

A tale of sex: Gene sharing between microbial species, genomes and microbiomes

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November 22, 2016

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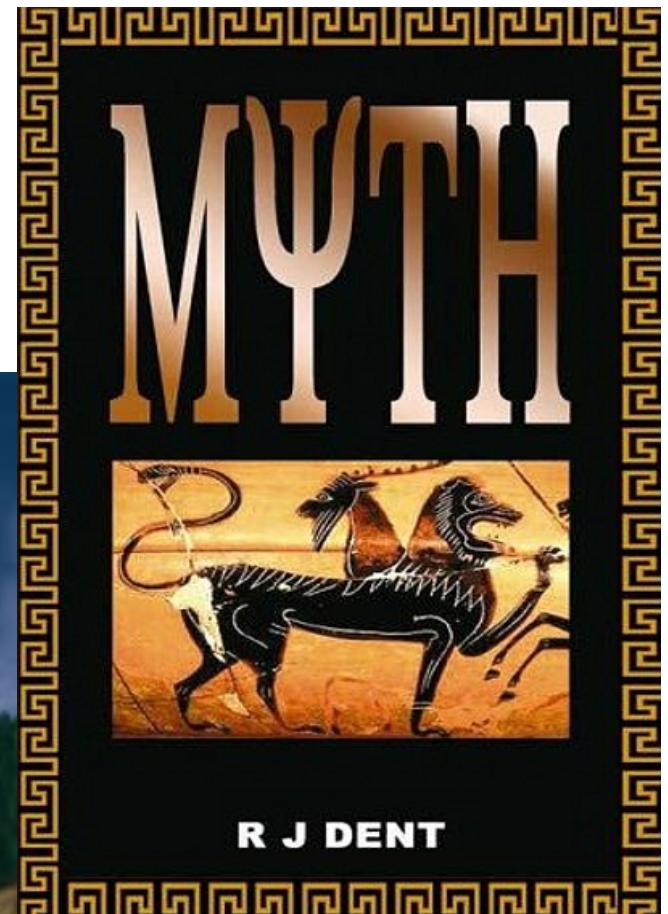
Acknowledgements

- Harvard U: Bill Hanage, Colin Worby, Rose Chang, Patrick Mitchell, Alanna Callendrello
- Cornell U: Daniel H. Buckley, Mallory Choudoir
- U. Connecticut: J. Peter Gogarten
- U. Connecticut, MIT: Greg Fournier
- Aalto U. (Finland): Pekka Marttinen
- U. Oslo (Norway): Jukka Corander
- U. Liverpool (UK): Chrispin Chaguza

OUTLINE

- Intro to HGT
- Ancient evolution and the Tree of Life
- Same species, different genes
- Crossing species barriers
- HGT between populations
- HGT in the age of genomics

Chimeras in the microbial world



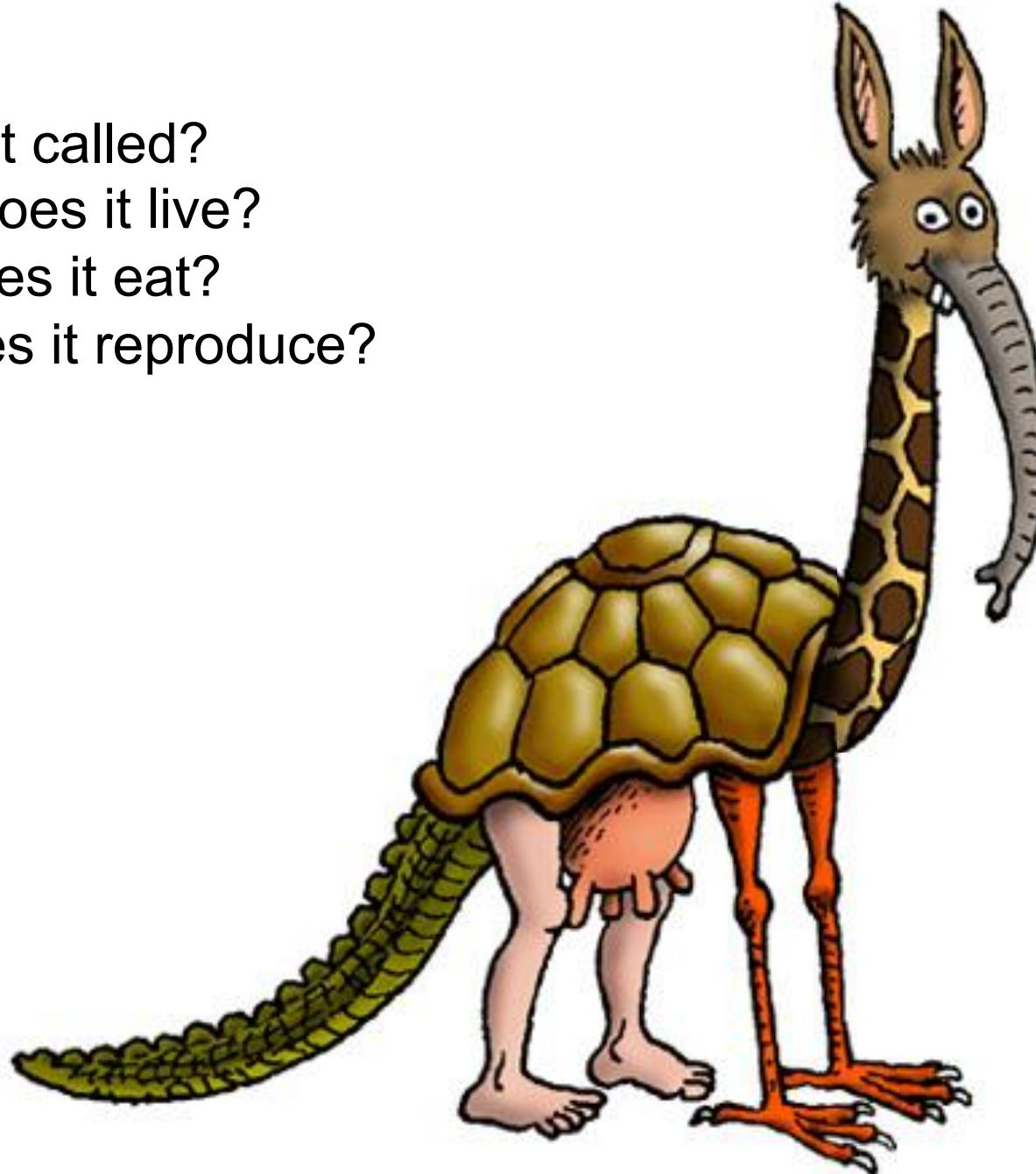
What is it called?

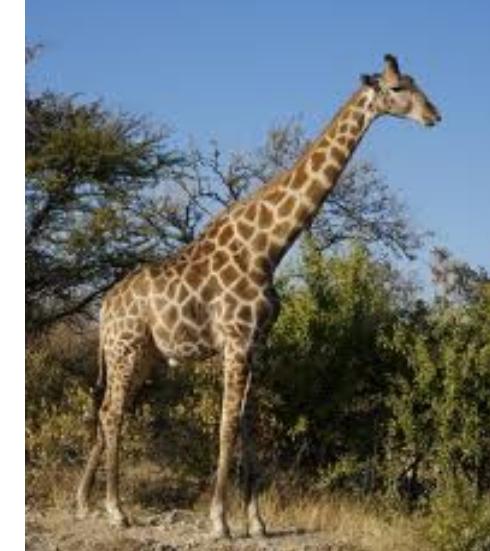
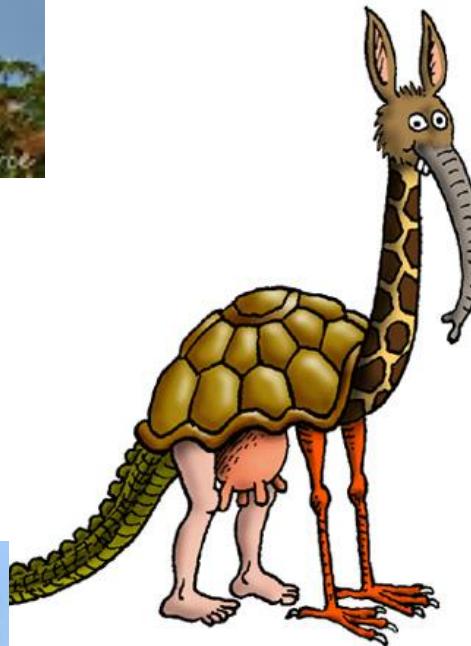
Where does it live?

What does it eat?

How does it reproduce?

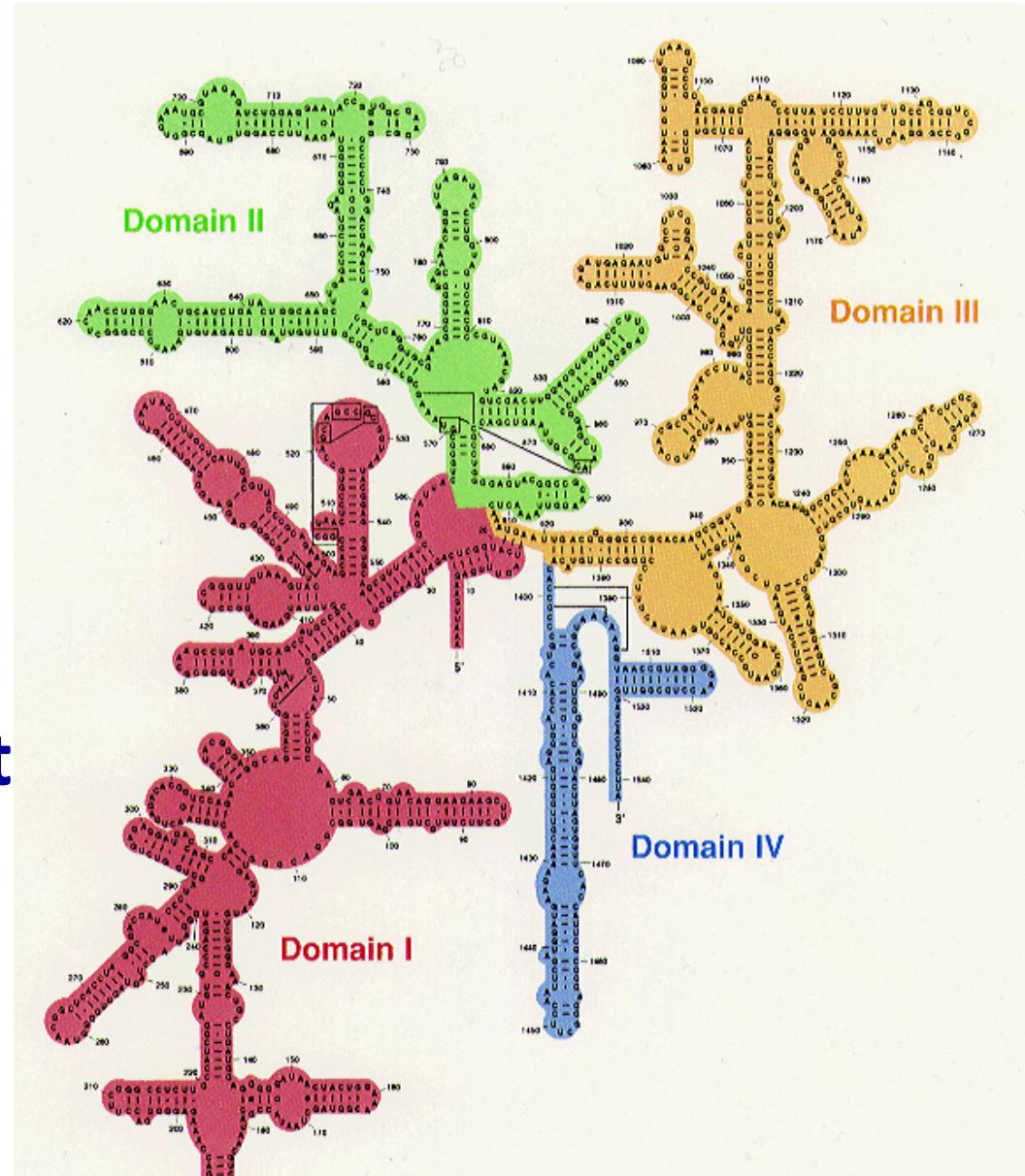
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Microbial taxonomy: 16S rRNA

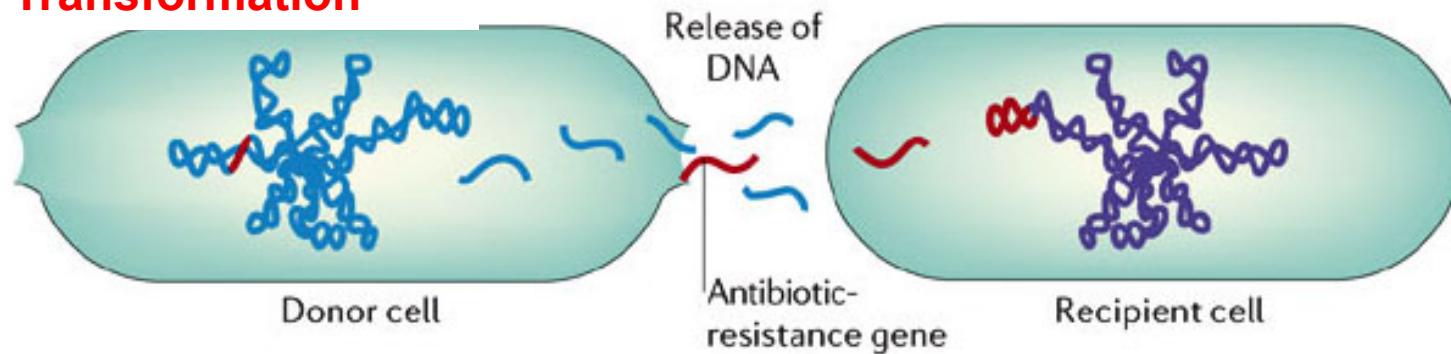
The evolutionary history of any one gene may be different from the history of other genes in the genome or of the organism itself.



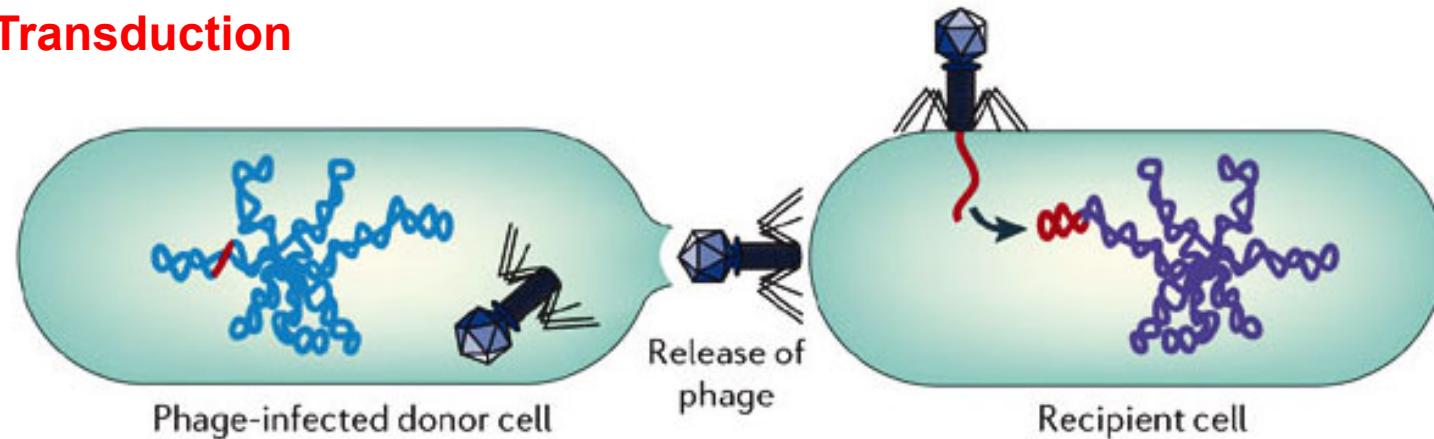
Horizontal gene transfer

- the acquisition of genetic material from a donor organism, regardless of the evolutionary distance between donor and recipient

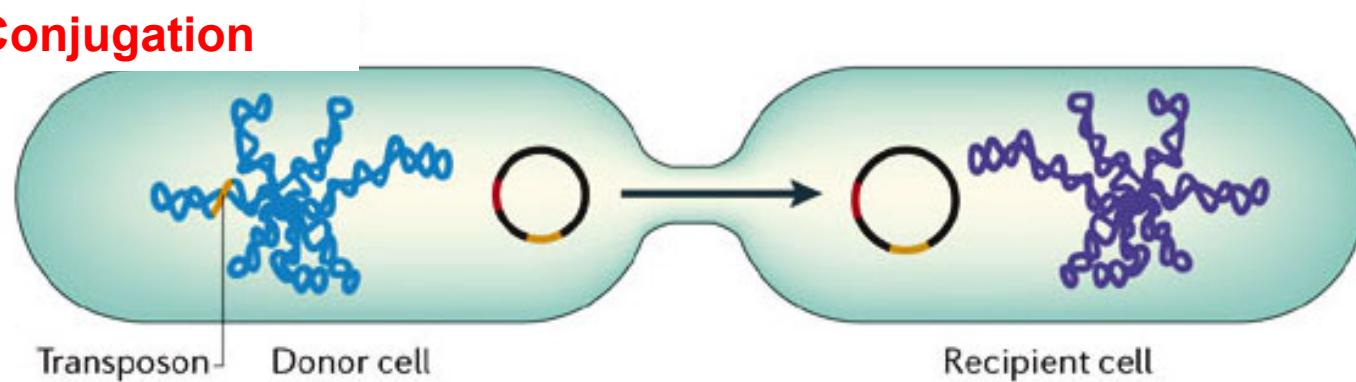
Transformation



Transduction



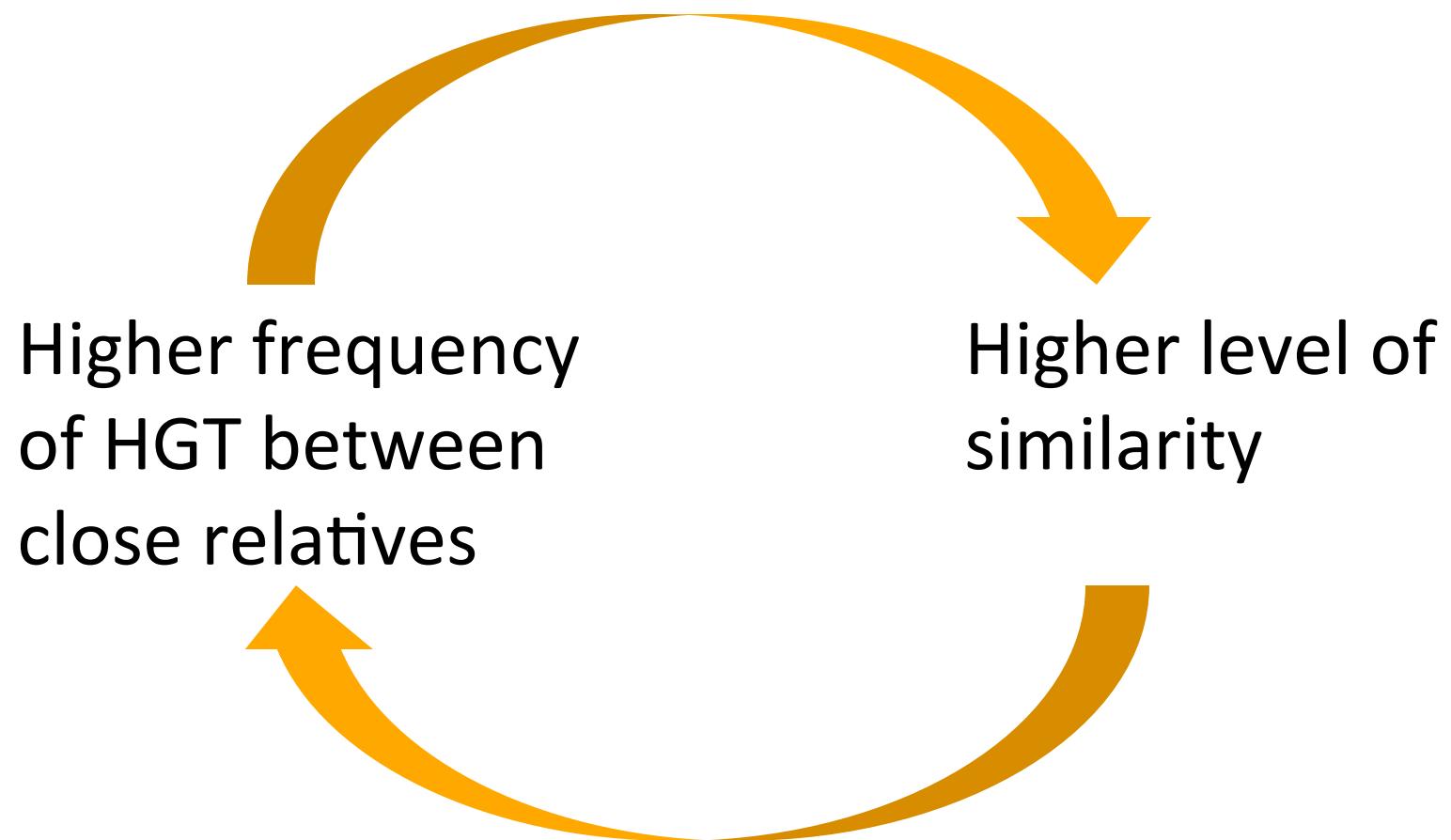
Conjugation



Ancient evolution and the Tree of Life

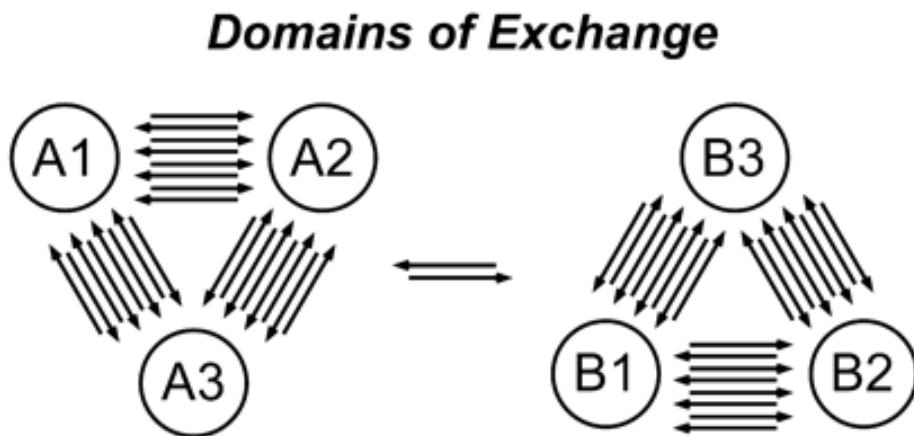
Biased gene transfer

Andam et al. PNAS 2010



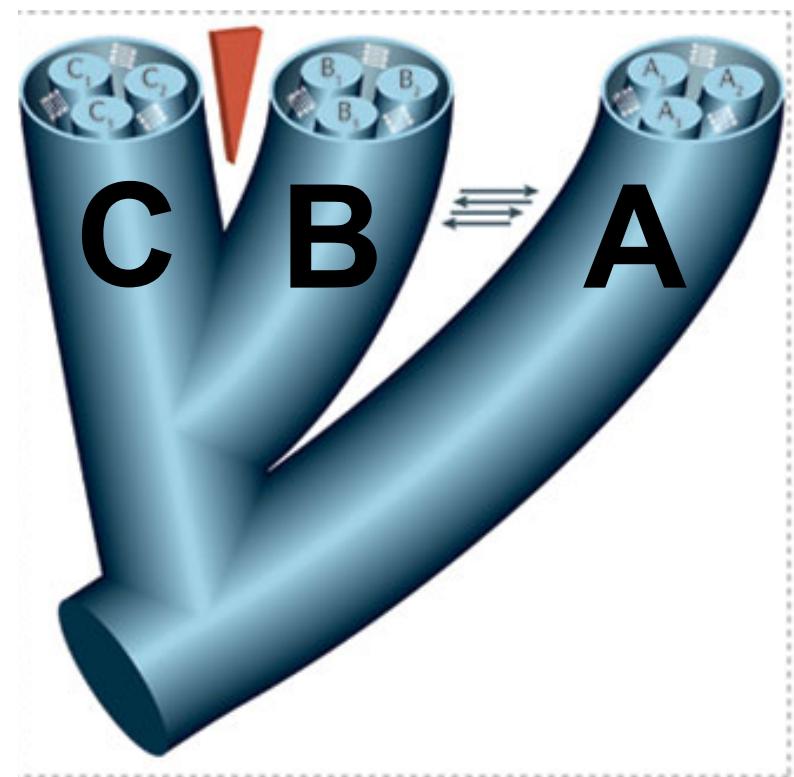
Biased HGT can mimic patterns of vertical inheritance

Andam et al., PNAS 2010; Andam & Gogarten, Nature Rev Microbio 2011; Andam & Gogarten, Biol Direct 2011



Gogarten, Doolittle, Lawrence MBE 2002

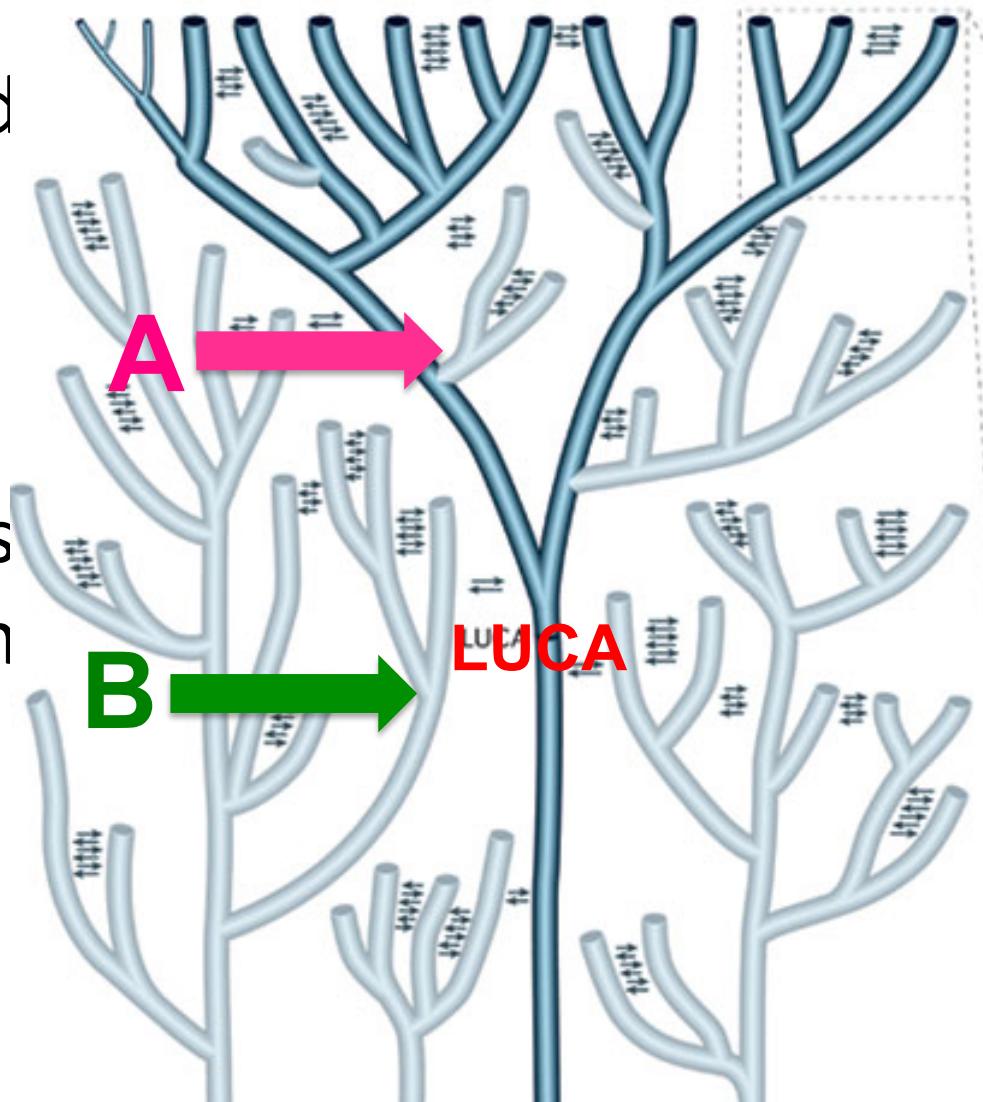
Recognized taxonomic groups created through a gradient of HGT



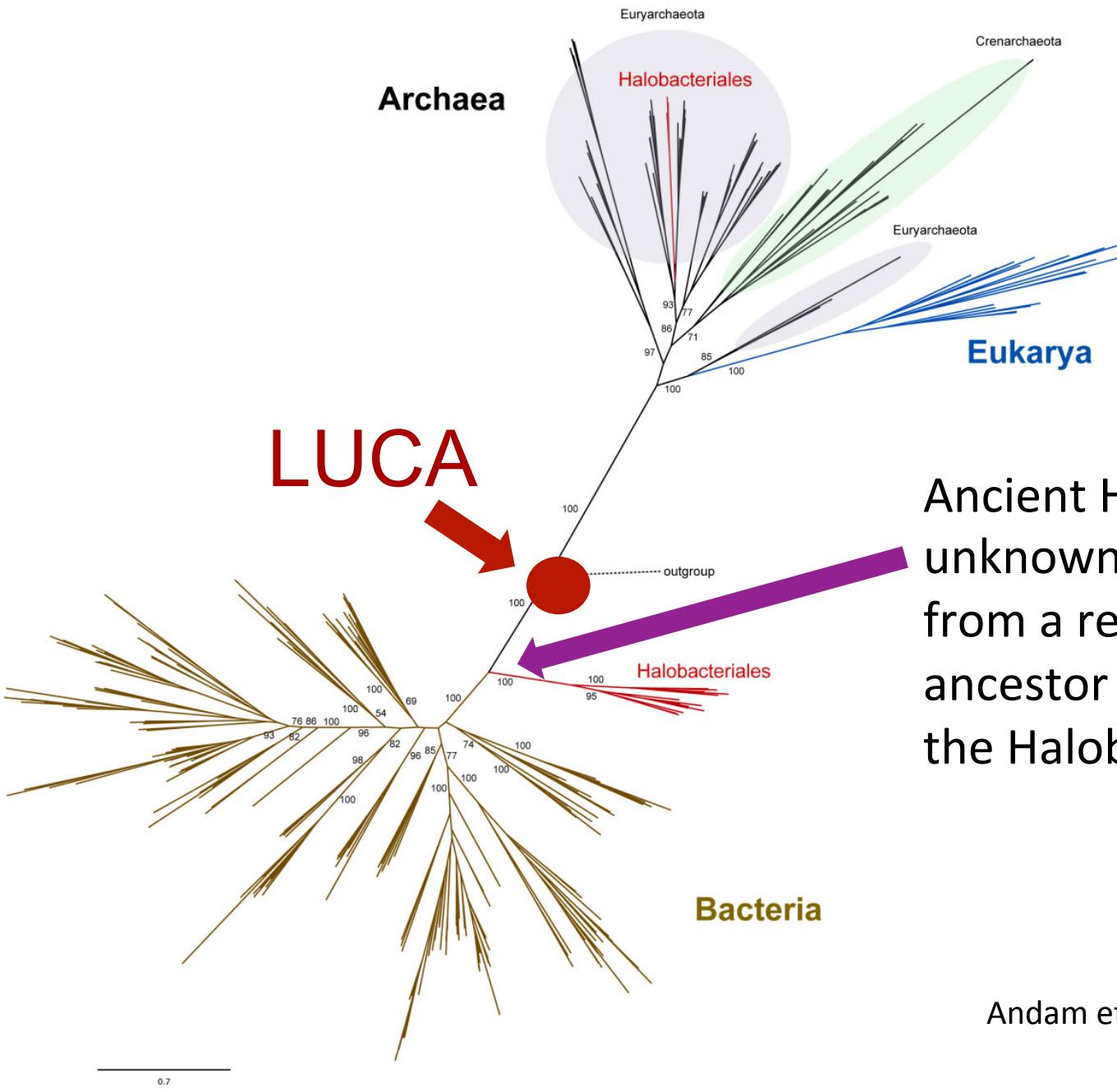
HGT as a homogenizing force

- Some genes diverged before LUCA.
- Molecular common ancestors of most ancient gene families did not all coincide in space and time.

LUCA: Last Universal Common Ancestor



Andam & Gogarten, Nature Rev Microbiol 2011
Fournier, Andam, Gogarten, BMC Evol Biol 2015



Ancient HGT of *leuS* from an unknown source, most likely from a relative of the ancestor of the Bacteria, to the Halobacteriales

Andam et al., BMC Evol Biol 2012

LUCA

Common Type

96/0.96

A

SerRS

100/1.00

Rare Type

100/0.99

Common Type



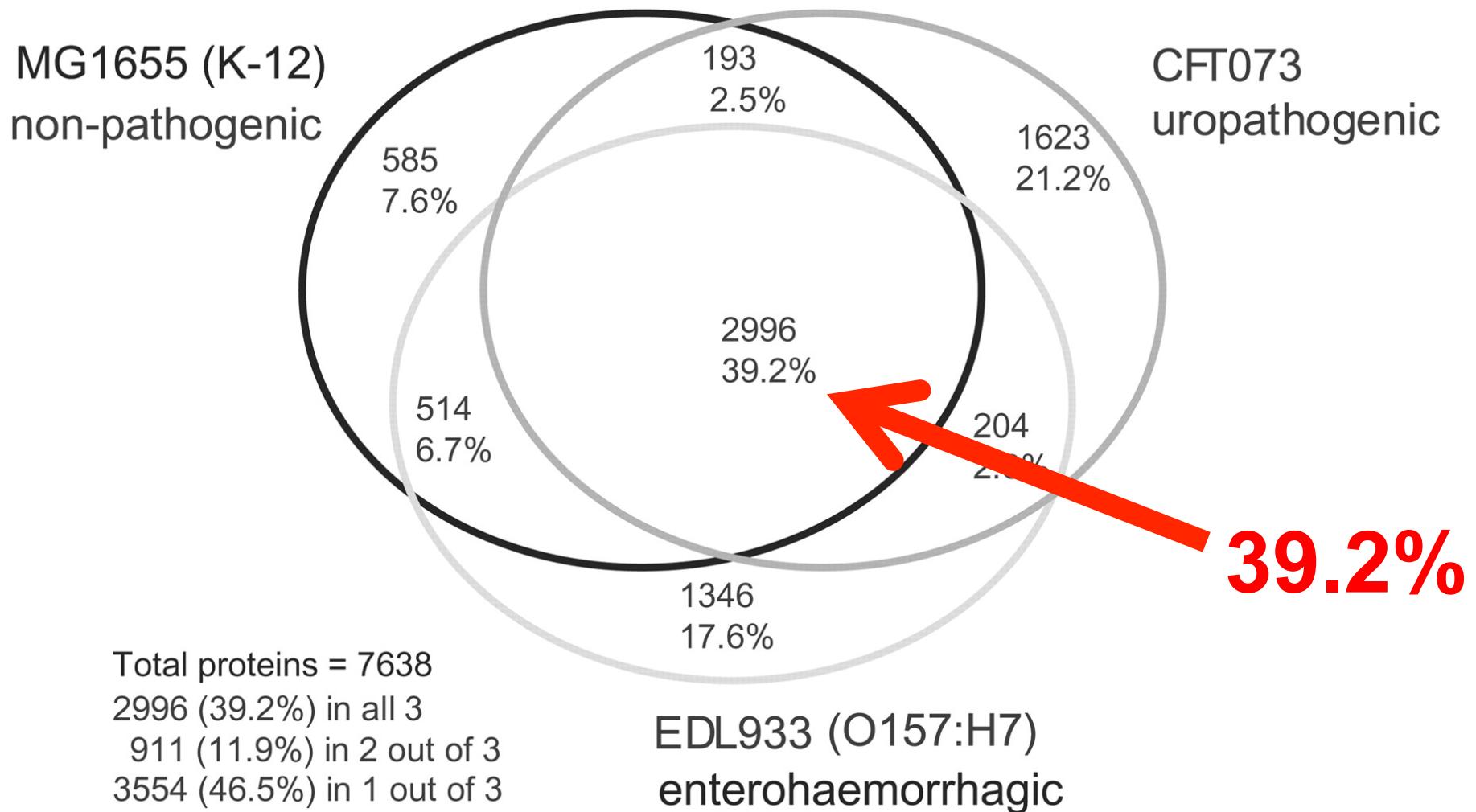
B

Divergence event prior to LUCA;
Other unknown or extinct lineages
co-existed at the time of LUCA

Fournier, Andam, Gogarten, BMC Evol Biol 2015

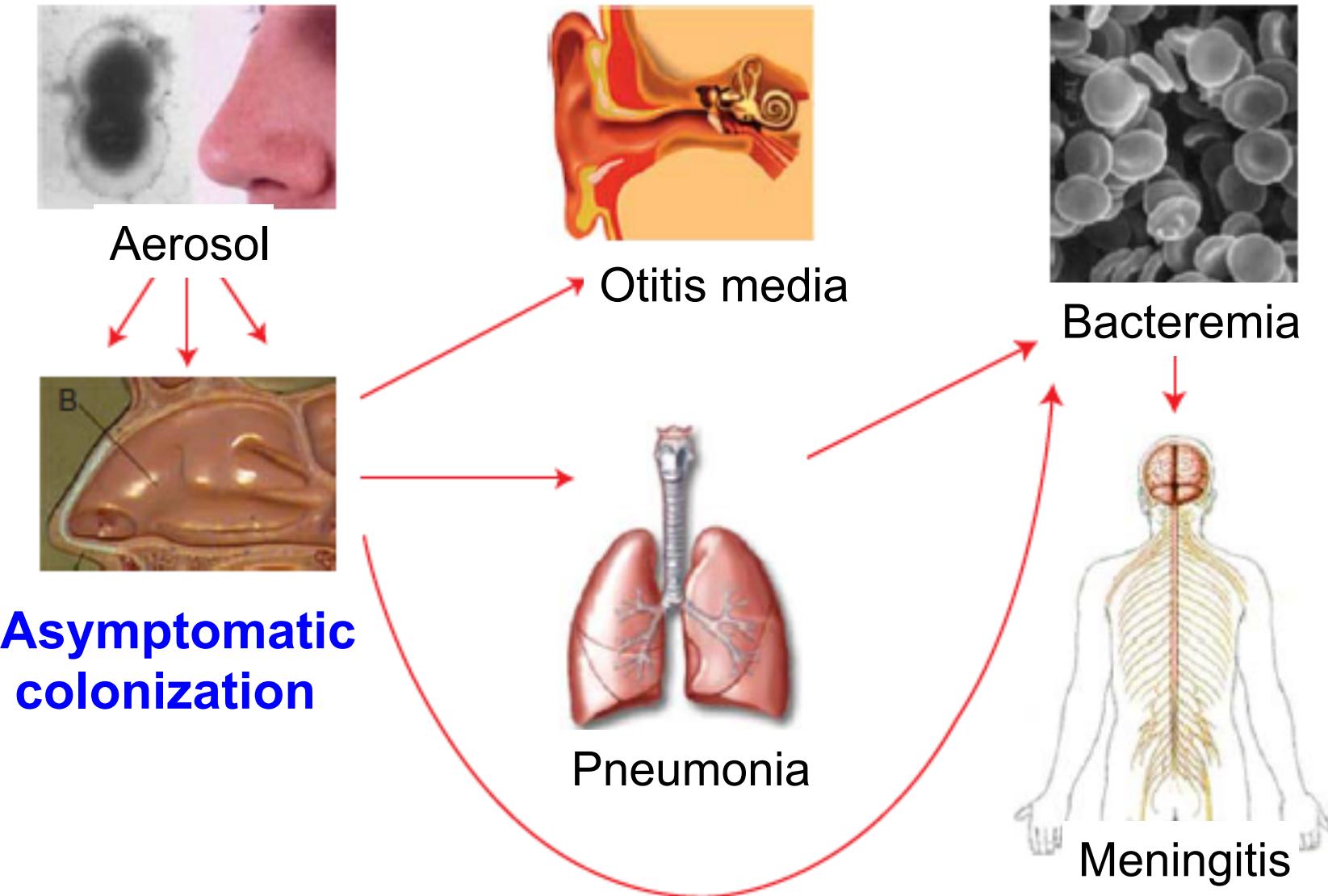
Same species, different genes

Shared *E. coli* genes



Welch et al. PNAS 2002

Streptococcus pneumoniae (pneumococcus)

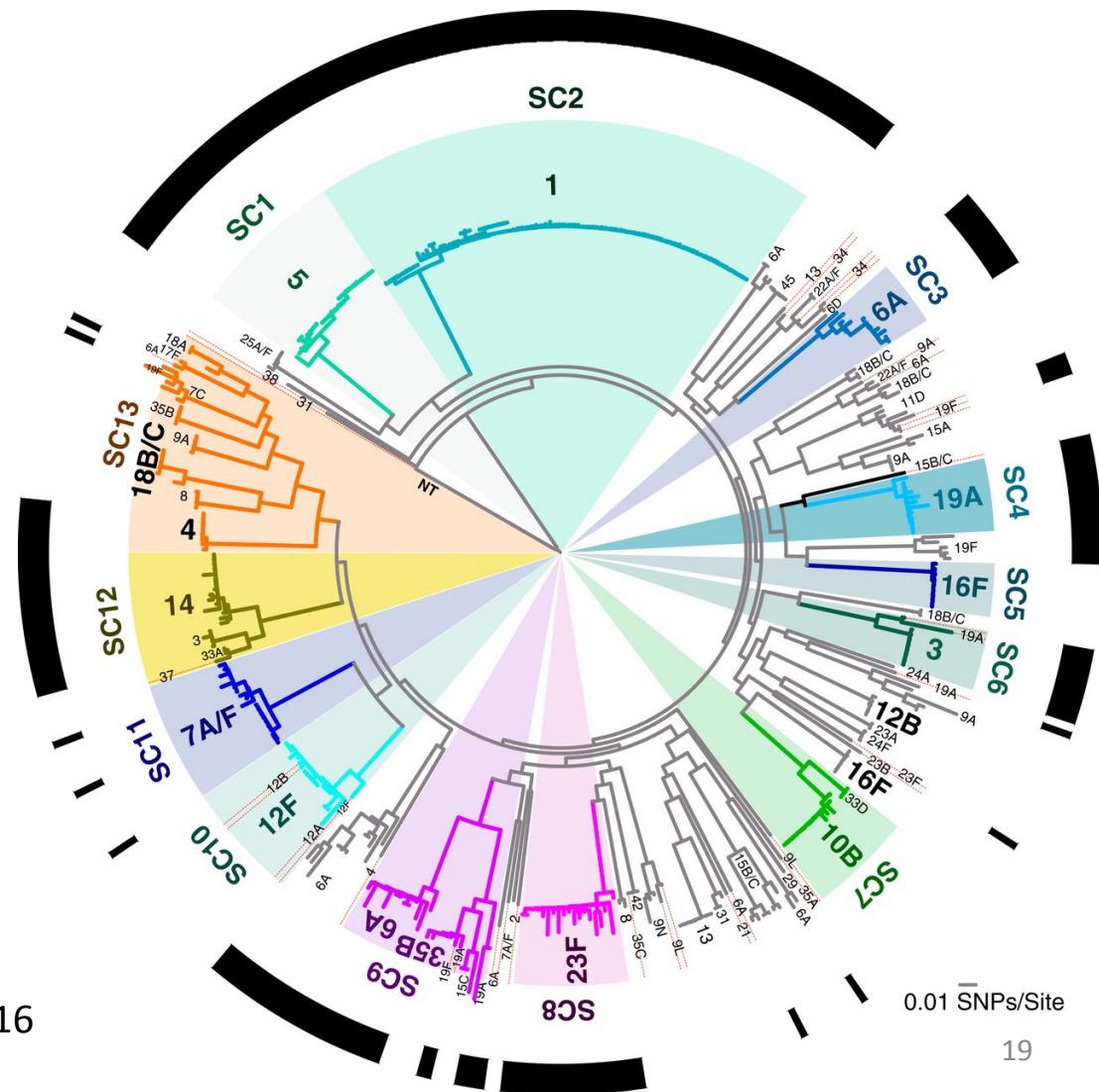


Normark & Tuomanen 2013
Cold Spr Harbor Persp Med

Invasive diseases: Isolated from normally sterile sites (e.g., blood, cerebrospinal fluid)
18

Core genome phylogeny of 439 pneumo from Malawi, Africa

- 0.79-Mb multiple-sequence alignment with 51,389 SNPs from 852 universally conserved (core) genes present in single copies

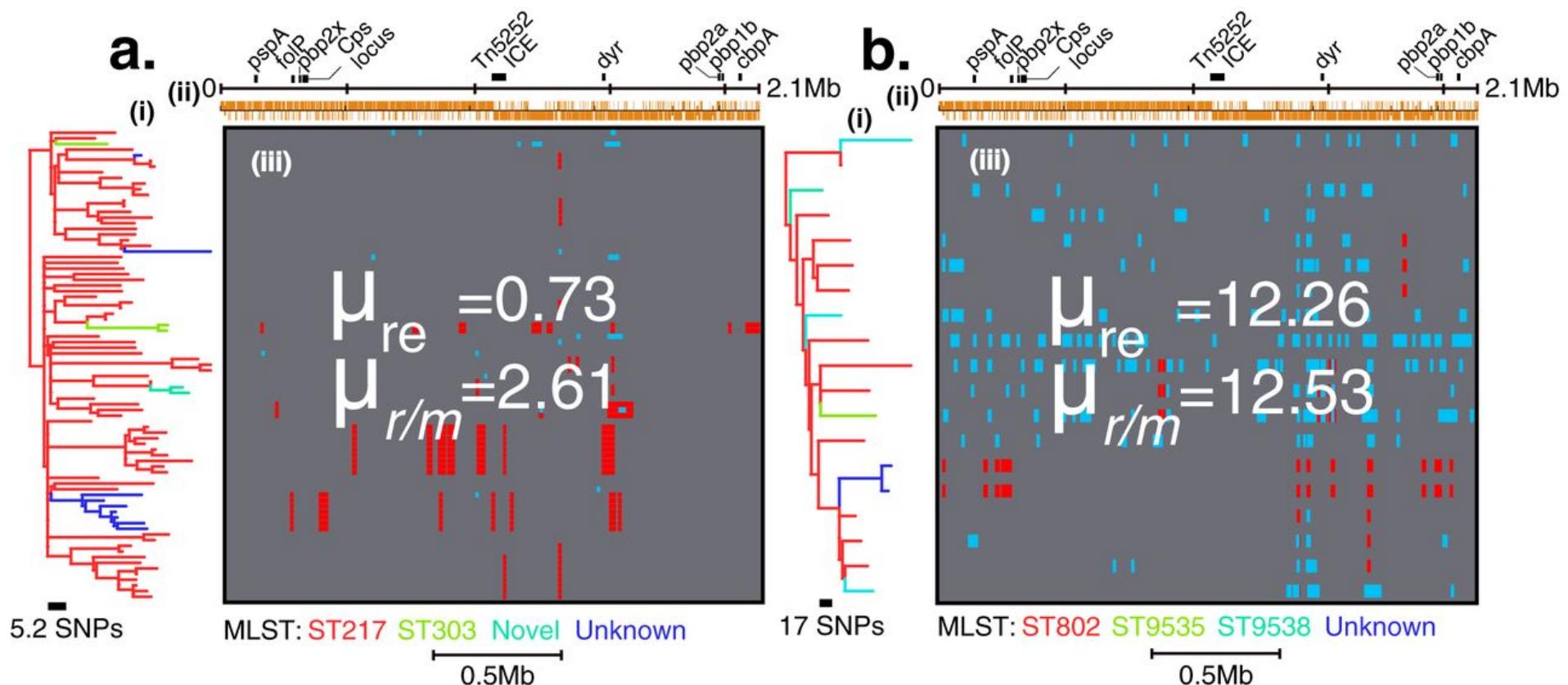


Chaguza, Andam, et al. mBio 2016

0.01 SNPs/Site

19

Within-species HGT via homologous recombination

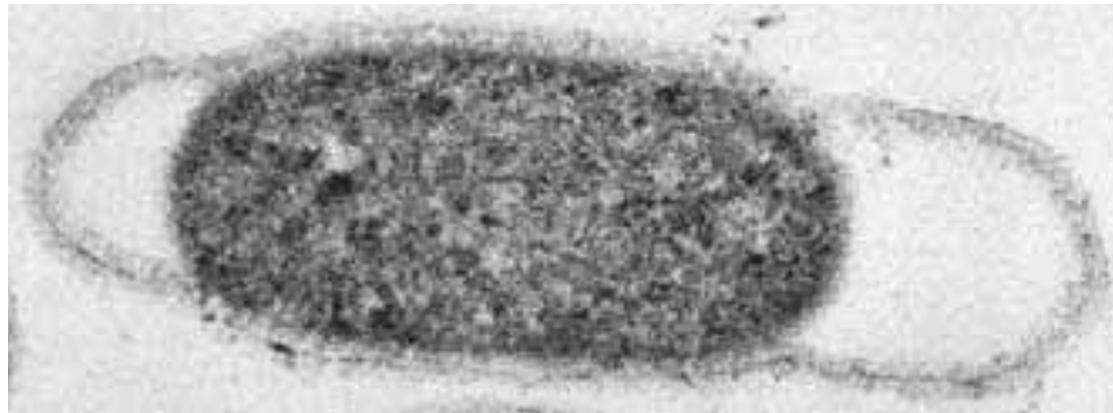


Chaguza, Andam, et al. mBio 2016

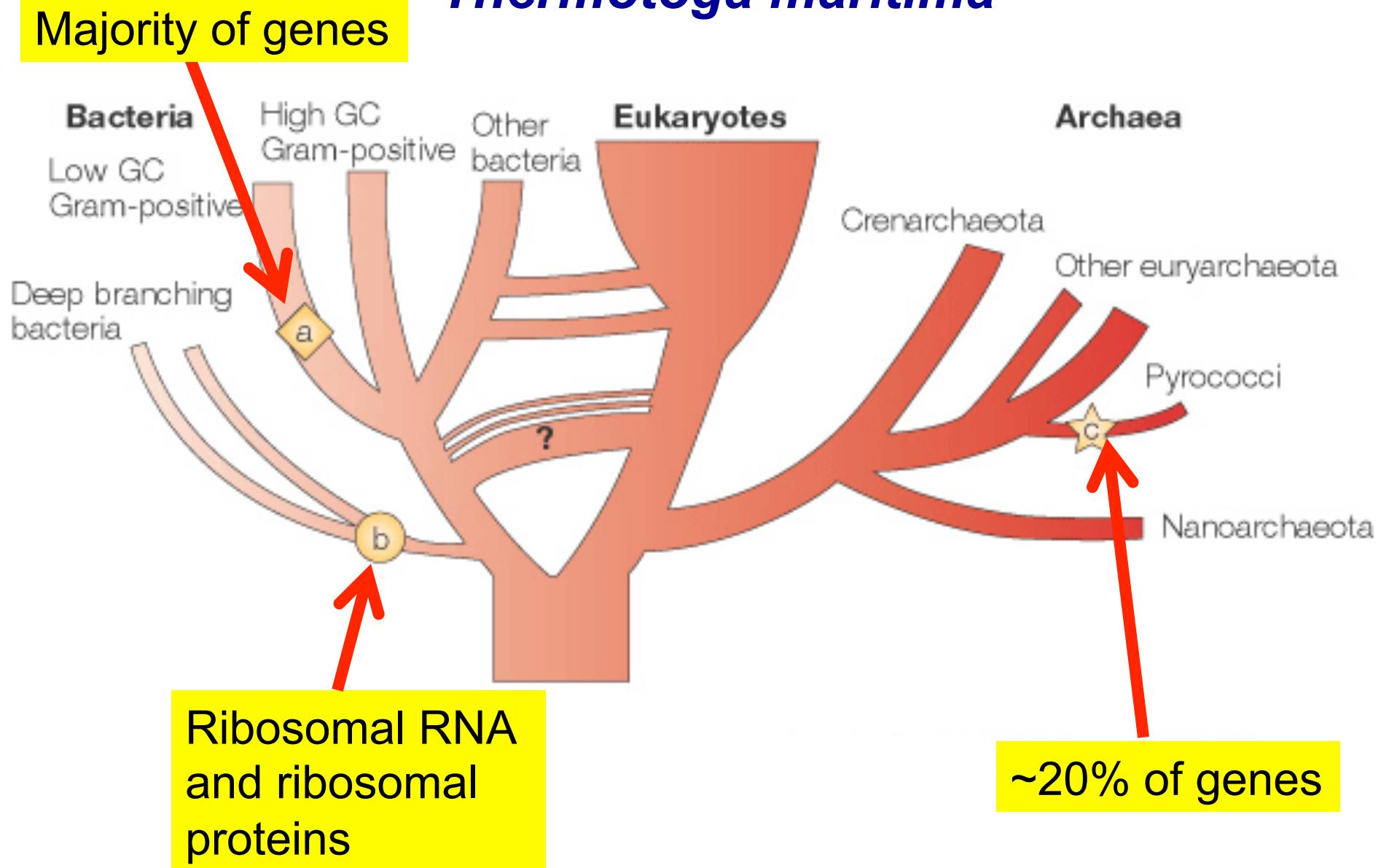
Crossing species barriers

Thermotoga

- Rod-shaped cell enveloped in an outer cell membrane (the 'toga')
- Thermophilic or hyperthermophilic, growing best around 80°C



Thermotoga maritima

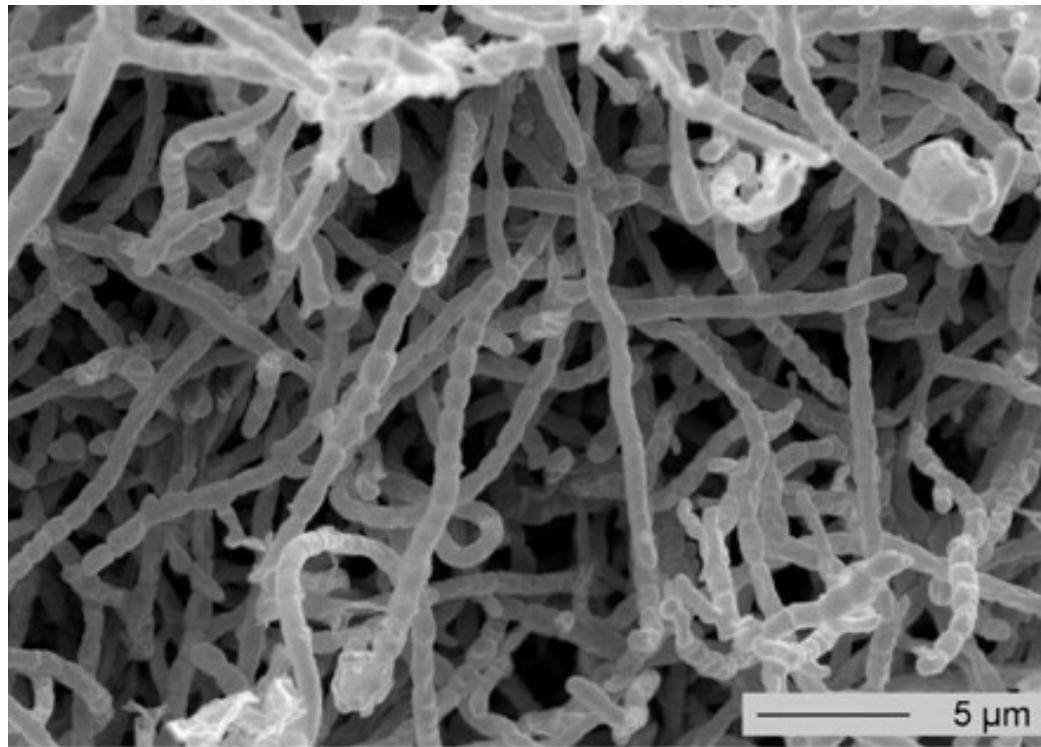




Streptomyces

- Gram +; Actinobacteria
- Ubiquitous in soils
- Geosmin – “earthy smell”
- Degrade complex polymers
- Major natural source of antibiotics and secondary metabolites
- 615 species (Labeda 2012)

Unique developmental stages

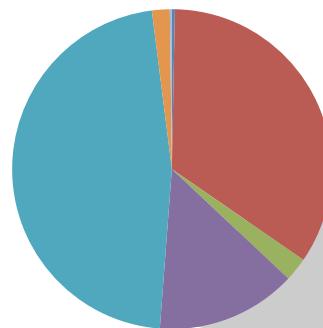


Nguyen et al. 2003



Widespread interspecies homologous recombination in *Streptomyces*

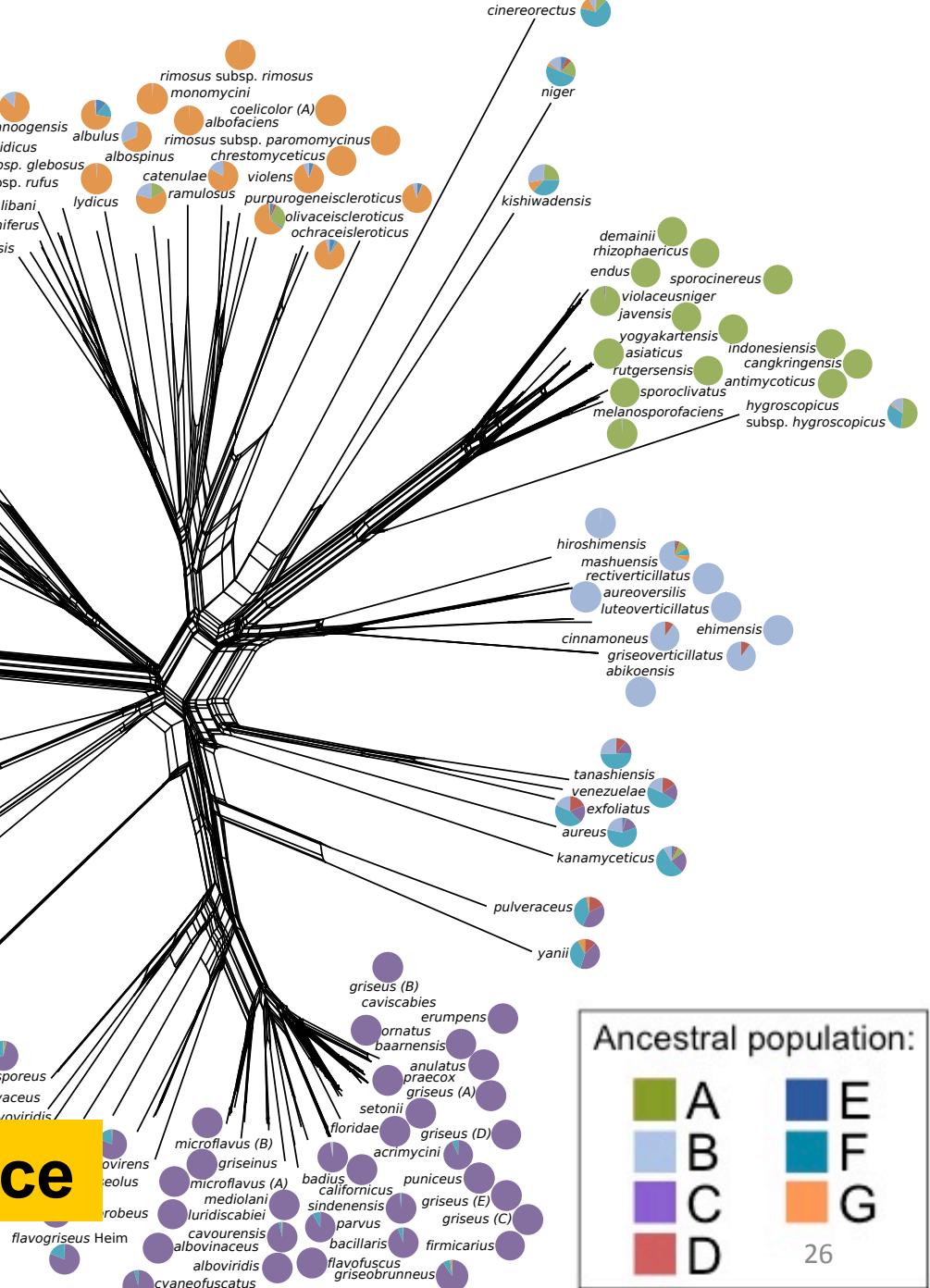
Andam et al., ISME J 2016

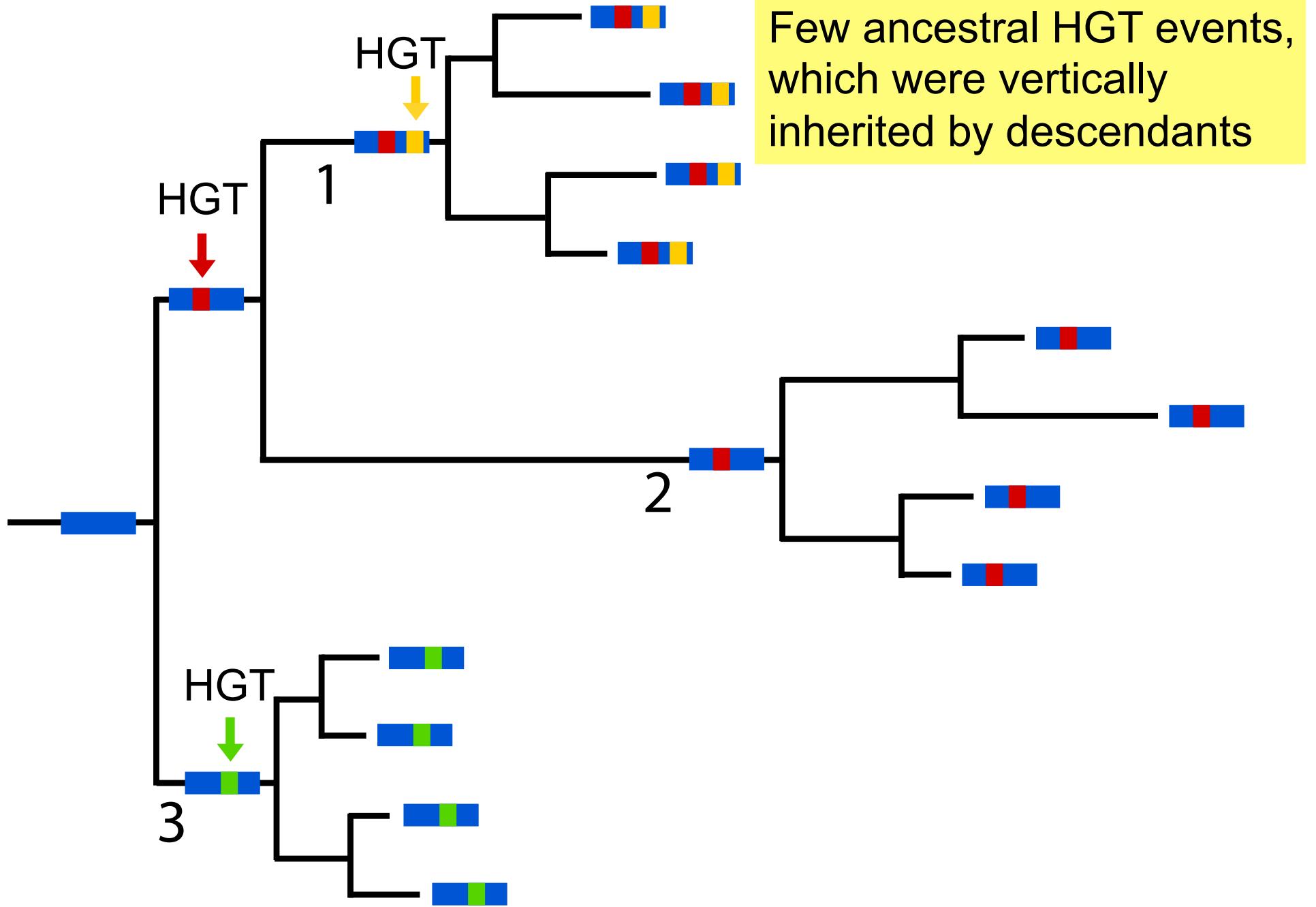


spiroveticillatus

HGT as a diversifying force

10.01





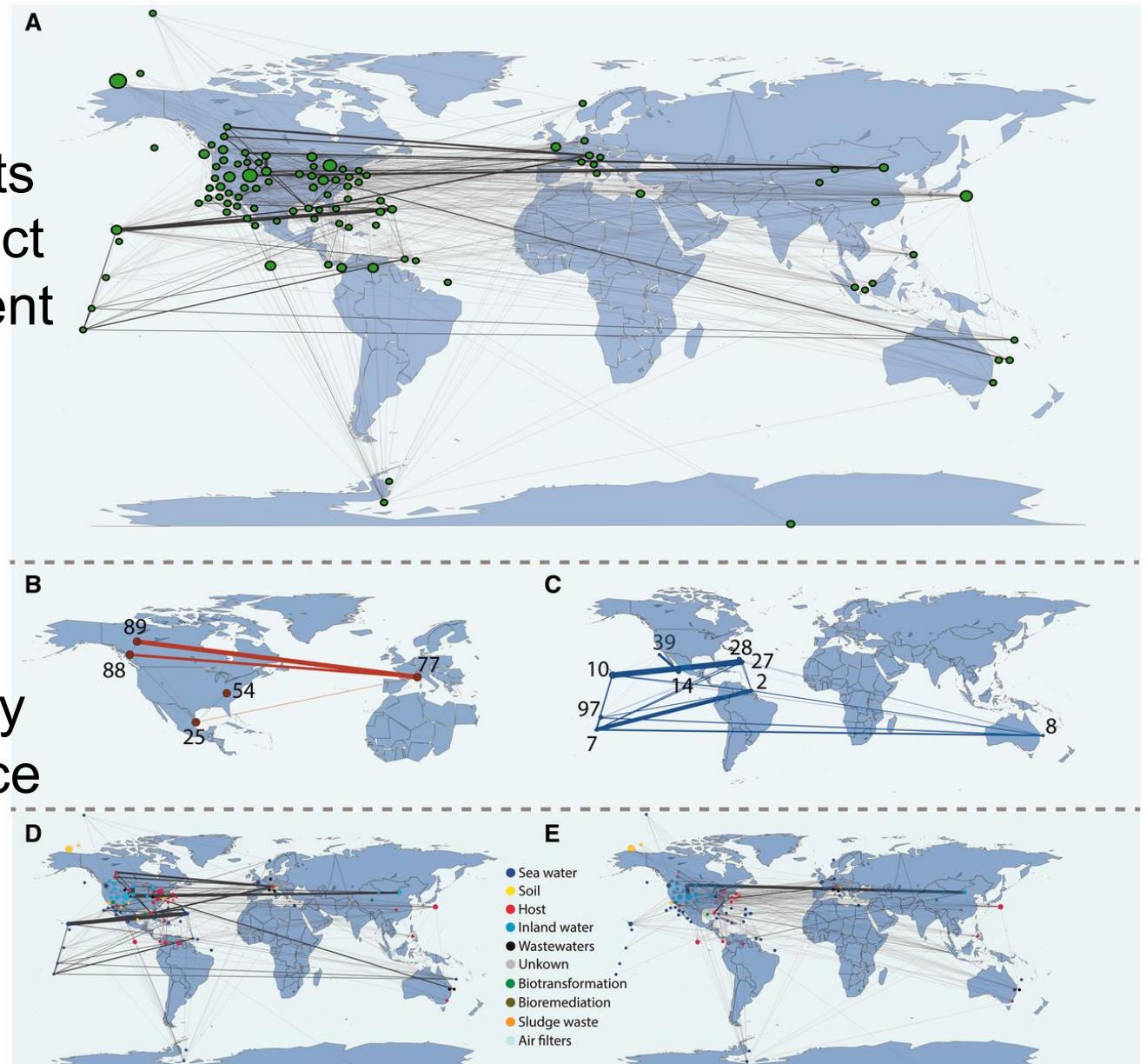
Gene sharing between populations

Global Geolocation of Gene Sharing

Fondi et al. GBE 2016

Each node represents a metagenome project and the links represent the presence of homologous sequences between them.

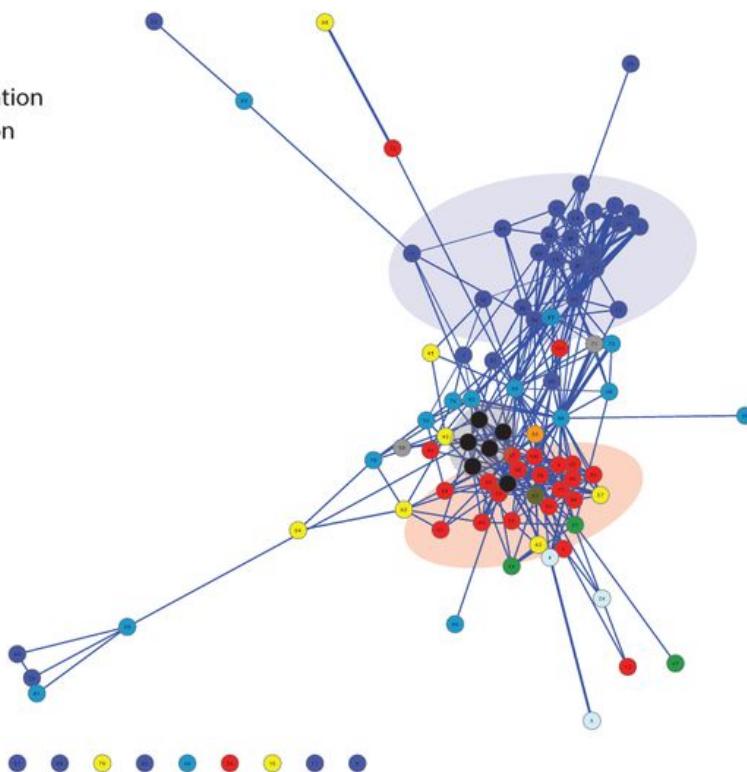
Cross-habitat mobility of antibiotic resistance genes



Global Geolocalization of Gene Sharing

Fondi et al. GBE 2016

- Sea water
- Soil
- Host
- Inland water
- Wastewaters
- Unknown
- Biotransformation
- Bioremediation
- Sludge waste
- Air filters

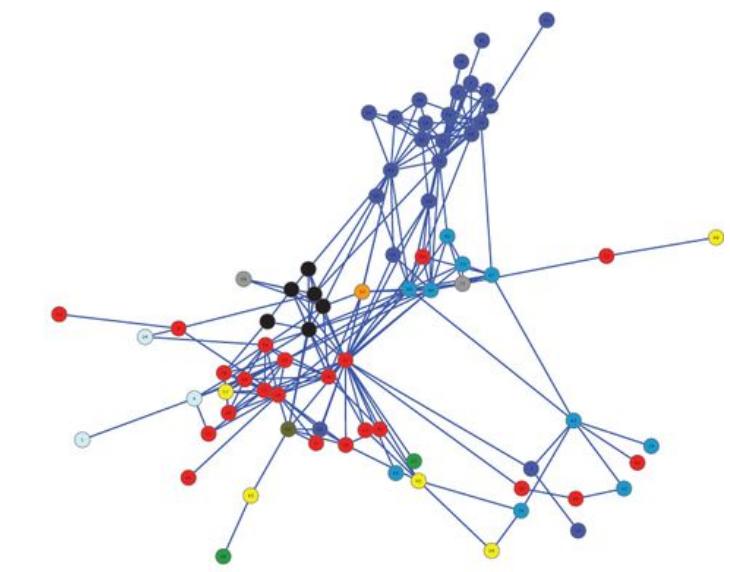


A

Metagenome network

Freshwater habitats act as a gene exchange bridge between otherwise disconnected habitats.

B



HGT network

Take-home message:

- HGT has been occurring for millions of years.
- HGT has altered the structure of the Tree of Life, and will continue to affect the diversification of all lineages today.

Take-home message:

- A (microbial) species is not a homogenous entity.
- Highly variable genome composition among members of the same species
- Is there such a thing as a microbial species?
- Presence of local gene pools in a globally distributed gene network → role of ecology

HGT in the age of genomics

- Thousands of genome sequences available for analysis
 - GenBank: ~80,000 complete prokaryotic genomes
 - *Streptococcus pneumoniae*: ~5,000 draft genomes
- Metagenomic data from different sources, habitats also available

Beyond identifying new species...

- How did lineages emerge?
- How does HGT contribute to speciation and adaptation?
- What are the driving factors and barriers to HGT?
- What causes high variability in rates of HGT via recombination within species?
- What genes are shared between clinic and environment?

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