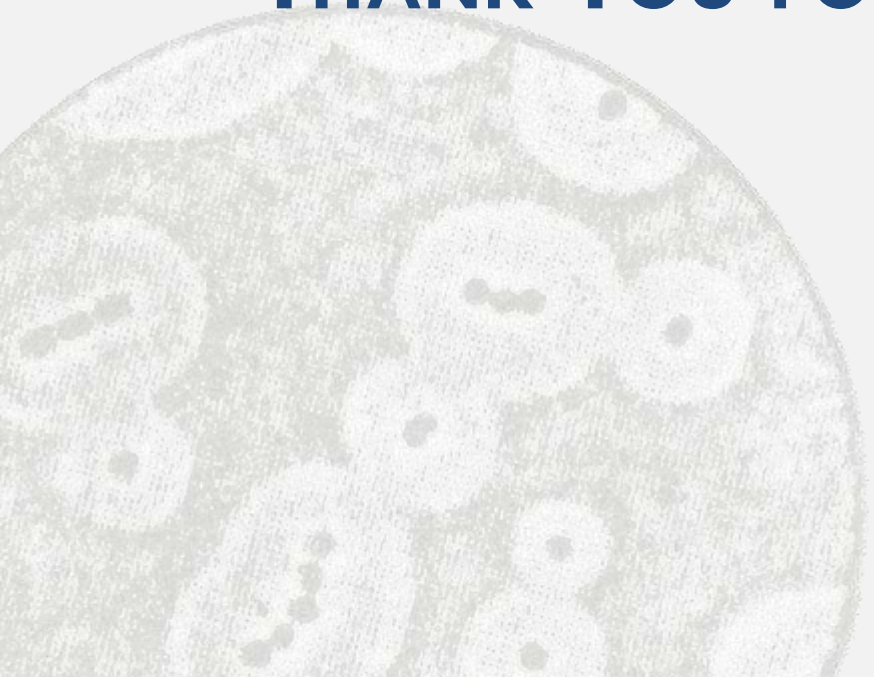
„THERE WILL NEVER BE A DEFINITIVE CLASSIFICATION OF BACTERIA…”

VANDAMME ET AL., 1996

„THE MODERN PRACTICE OF POLYPHASIC TAXONOMY IS COUNTERPRODUCTIVE IN LIGHT OF THE TREMENDOUS NUMBER OF BACTERIAL SPECIES THAT AWAITS FORMAL DESCRIPTION AND NAMING. BACTERIAL TAXONOMISTS MUST URGENTLY RECONSIDER HOW TO DESCRIBE AND NAME NOVEL BACTERIA IN THE GENOMIC ERA, AND SHOULD CONSIDER USING A FULL GENOME SEQUENCE AND A MINIMAL DESCRIPTION OF PHENOTYPIC CHARACTERISTICS AS A BASIC, SUFFICIENT, COST-EFFECTIVE AND APPROPRIATE BIOLOGICAL IDENTITY CARD FOR A SPECIES DESCRIPTION.”

VANDAMME, 2014

STANDARD CONSENSUS METHOD:

MULTI-LOCUS SEQUENCE ANALYSIS, BASED ON PHYLOGENETIC MARKER (CHRONOMETER) GENES TOGETHER WITH ECOLOGICALLY RELEVANT FUNCTIONAL GENES, AND PARALLEL APPLICATION OF HOMOLOGY AND SIMILARITY ASSESSMENTS.

THANK YOU FOR YOUR ATTENTION!