Welcome to Bacterial Population Genomics!

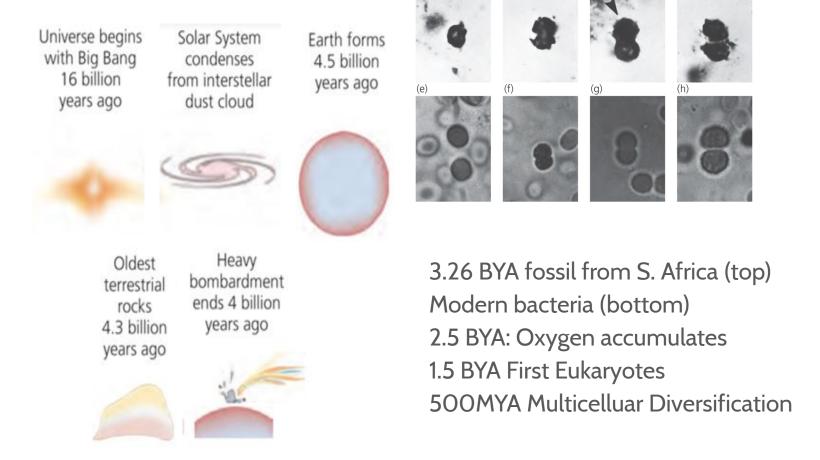
Introductions – Name, Academic Stage, Research Interests, Goal for this seminar

Introductory Concepts

- Bacterial diversity, evolution and ecology in relation to hosts
- Genomes, HGT and the "pan-genome"
- Biogeography
- Local adaptation

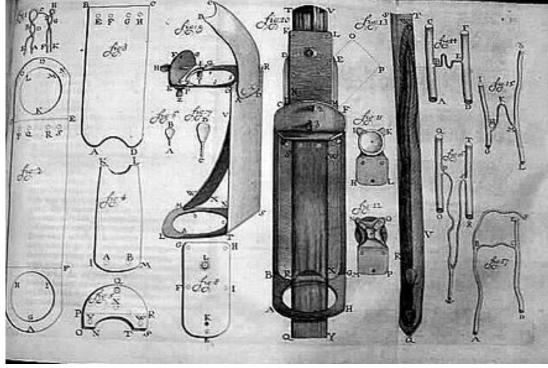
Resource Introduction: command line & kamiak accounts

Origin of Bacteria



Antonie van Leeuwenhoek (Dutch scientist)





Louis Pasteur (French microbiologist)





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Robert Koch (German physician)



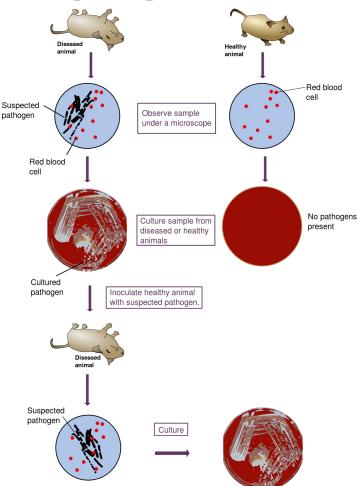
Koch's Postulates:

The microorganism must be found in abundance in all organisms suffering from the disease, but should not be found in healthy organisms.

② The microorganism must be isolated from a diseased organism and grown in pure culture.

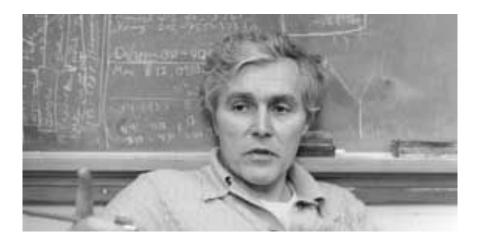
③ The cultured microorganism should cause disease when introduced into a healthy organism.

The microorganism must be reisolated from the inoculated, diseased experimental host and identified as being identical to the original specific causative agent.



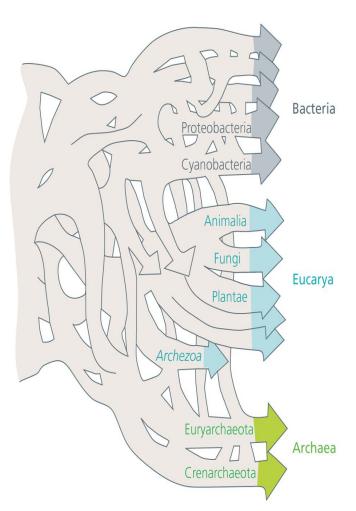
Carl Woese

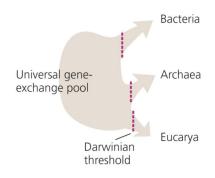
ribosomal tree of life



		1	2	3	4	5	6	7	8	9	10	11	12	13
1	Saccharomyces cerevisiae, 18S	_	0.29	0.33	0.05	0.06	0.08	0.09	0.11	0.08	0.11	0.11	0.08	0.08
	Lemna minor, 18S	0.29	_	0.36	0.10	0.05	0.06	0.10	0.09	0.11	0.10	0.10	0.13	0.07
3	L cell, 18S	0.33	0.36	_	0.06	0.06	0.07	0.07	0.09	0.06	0.10	0.10	0.09	0.07
4	Escherichia coli	0.05	0.10	0.06	_	0.24	0.25	0.28	0.26	0.21	0.11	0.12	0.07	0.12
5.	Chlorobium vibrioforme	0.06	0.05	0.06	0.24	· -	0.22	0.22	0.20	0.19	0.06	0.07	0.06	0.09
6.	Bacillus firmus	0.08	0.06	0.07	0.25	0.22	_	0.34	0.26	0.20	0.11	0.13	0.06	0.12
7.	Corynebacterium diphtheriae	0.09	0.10	0.07	0.28	0.22	0.34	_	0.23	0.21	0.12	0.12	0.09	0.10
8.	Aphanocapsa 6714	0.11	0.09	0.09	0.26	0.20	0.26	0.23		0.31	0.11	0.11	0.10	0.10
9.	Chloroplast (Lemna)	0.08	0.11	0.06	0.21	0.19	0.20	0.21	0.31	_	0.14	0.12	0.10	0.12
10.	Methanobacterium thermoautotrophicum	0.11	0.10	0.10	0.11	0.06	0.11	0.12	0.11	0.14	-	0.51	0.25	0.30
11.	M. ruminantium strain M-1	0.11	0.10	0.10	0.12	0.07	0.13	0.12	0.11	0.12	0.51	_	0.25	0.24
12.	Methanobacterium sp., Cariaco isolate JR-1	0.08	0.13	0.09	0.07	0.06	0.06	0.09	0.10	0.10	0.25	0.25	-	0.32
	Methanosarcina barkeri	0.08	0.07	0.07	0.12	0.09	0.12	0.10	0.10	0.12	0.30	0.24	0.32	_

LUCA: Last Universal Common Ancestor



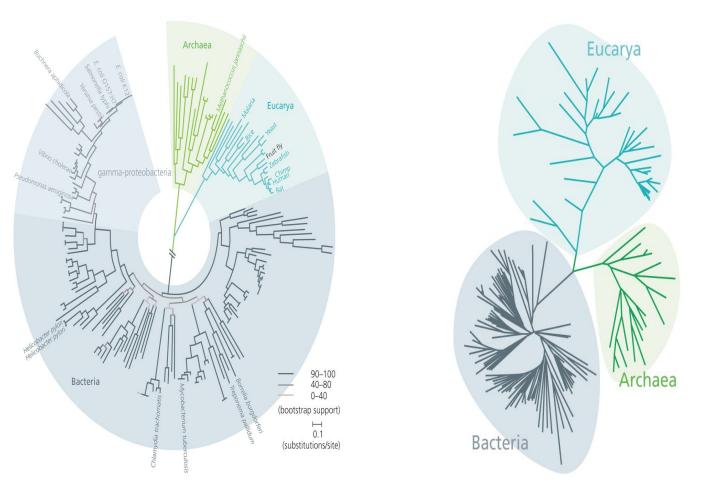


- Carl Woese (originator of 16S universal tree of life) conjectured "communal evolution" early in the tree of life; community trading genes
- However, LUCA as a community is mathematically unstable

Universal Phylogeny of Life

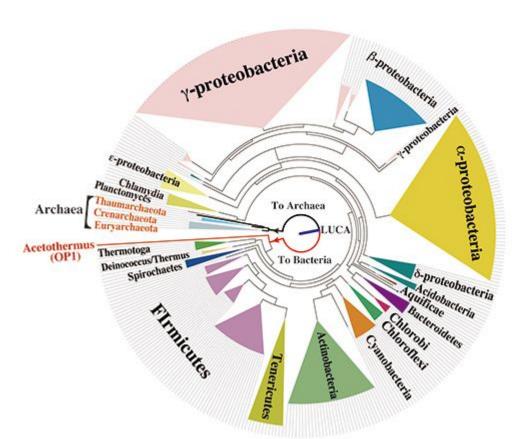
Based on 31 universal genes

Based on protein super-families



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Bacteria are ancient and very diverse



Some characters:

Peptidoglycan cell wall +/- (gram stain)

Ability to grow with oxygen +/Metabolic capabilities:
heterotroph/ oligotroph
(including things like jet fuel),
autotroph (photosynthesis),
chemi-autotroph (e.g., CO,
sulfide, hydrogen gas, metals)
Thermal, UV, radiation tolerance
Live in rocks, clouds, water, soil,
animals, plants

Plant-associated Bacteria

Compartments:

Phyllosphere - bacteria found on above ground portion of plant

Rhizosphere- bacteria found below ground at the plant root and soil interface

Endosphere- bacteria occupying the internal spaces of a plant

<u>Organisms:</u>

Epiphyte- bacteria which live on the surface of a plant

Endophyte- endosymbiont that lives within plant tissue

Endosymbiont- any organism that lives within another

Plant-associated Bacteria

Phyllosphere

Rhizosphere

Endosphere

Epiphyte

Endophyte

Endosymbiont

Individually, write down your prediction of how many bacterial cells fall into each category for a single plant.

Plant-associated Bacteria

Phyllosphere

Rhizosphere

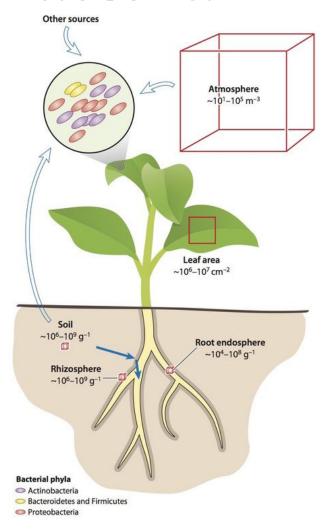
Endosphere

Epiphyte

Endophyte

Endosymbiont (intra-cellular)

Do these numbers match your predictions? Discuss any discrepancies.



Types of Interactions



Interaction (effect on bacteria, effect on plant)

Pathogenic (+,-)

Mutualistic (+,+)

Commensal (+,0) or

(0,+)

Amensal (0,-) or (-,0)

Bacterial Pathogens

Bacterial Diseases

from Agrios, G. N. 2004. Plant Pathology – 5th

Edition. Elsevier Academic Press. 922 pp. (ISBN 10

= 0120445654; ISBN-13 = 978-0120445653)

Bacterial blights of beans

Fire blight

Black rot of cabbage

Bacterial soft rot

Crown gall

Citrus canker

Common scab

Fastidious vascular bacteria

"Plant pathogenic bacteria cause many serious diseases of plants throughout the world (Vidhyasekaran 2002; Figure 2), but fewer than fungi or viruses, and they cause relatively less damage and economic cost (Kennedy and Alcorn 1980)."

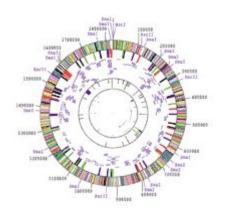
https://www.apsnet.org/edcenter/intropp/PathogenGroups/Pages/Bacteria.aspx

Beneficial Bacteria

- 1. Nutritional mutualists:
 - a. Nitrogen-fixation
 - b. Phosphate solubilization
- 2. Protection from pathogens:
 - a. Direct inhibition of pathogens
 - b. Priming of plant immune system
- 3. Enhanced tolerance of abiotic stress
 - a. Produce osmolytes
 - b. Phytohormone production

(Friesen et al. 2011)

J. Craig Venter







RESEARCH ARTICLES

Whole-genome random sequencing and assembly of Haemophilus influenzae Rd

RD Fleischmann, MD Adams, O White, RA Clayton, EF Kirkness, AR Kerlavage, CJ Bult, JF Tomb, BA Dougherty, JM Merrick, et al.

+ See all authors and affiliations

Science 28 Jul 1995: Vol. 269, Issue 5223, pp. 496-512 DOI: 10.1126/science.7542800

http://www.genomenewsnetwork.org/resources/timeline/1995_Haemophilus.php

What is a species?

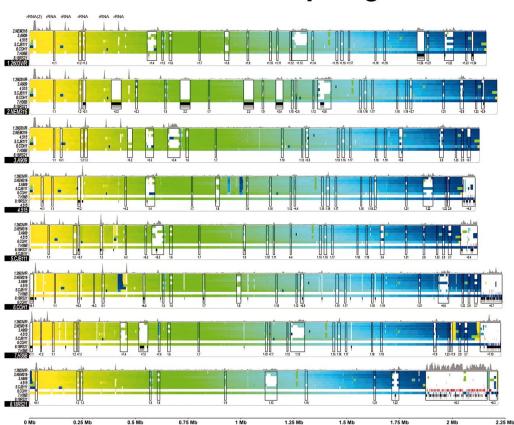
- Interbreed & share a similar niche
- Morphological features

Ecotype: subpopulation of a species that has distinct ecological characteristics, i.e., expresses phenotypes that are adaptive to a subset of environments [genotype fits the environment]

The Pan-genome

Pan = All, the union of all branches of a group.

Genome analysis of multiple pathogenic isolates of *Streptococcus agalactiae*: Implications for the microbial "pan-genome"



Tettelin et al. 2005

8 strains, only share ~80% of genes!

Conclude that hundreds of genomes will not capture diversity in this species!!

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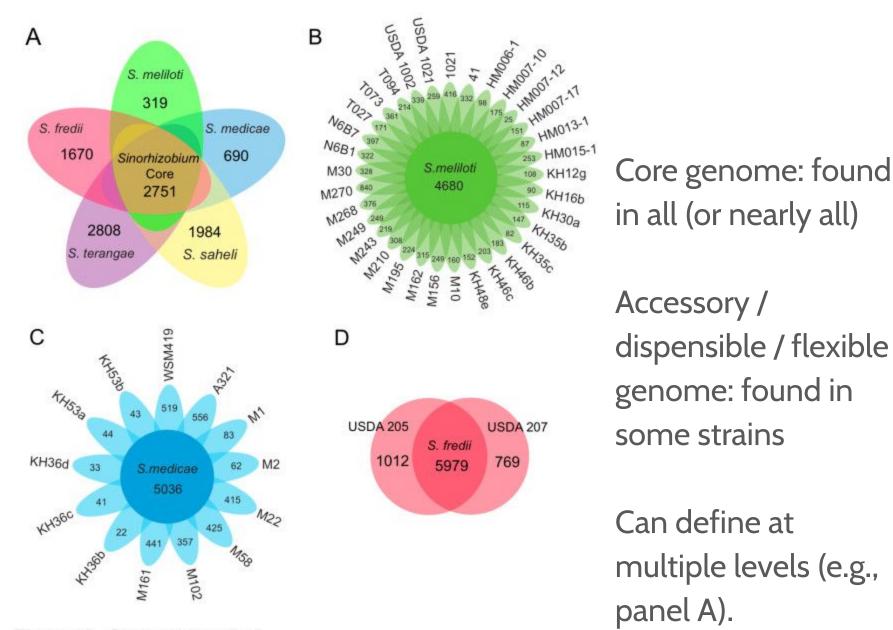
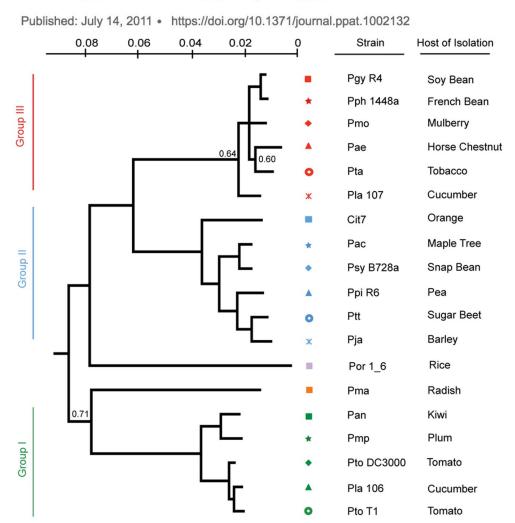


Figure 3. Sugawara et al.

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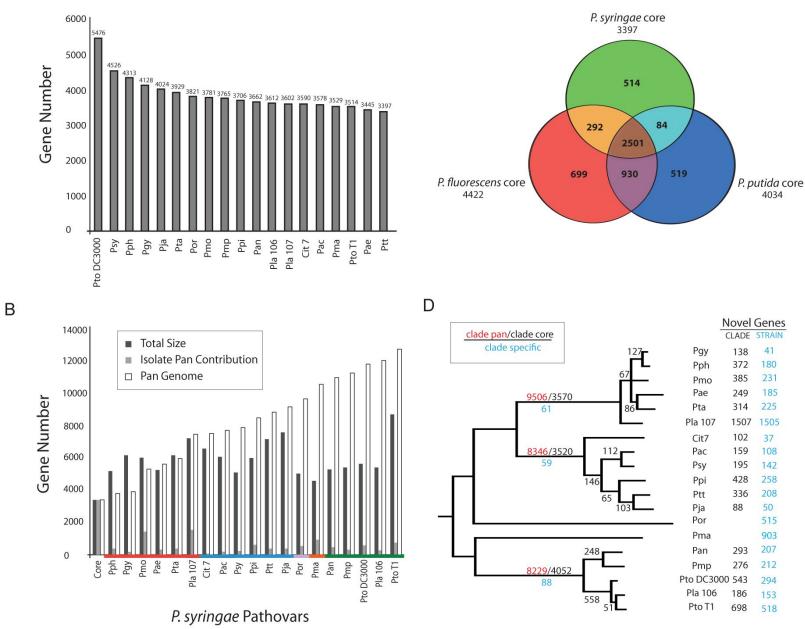
Dynamic Evolution of Pathogenicity Revealed by Sequencing and Comparative Genomics of 19 *Pseudomonas syringae* Isolates

David A. Baltrus , Marc T. Nishimura , Artur Romanchuk, Jeff H. Chang, M. Shahid Mukhtar, Karen Cherkis, Jeff Roach, Sarah R. Grant, Corbin D. Jones , Jeffery L. Dangl □



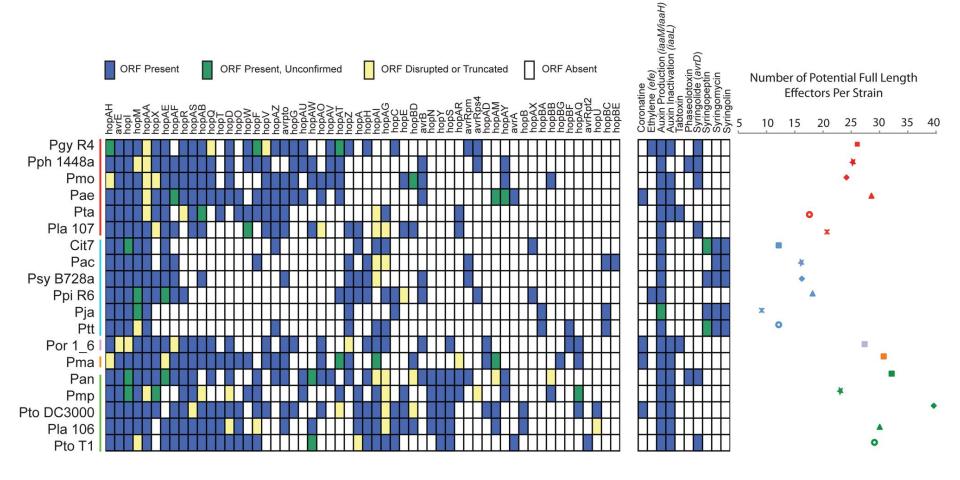
Phylogenetic analysis of the 19 strains included in this study based on nucleotide sequence of seven conserved loci. Bayesian posterior probabilities are displayed on the phylogeny only at nodes where these values are <0.95. For these unresolved notes, we used an independent phylogenetic approach on another 324 genes that confirmed that this tree captures the evolutionary history of these nodes

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Command line Terminal (Unix)

Mac: Terminal

Windows: PUTTY

Chrome: Secure Shell (extension; runs command line in your

browser! How cool is that?)



Open a terminal

Type pwd

-> tell me where your are?

Type ls

-> tell me what you see?

Type touch file.txt

Type ls

-> what happened?

```
cd - Change directory
pwd - your full path of directory
mkdir - make a new directory
rm - remove a file
head - first 5 lines of a file
tail - last 5 lines of a file
more - scroll file top to bottom
  - what is this symbol in unix?
mv - move a folder/file or rename?
touch - create a file
```

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More of a detailed introduction listed here:

https://github.com/raw937/bacterialpopulationgenomics/tree/master/doc

PLEASE EMAIL ASAP KAMIAK TO GET AN ACCOUNT

You use your wsu email and password as login.

kamiak.support@wsu.edu.

Command line - Homework

- I will post a command line survey to see what you know
- It will also help me cover material needed to get you ready for next week assembly lecture