Structure and evolution of bacterial genomes

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Data is coming ...

Bacteria

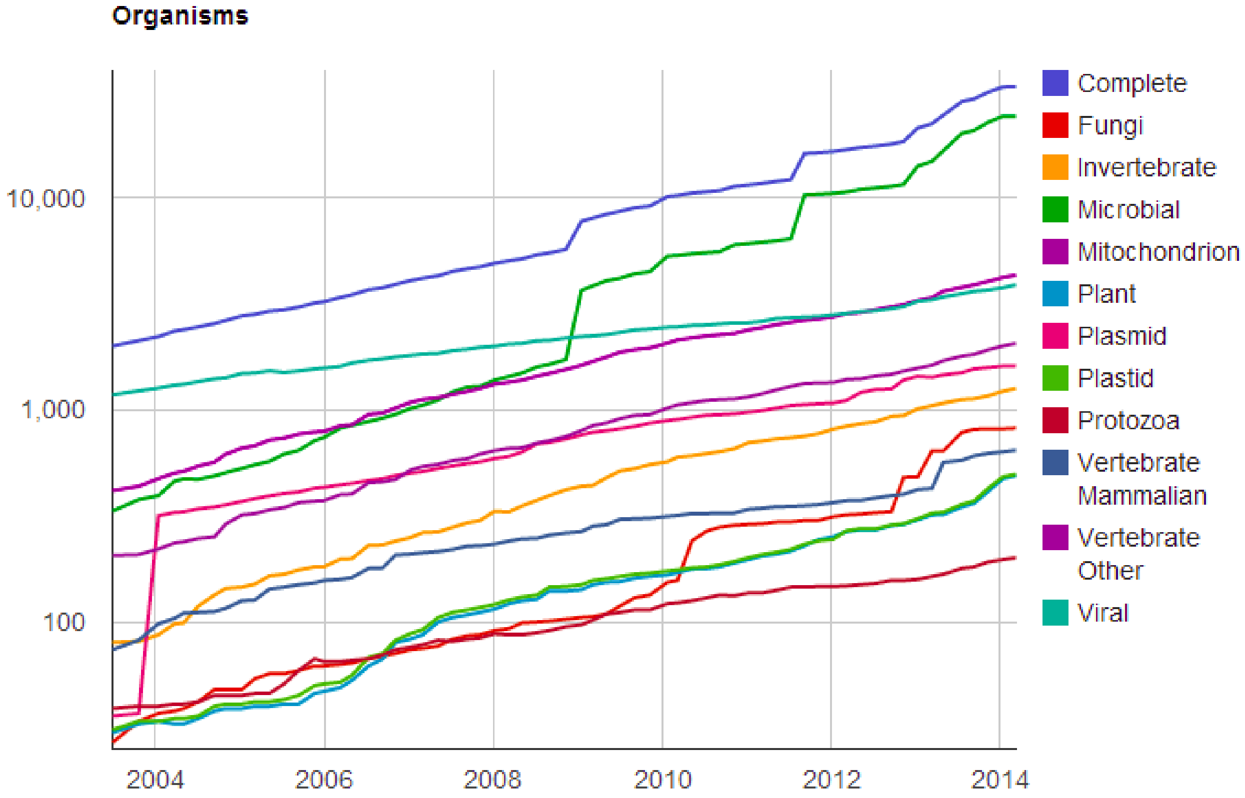
479 320 assemblies

↓

16 527 complete genome assembly level

↓

1 631 representative genomes



https://www.ncbi.nlm.nih.gov/refseq/statistics/

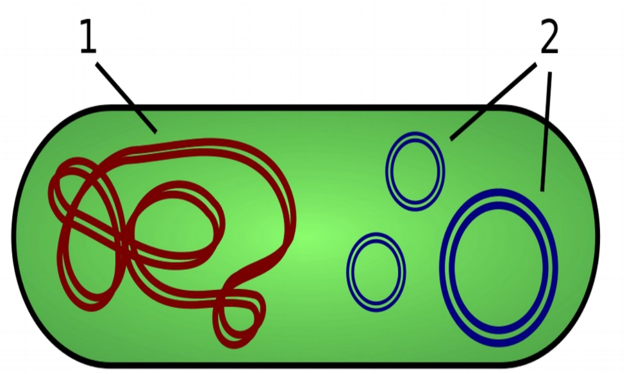
What is bacterial genome?

1. Chromosome(-s)

- circular, double-stranded DNA molecule
- 1Mb – 6 Mb
- one origin of replication
- carry house-keeping genes

2. Plasmids

- circular, double-stranded DNA molecules
- 15 kb – 200 kb
- replicate independently
- carry genes that benefit the survival of the organism.

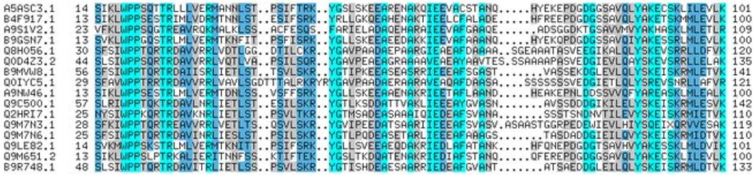


wikipedia.org

How does it evolve?

What we can observe in genomes

- Mutations – genes sequences



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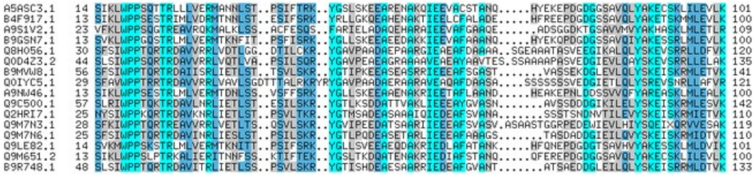

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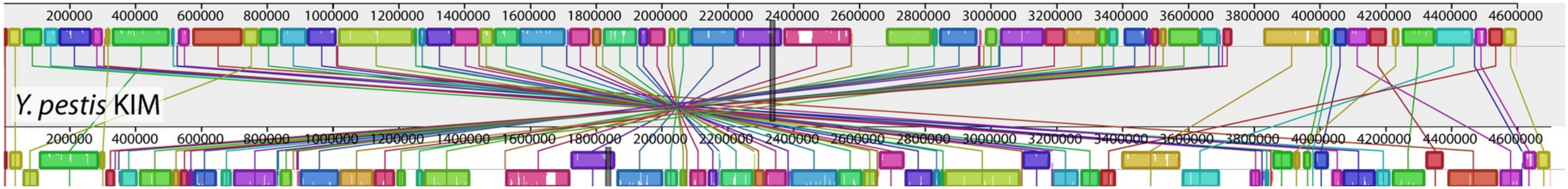
- Gene gain/loss – genes content

- Rearrangements - genes order



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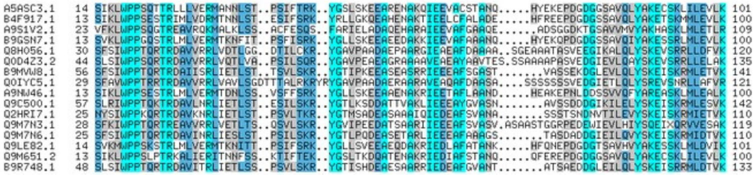

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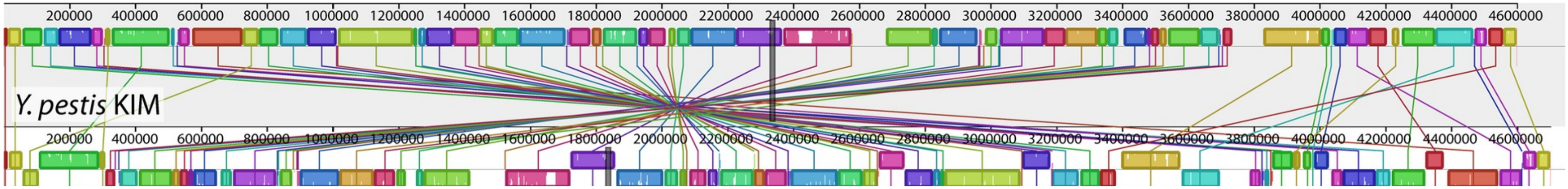
What are the mechanisms?

1. Homologous recombination

2. Intra-genomic recombination

3. Horizontal gene transfer:

- transformation
- transduction
- bacterial conjugation

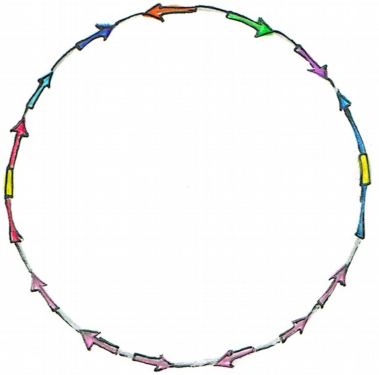


From Biology to Maths

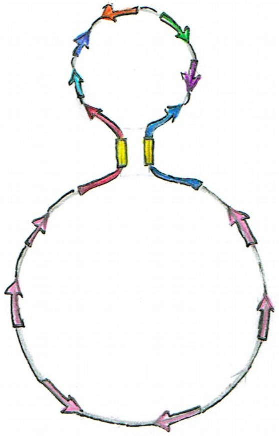
Rearrangement	Math illustration
> Deletion	1 2 -3 4 -5 6 ⇒ 1 2 -3 -5 6
> Insertion	1 2 -3 4 -5 6 ⇒ 1 2 -3 4 7 -5 6
> Translocation	1 2 -3 4 -5 6 ⇒ 1 -3 4 -5 2 6
> Inversion	1 2 -3 4 -5 6 ⇒ 1 2 5 -4 3 6
> Duplication	1 2 -3 4 -5 6 ⇒ 1 2 -3 -3 4 -5 6

Intra-genomic recombination

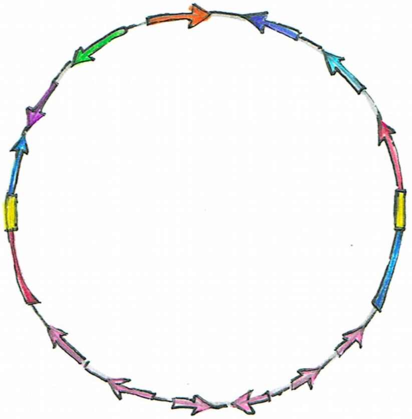
Circular chromosome with repeats



Intra-chromosome recombination



Inversion of the segment between repeats



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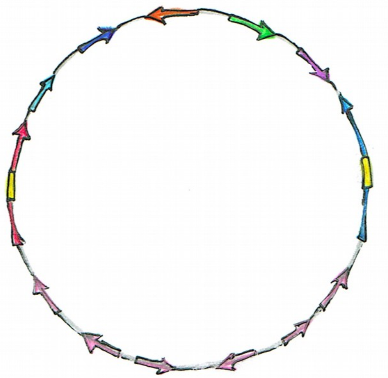

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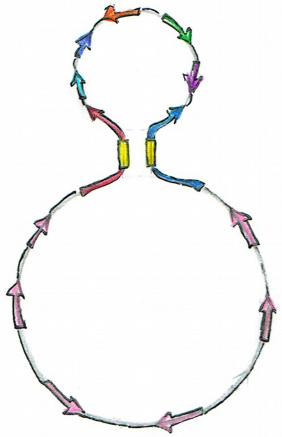

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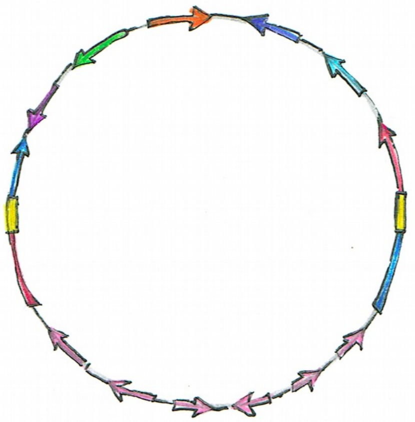
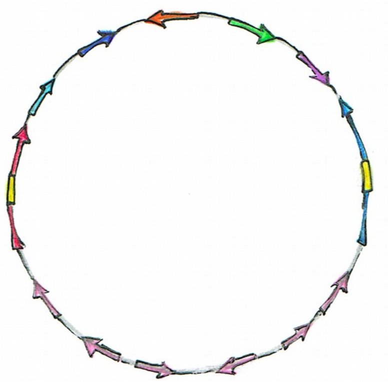


Genomic repeats:

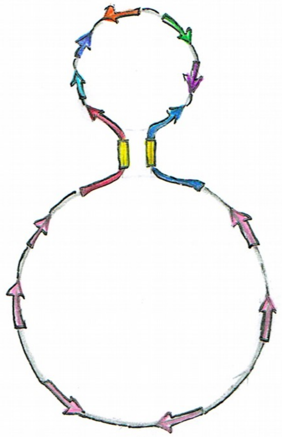
- mobile elements (transposase) – up to 100 copies per genomes
- rRNA gene operons – up to 15 copies per genomes
- gene paralogs

Intra-genomic recombination

Circular chromosome with repeats



Intra-chromosome recombination



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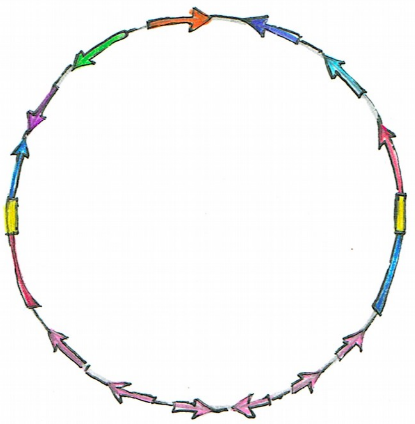

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- mobile elements (transposase) – up to 100 copies per genomes
- rRNA gene operons – up to 15 copies per genomes
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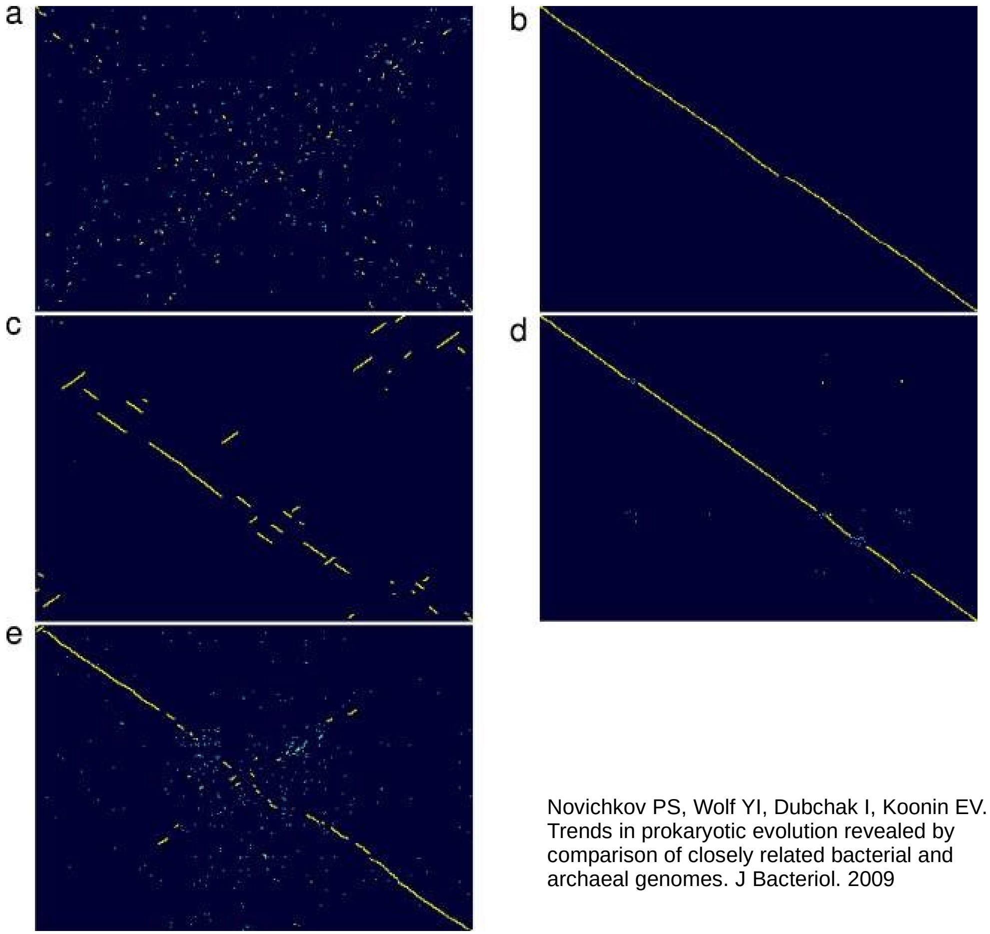
- short fragments Site-specific inversion

Is gene order conserved?



(a) Nearly complete decay of synteny; *Streptococcus sanguinis* SK36 and *Streptococcus pneumoniae* R6.

(b) Virtual absence of rearrangements; *Chlamydophila caviae* GPIC and *Chlamydophila abortus* S26/3.

(c) Multiple inversions with limited transposition of individual genes; *Yersinia pestis Antiqua* and *Y. pestis CO92*.

(d) No inversion; hot spots of transposition of individual genes; *P. marinus* AS9601 and *P. marinus* MIT 9215.

(e) Multiple inversions and transposition of individual genes; *Pseudomonas fluorescens* PfO-1 and *P. fluorescens* Pf-5.

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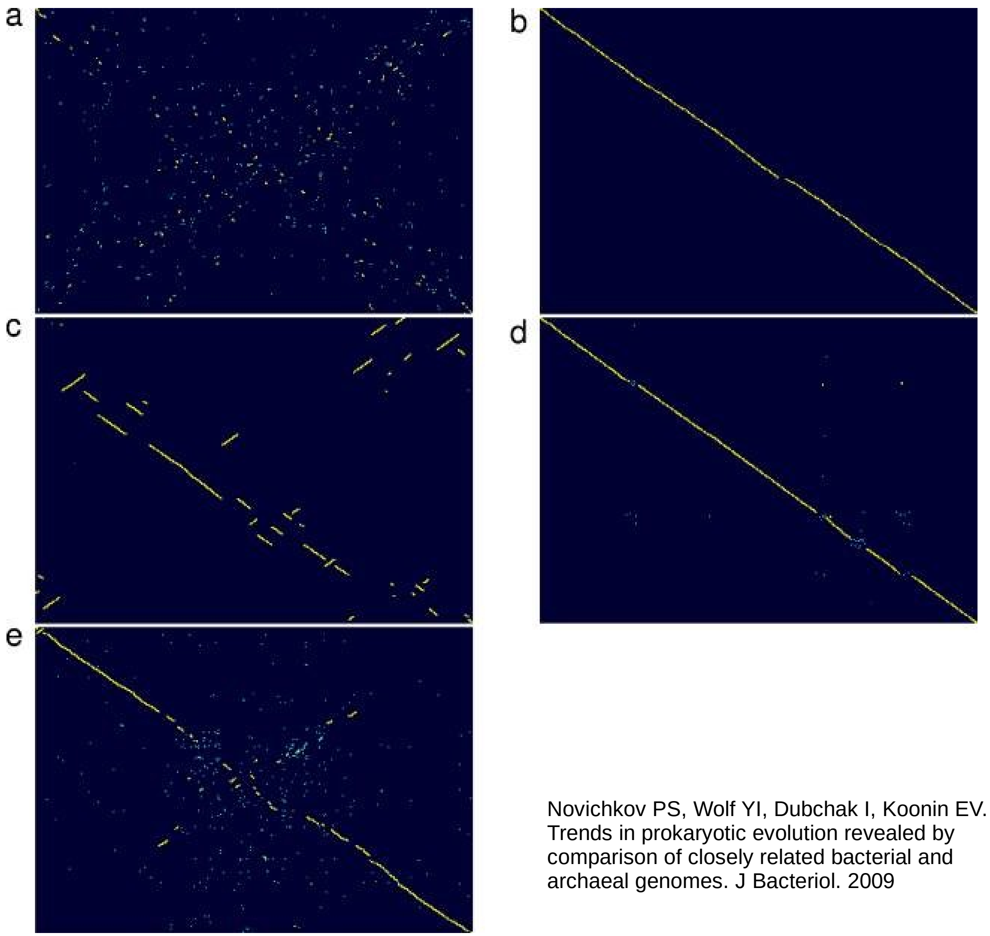

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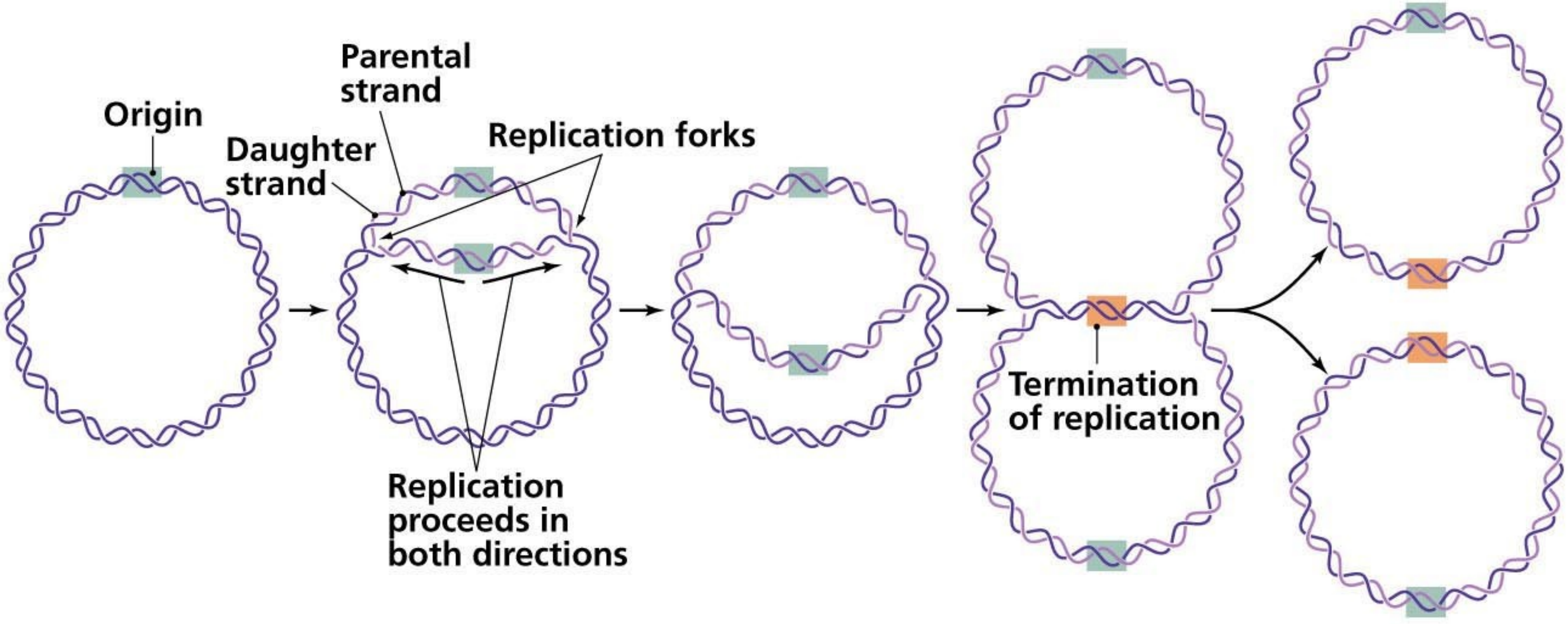
symmetric inversions
around the replication origin

Chromosome structure



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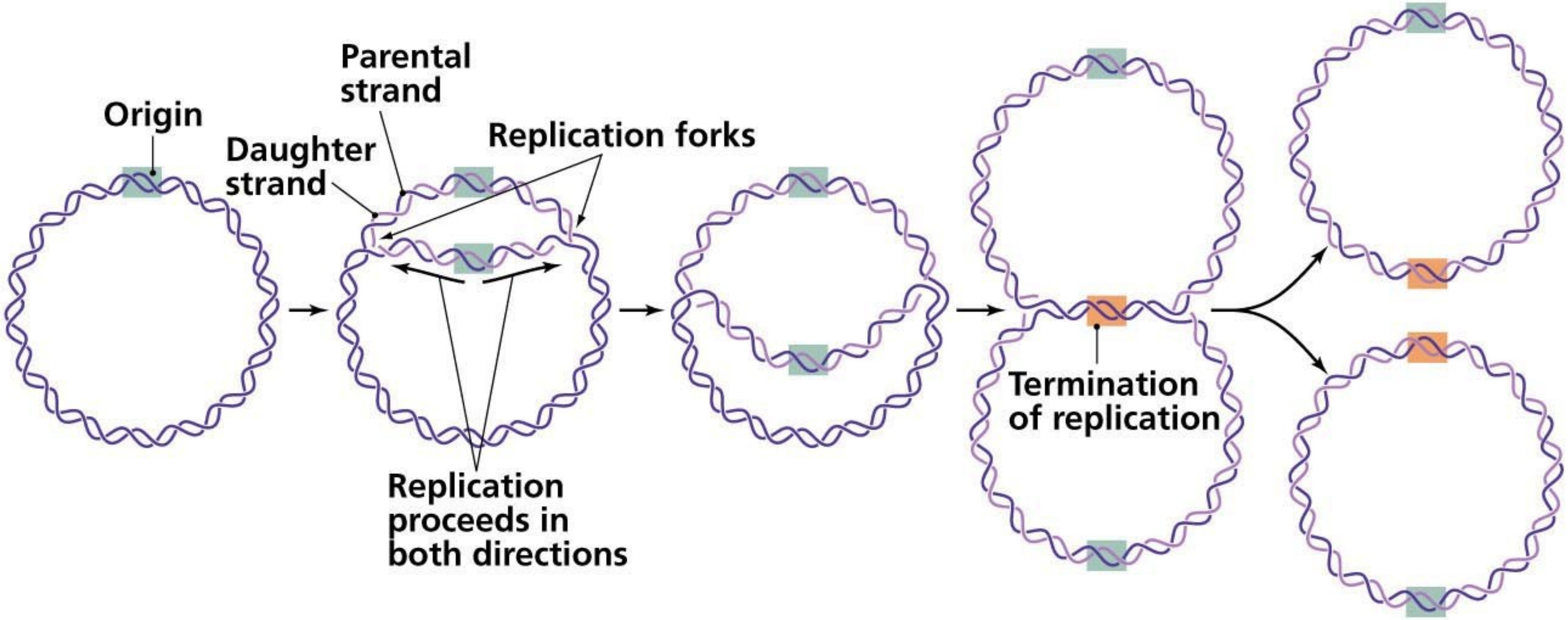
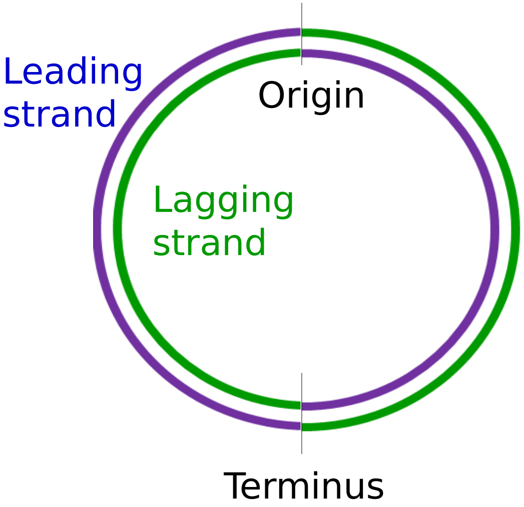


Selection on genome rearrangements / gene transfer:

1. Highly-expressed genes placed closed to origin of replication
2. Highly-expressed genes placed on the leading strand (co-direction of replication and transcription processes)
3. Origin and terminus of replication placed symmetrically (equal replicore lengths)

If the inversion occurred



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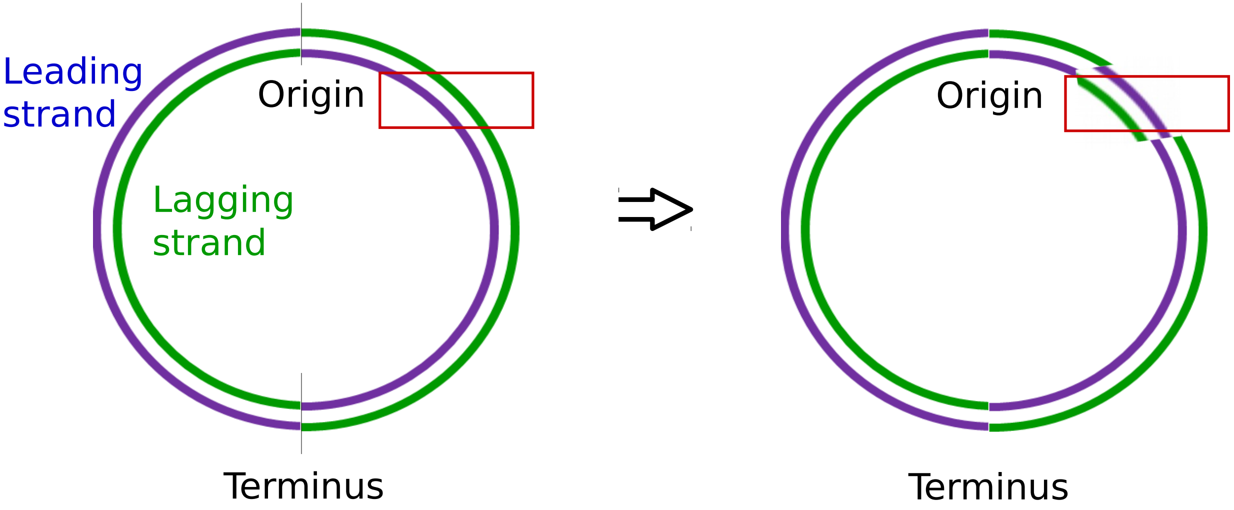


Leading strand

Lagging strand

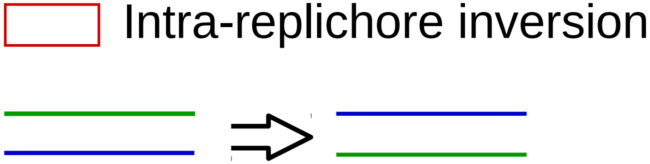
Origin

Terminus

⇒

Origin

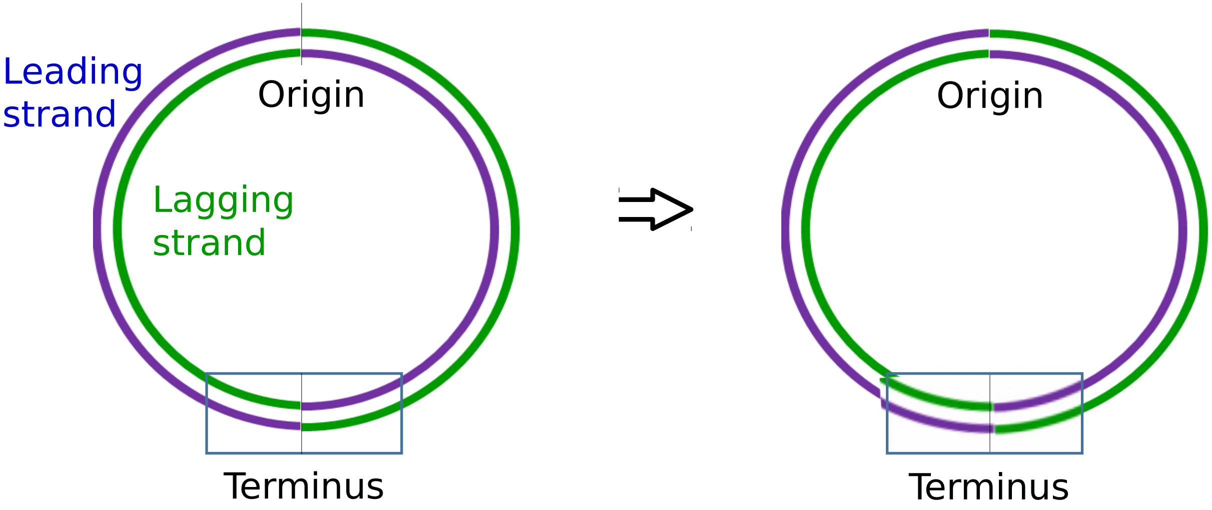
Terminus



🟥 Intra-replichore inversion

⇒

If the inversion occurred



Leading strand

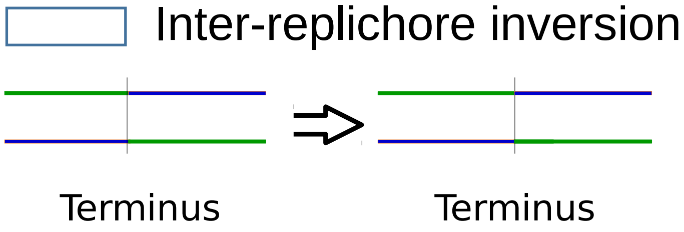
Lagging strand

Origin

Terminus

Origin

Terminus

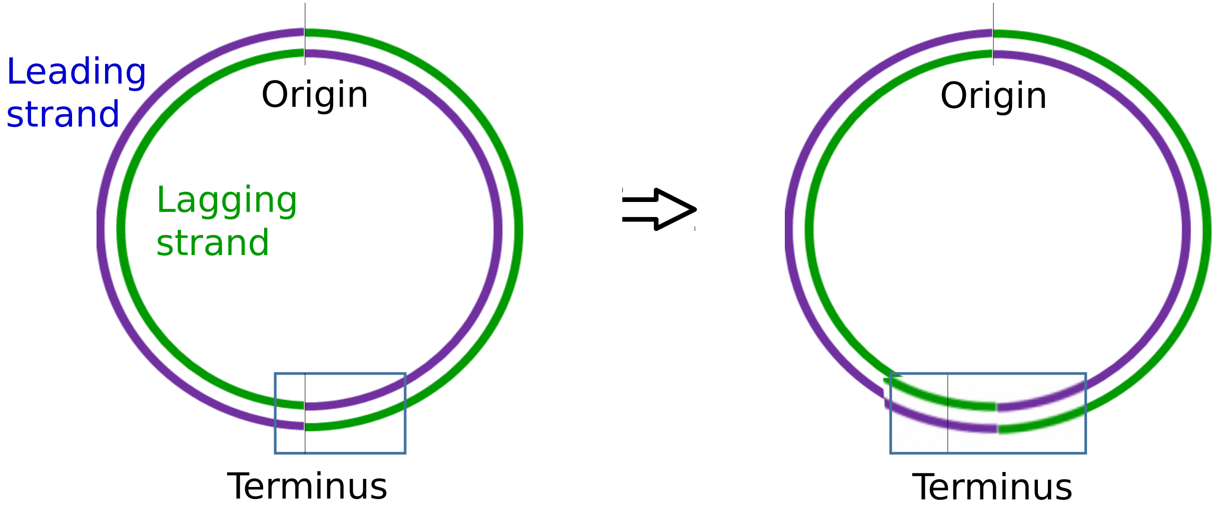


Inter-replichore inversion

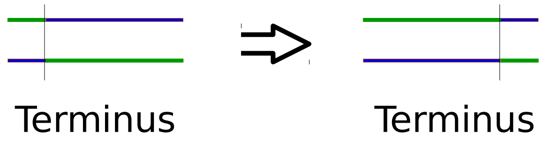
Terminus

Terminus

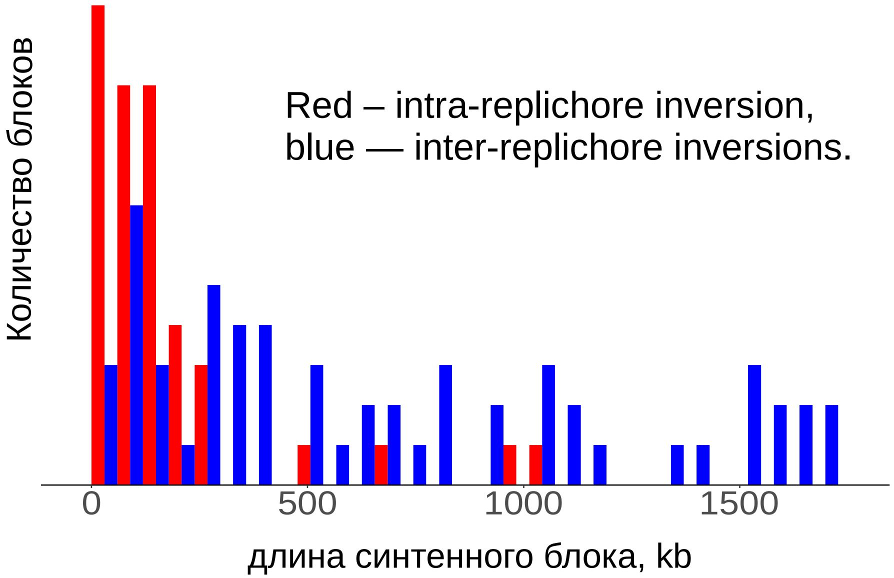
If the inversion occurred



▭ Inter-replichore inversion



What we see on the data



Red – intra-replichore inversion,
blue — inter-replichore inversions.

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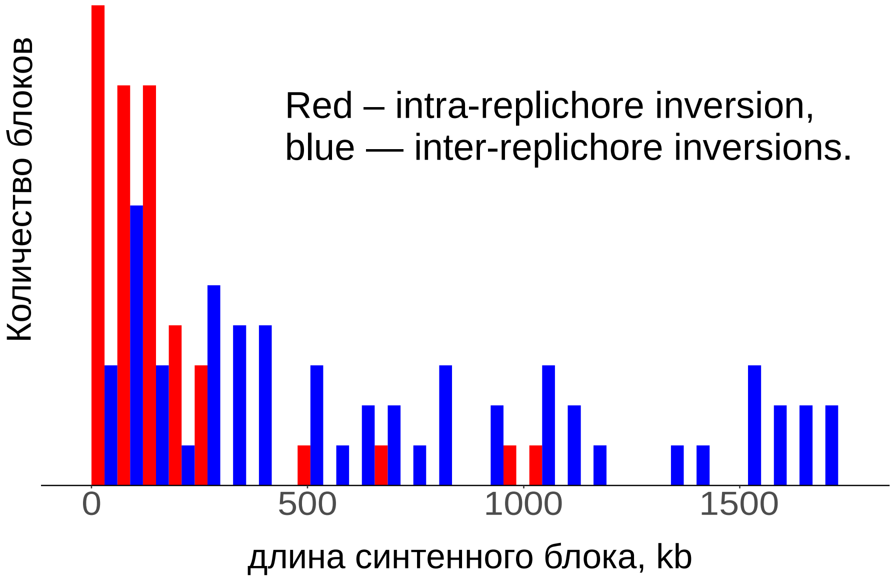

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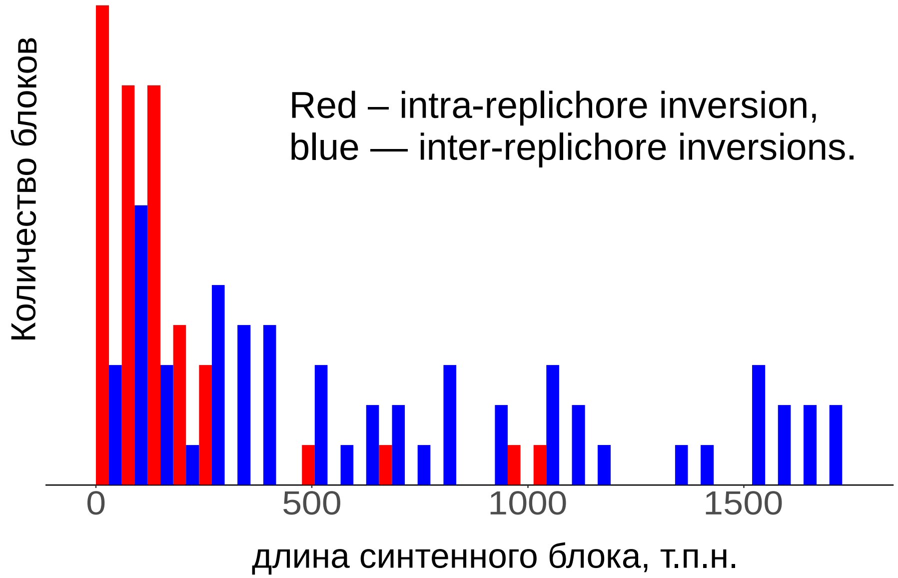
Вероятность инверсии длиной *m* пройти через точку начала (конца) репликации:

p(l)=m/L,
где L – размер реплихоры.

Доля инверсий
с концами на разных реплихорах:
58 из 101

Вероятность получить такой набор инверсий:
$p \sim 10^{-33}$

What we see on the data



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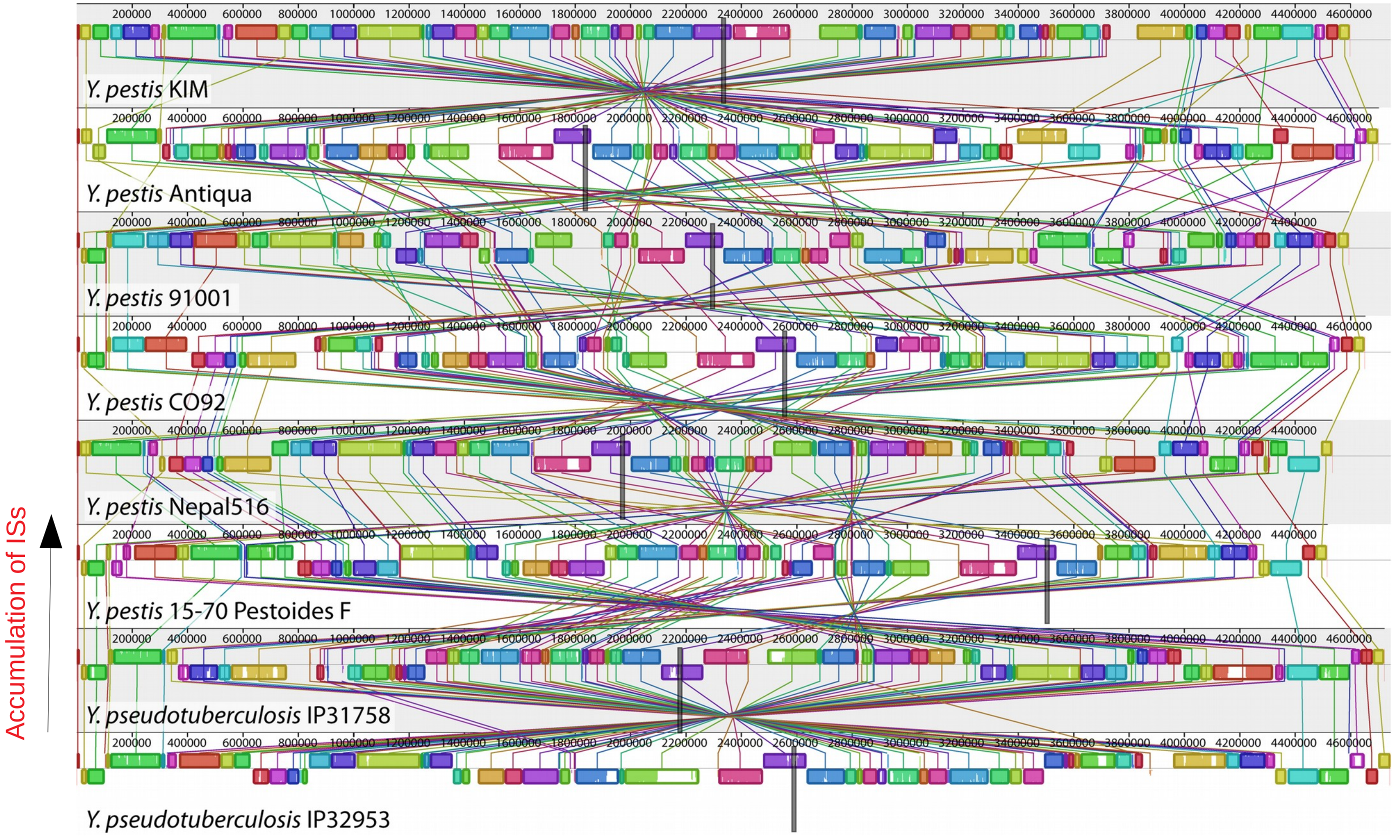
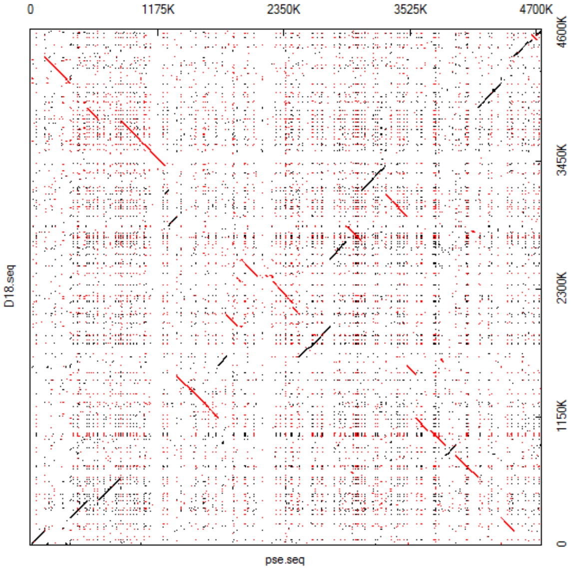
Darling AE, Miklós I, Ragan MA. Dynamics of genome rearrangement in bacterial populations. PLoS Genet. 2008

ISs expansion drives rearrangements

Yersinia pseudotuberculosis –> Y. pestis





AE, Miklós I, Ragan MA. Dynamics of genome rearrangement in bacterial populations. PLoS Genet. 2008

Pathogenic E.coli

enteropathogenic (EPEC),

enterotoxigenic (ETEC),

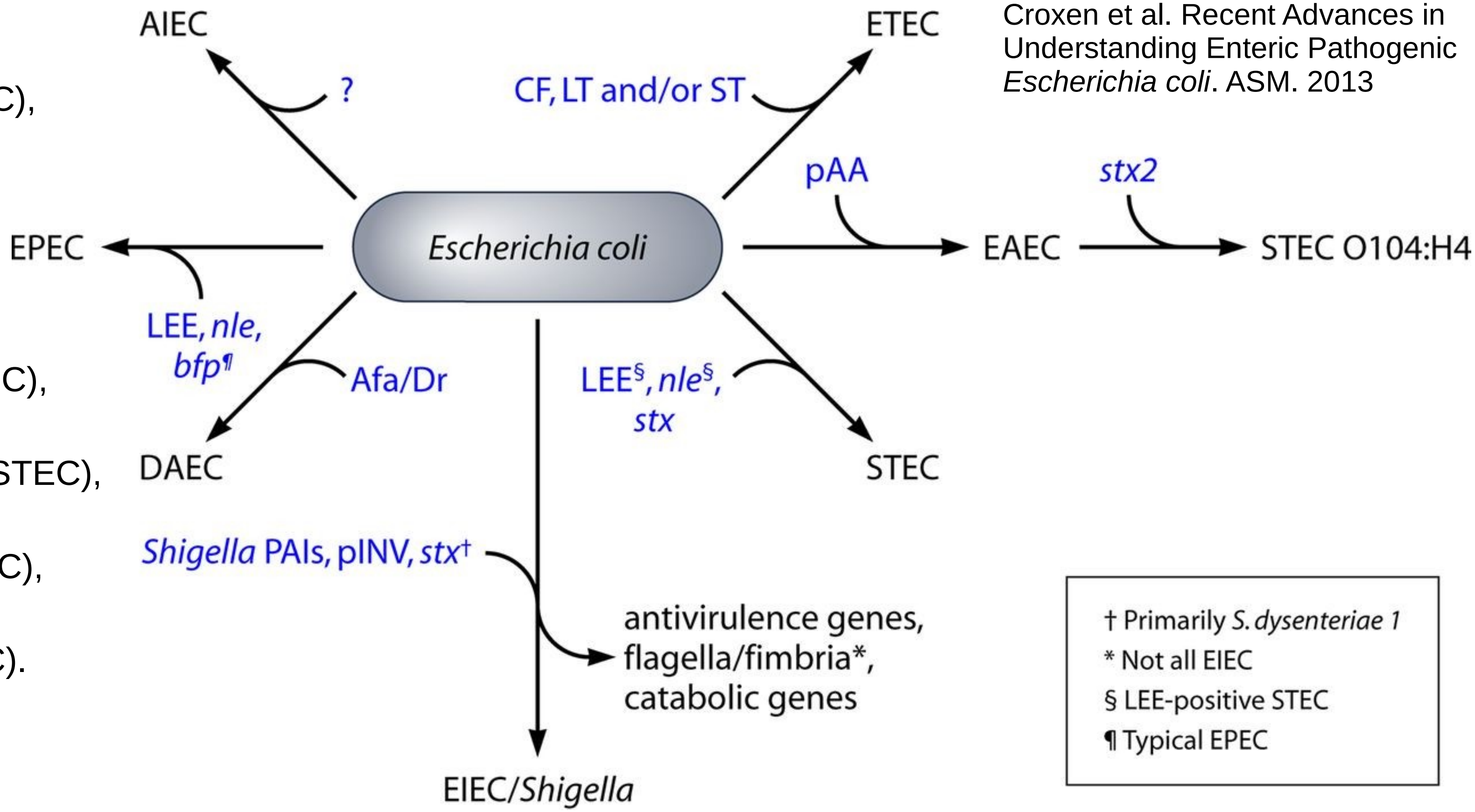
enteroinvasive (EIEC),

enteroaggregative (EAEC),

Shiga toxin-producing (STEC),

diffusely adherent (DEAC),

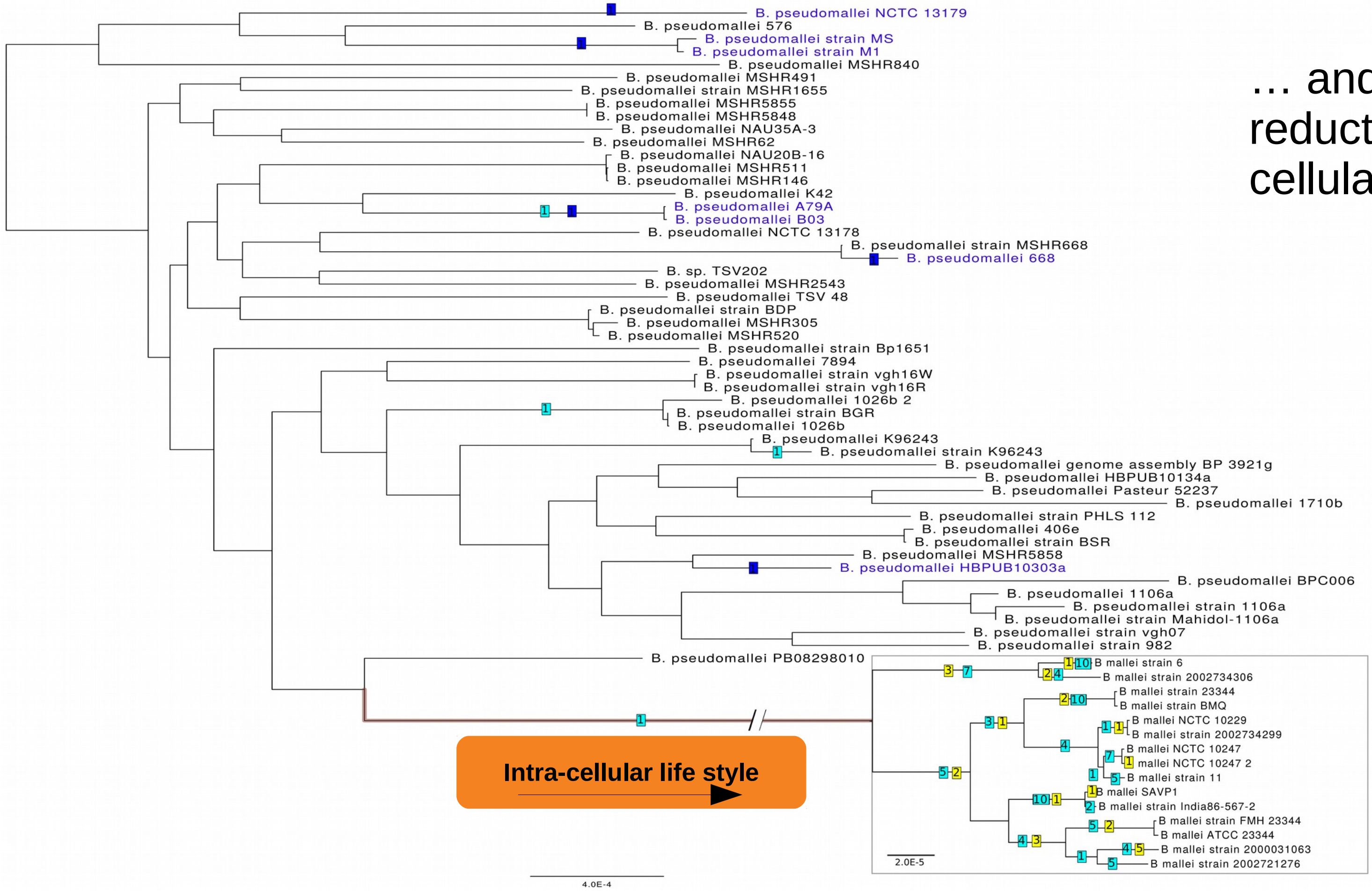
adherent invasive (AIEC).



Croxen et al. Recent Advances in Understanding Enteric Pathogenic *Escherichia coli*. ASM. 2013

Shigella strains are distinguished from *E. coli* by their nonmotility, absense of decarboxylated lysine and several biochemical characteristics, such as inability to ferment lactose and mucate.

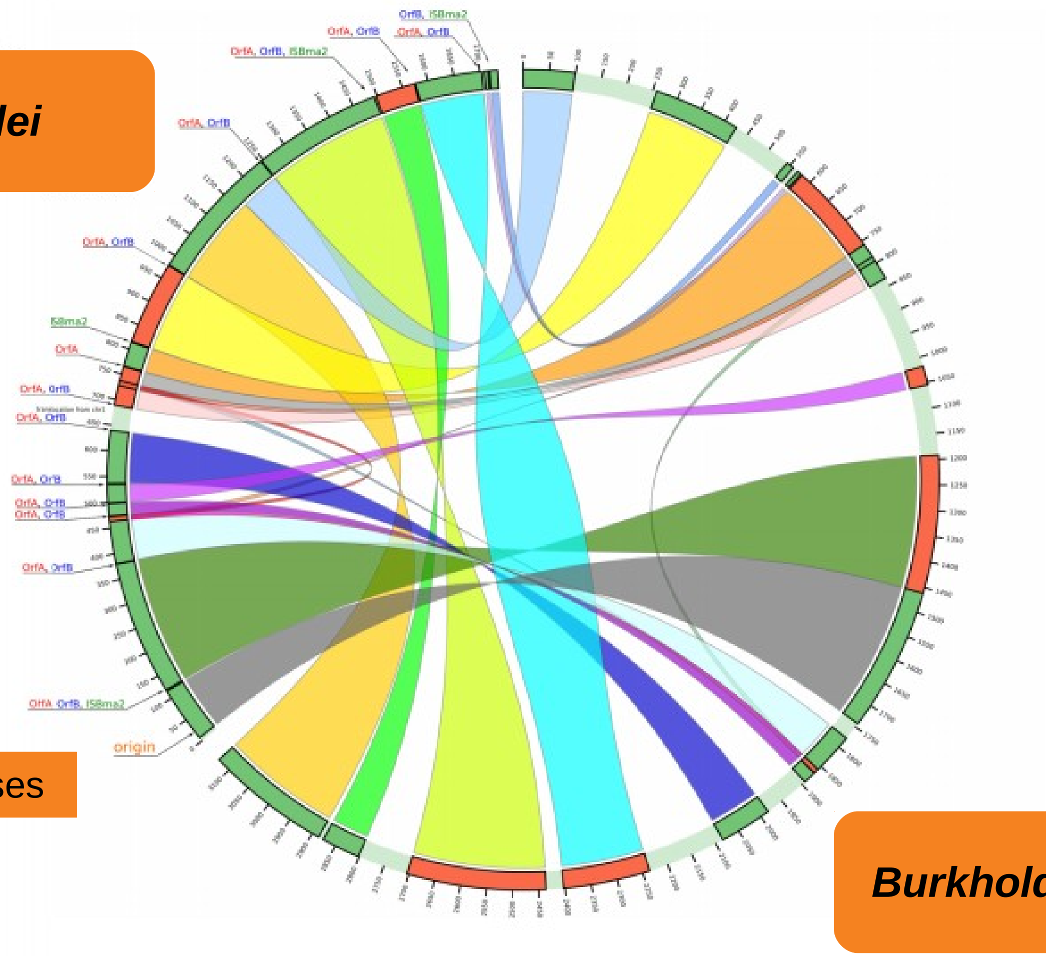
ISs expansion drives rearrangements



… and results in genome reduction in young intra-cellular pathogens

Genome reduction by deletions

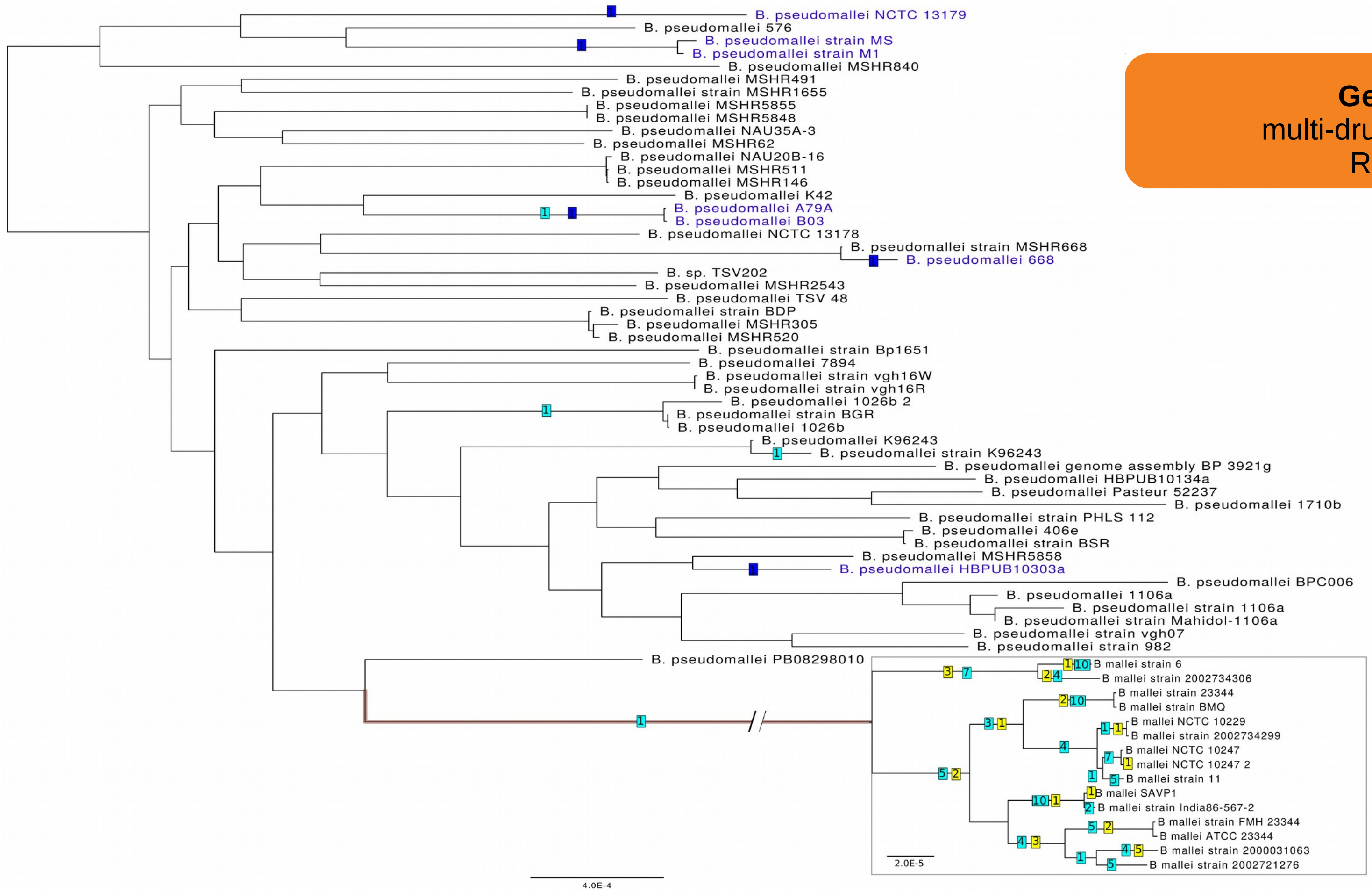
Burkholderia mallei



transposases

Burkholderia pseudomallei

Parallel inversions – genomic switch?

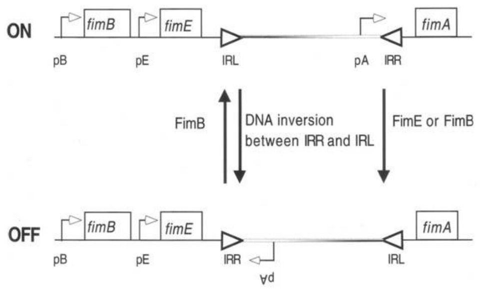


Genomic repeats:
multi-drug resistance complex,
RND efflux system

Site-specific micro-inversions

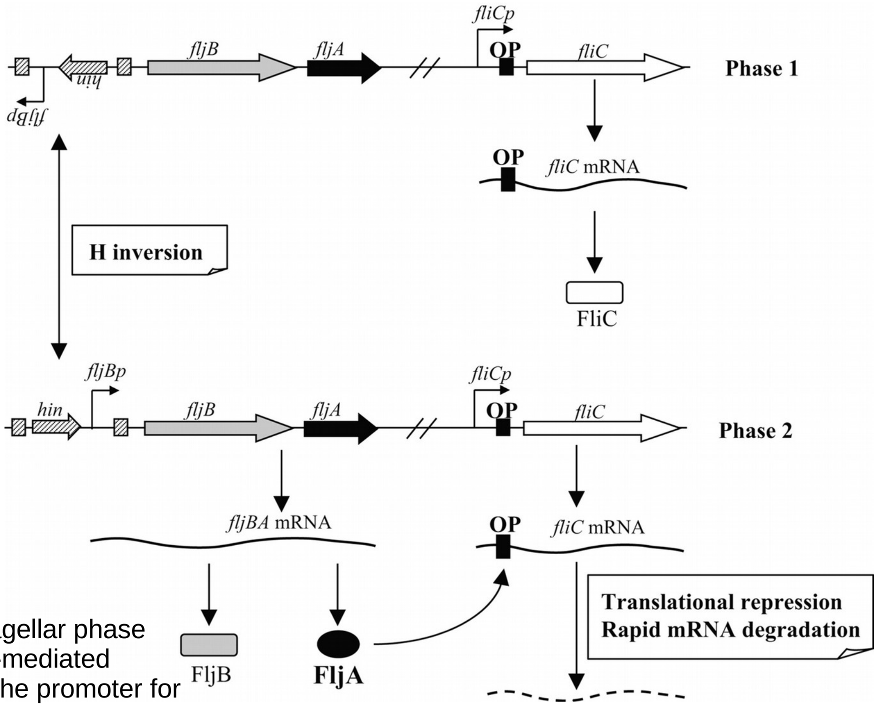
Phase variation – Site specific inversion

E. coli



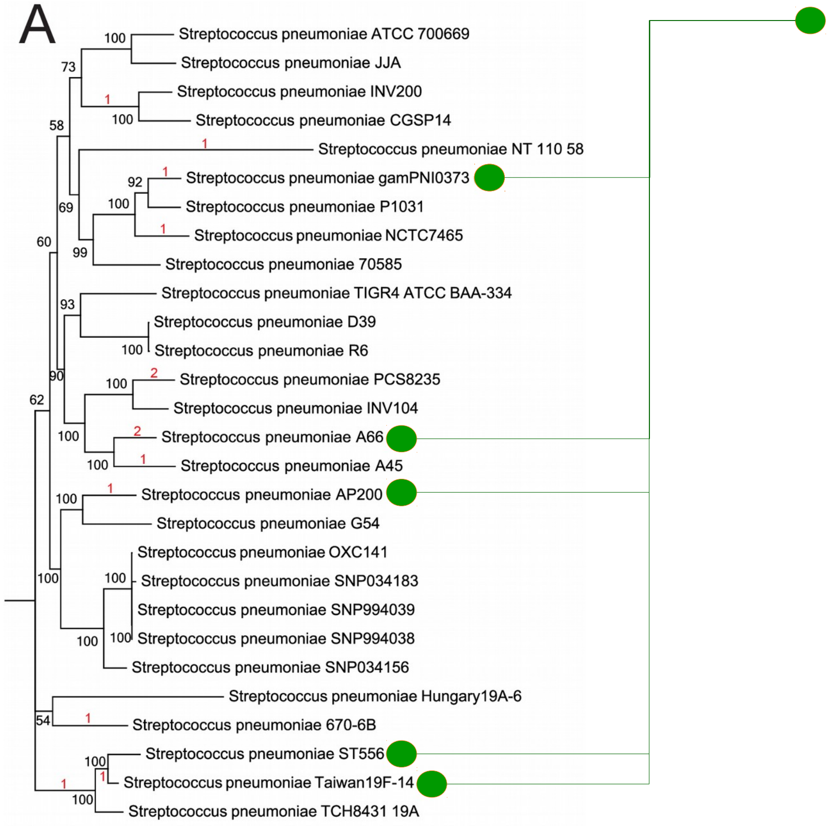
Phase variation – site specific inversion. pB, pE and pA are promoters for the genes *fimB, fimE* and *fimA* respectively. IRL and IRR are inverted repeats. FimB and FimE are recombinases that bind to the open triangles IRL an IRR. The result is an inversion of the DNA sequence (shaded bar) that turns ON or OFF the transcription of *fimA*.

Expression of multiple types of flagellin by *S. typhimurium*



The dual controlling system governs flagellar phase variation; one part of the system is Hin-mediated inversion of the H segment containing the promoter for the fljBA operon, and the other is FljA-mediated inhibition of fliC expression. FljA binds to the 5′-UTR of fliC mRNA, which inhibits its translation and facilitates its degradation.

Parallel inversions – genomic switch?

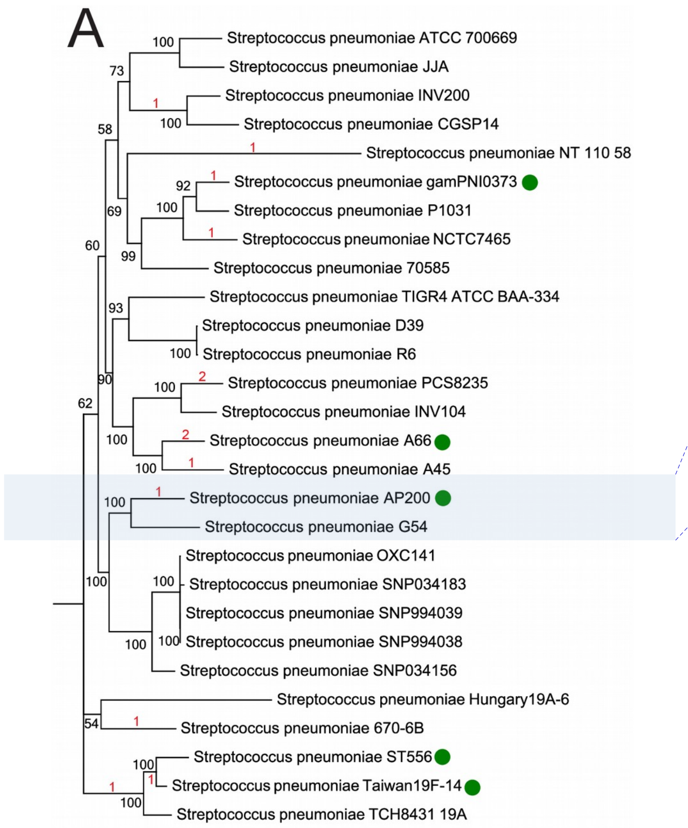


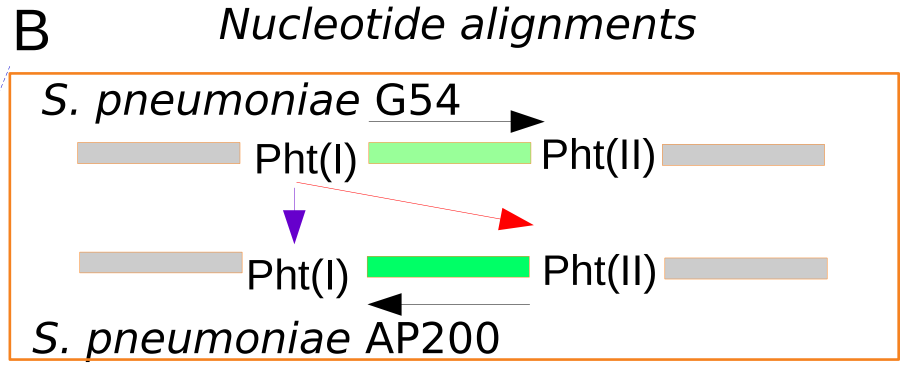
The same inverted sequence length 15kB
Breakpoints are formed by genes encoding proteins PhtB and PhtD

Белки гистидиновой триады (Pht)

- белки внешней мембраны, антигены
- характеризуются наличием мотива *HxxHxH*

Parallel inversions – genomic switch?

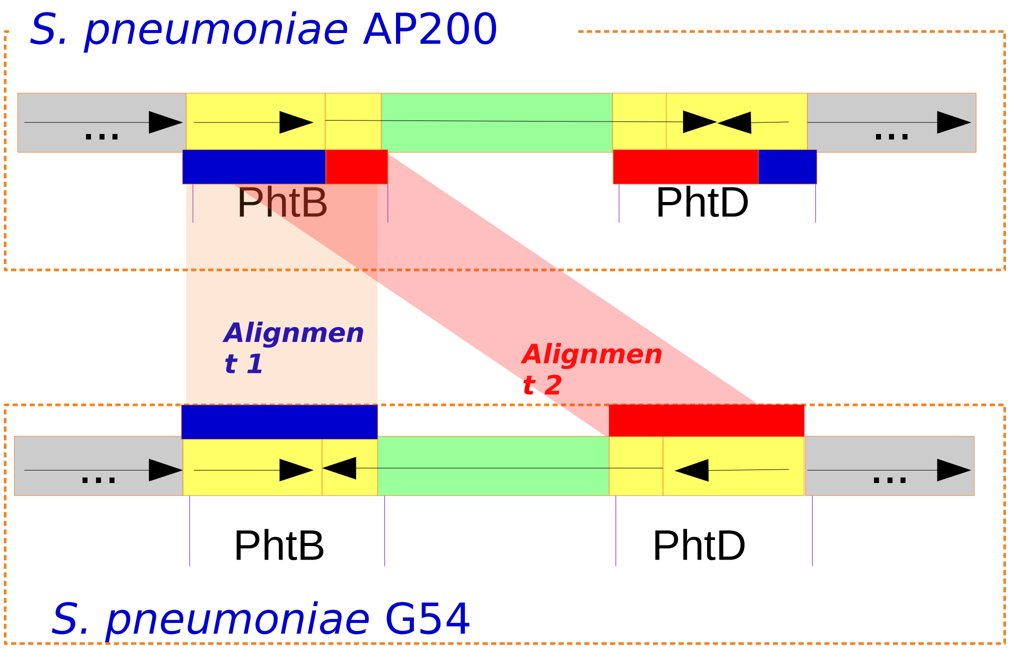




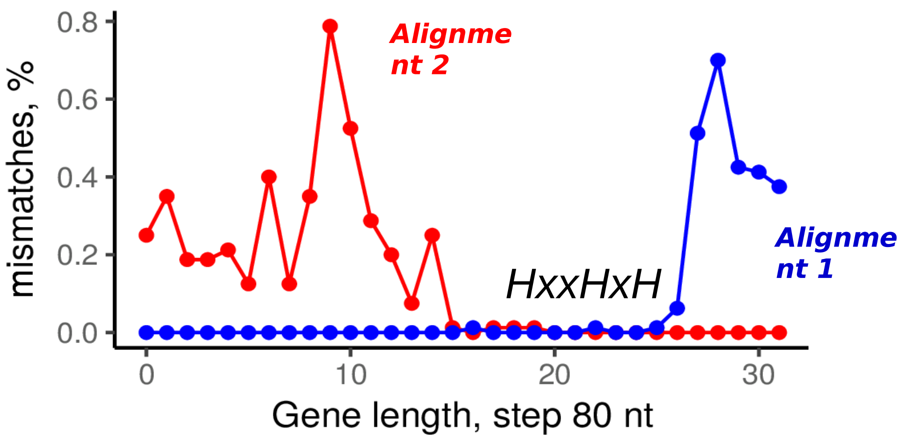
● The same inverted sequence length 15kB
Breakpoints are formed by genes encoding proteins PhtB and PhtD

Parallel inversions – genomic switch?

Phts' alignment



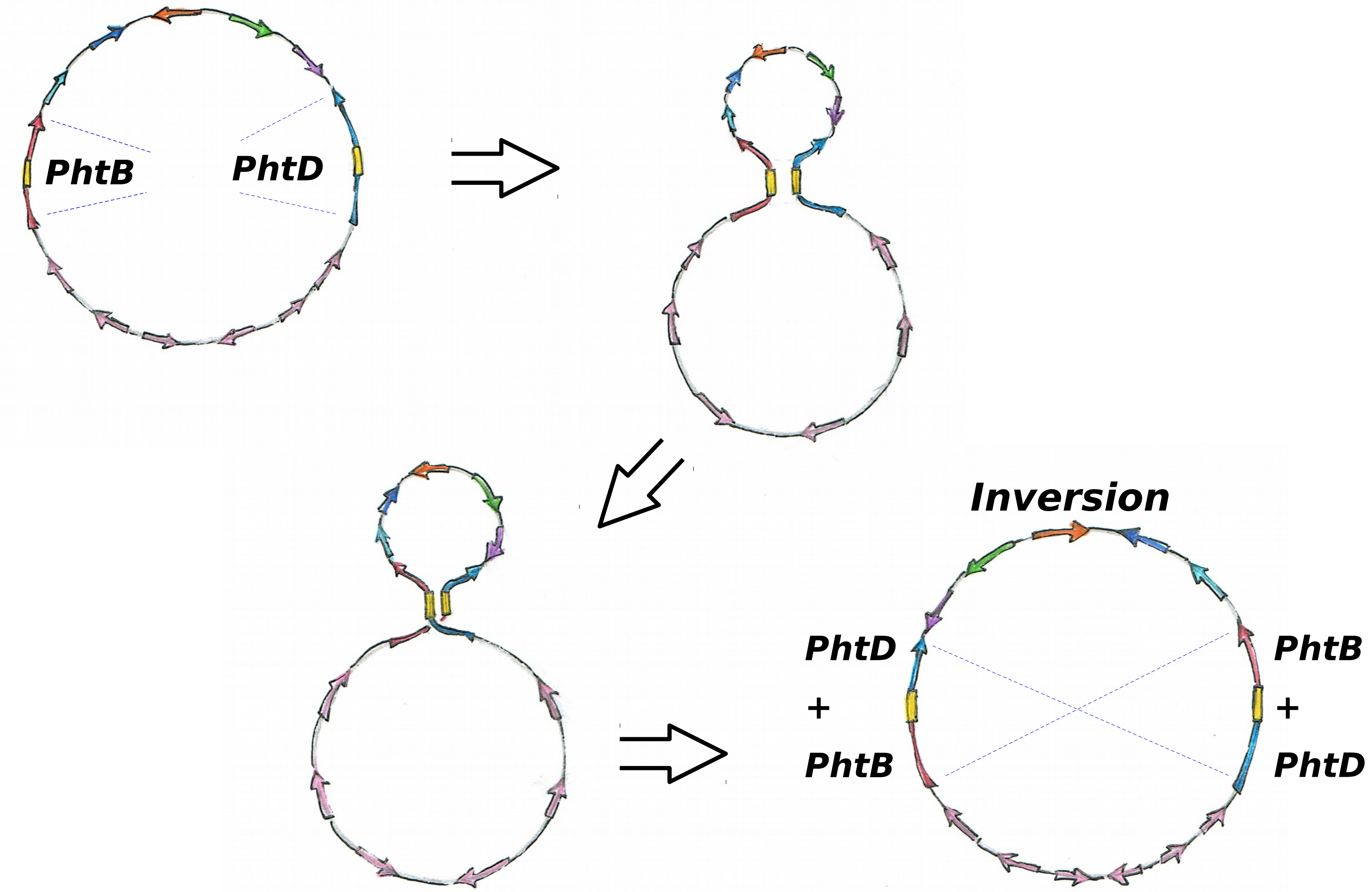
Mismatches



```
WP_0018462    1  MKINKKYVAGSVAVLALSVCSYELGRYQAGQDKKESNRVAYIDGDQAG
WP_0018475    1  MKINKKYLAGSVATLVLSVCAYELGLHQA-QTVKENNRVSYIDGKQAT

cons          1  *******:*****.*.****:****  :** *  **.***:****.** 
```

Parallel inversions – genomic switch?



Parallel inversions – genomic switch?

Биоинформатическое предсказание

Micro-evolution of three *Streptococcus* species: selection, antigenic variation, and horizontal gene inflow

Pavel V. Shelyakin [†], Olga O. Bochkareva [†], Anna A. Karan and Mikhail S. Gelfand

[†]Contributed equally

BMC Evolutionary Biology 2019 **19**:83
https://doi.org/10.1186/s12862-019-1403-6 | © The Author(s) 2019
Received: 22 December 2017 | **Accepted:** [redacted] | **Published:** [redacted]

Parallel inversions – genomic switch!!!

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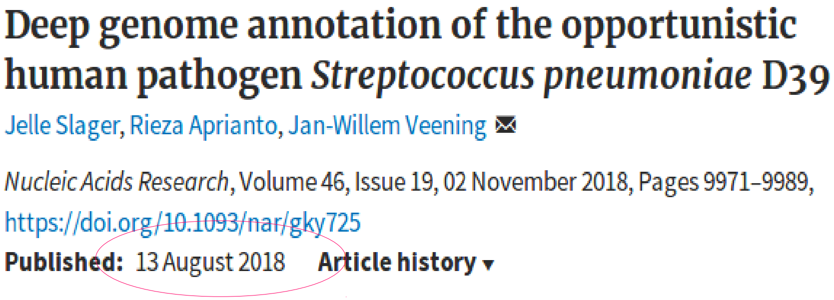
Received: 22 December 2017 | **Accepted:** 25 February 2019 | **Published:** 27 March 2019

Экспериментальное подтверждение



Deep genome annotation of the opportunistic human pathogen *Streptococcus pneumoniae* D39

Jelle Slager, Rieza Aprianto, Jan-Willem Veening

Nucleic Acids Research, Volume 46, Issue 19, 02 November 2018, Pages 9971–9989, https://doi.org/10.1093/nar/gky725

Published: 13 August 2018 **Article history** ▾

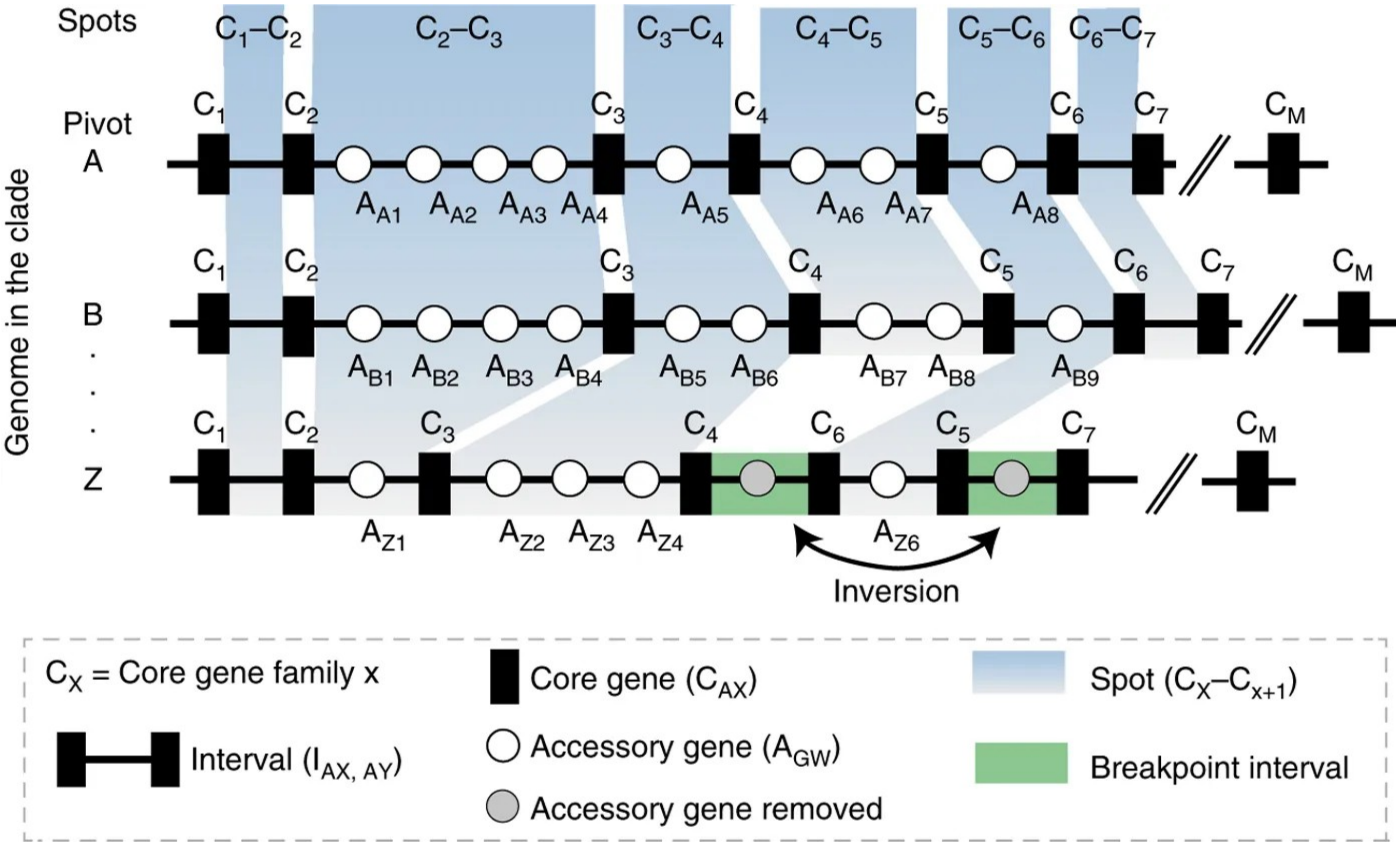
Parallel inversions – genomic switch!!!

These two out of four pneumococcal histidine triad (Pht) proteins **are considered to be good vaccine candidates.**

PhtD was already used in several phase I/II clinical trials.

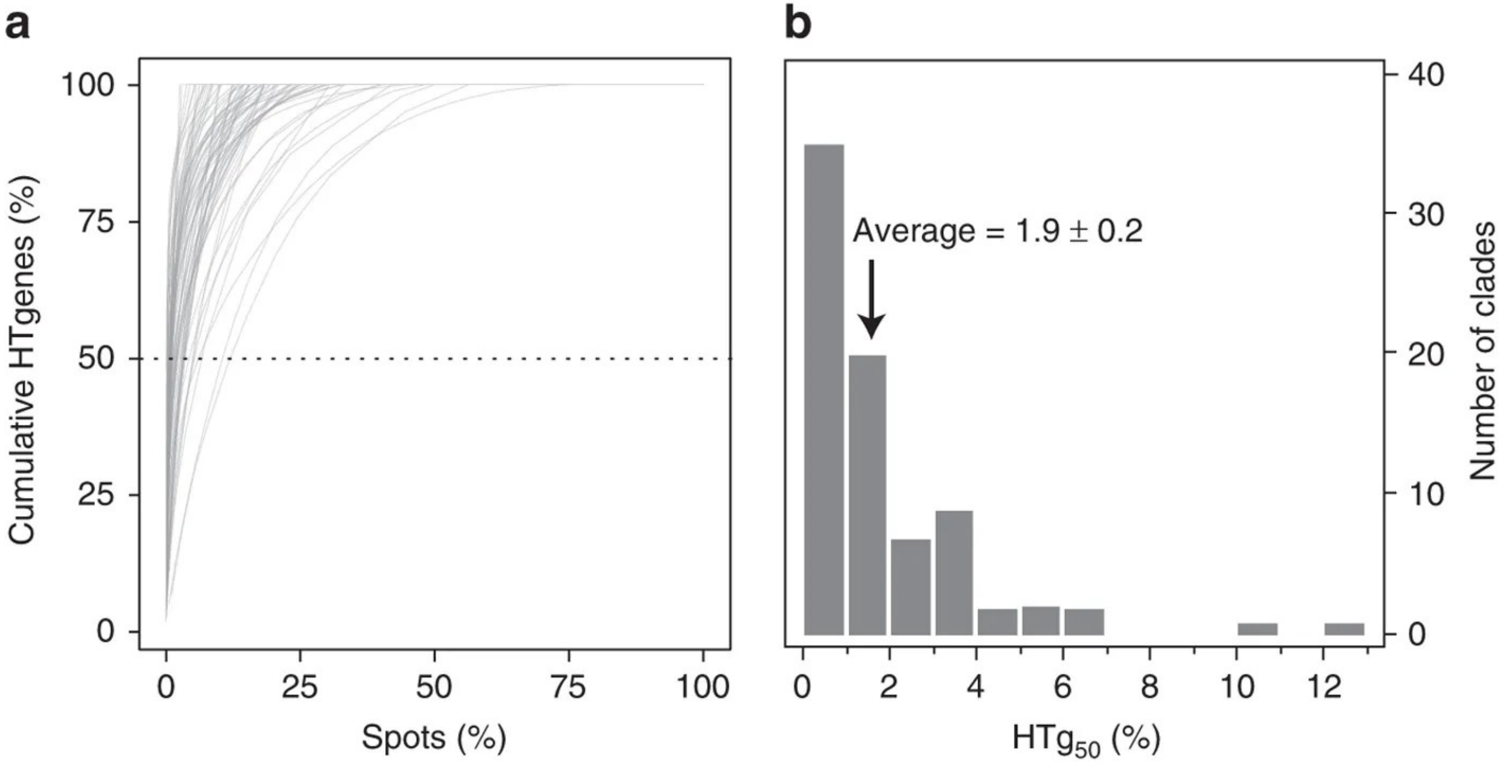
Yun et al.* (PLoS One. 2015) analyzed the diversity of phtD alleles from 172 clinical isolates and concluded that **the sequence variation was minimal.**

Evolution of gene content



Oliveira, P.H., Touchon, M., Cury, J. et al. The chromosomal organization of horizontal gene transfer in bacteria. Nat Commun. 2017

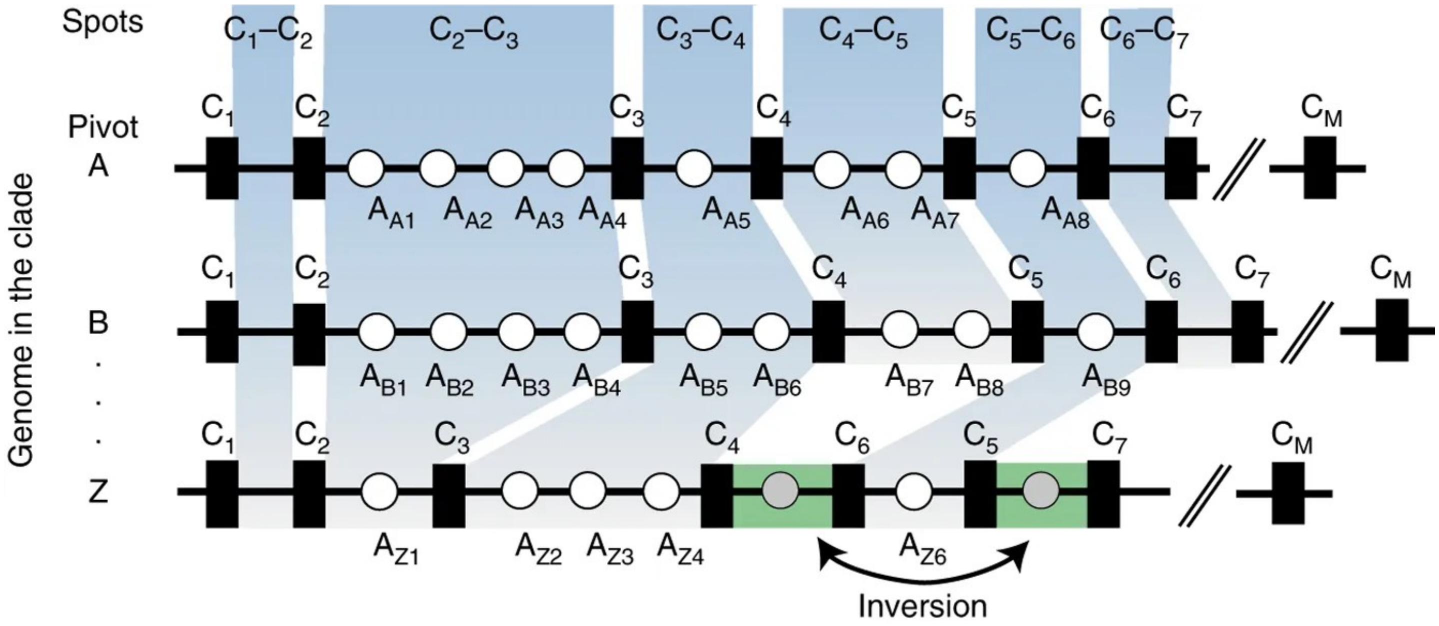
Evolution of gene content



“A total of 1841 hotspots in the 80 clades. They represent only 1.2% of the spots, but they concentrate 47% of the accessory gene families and 60% of the HTgenes.”

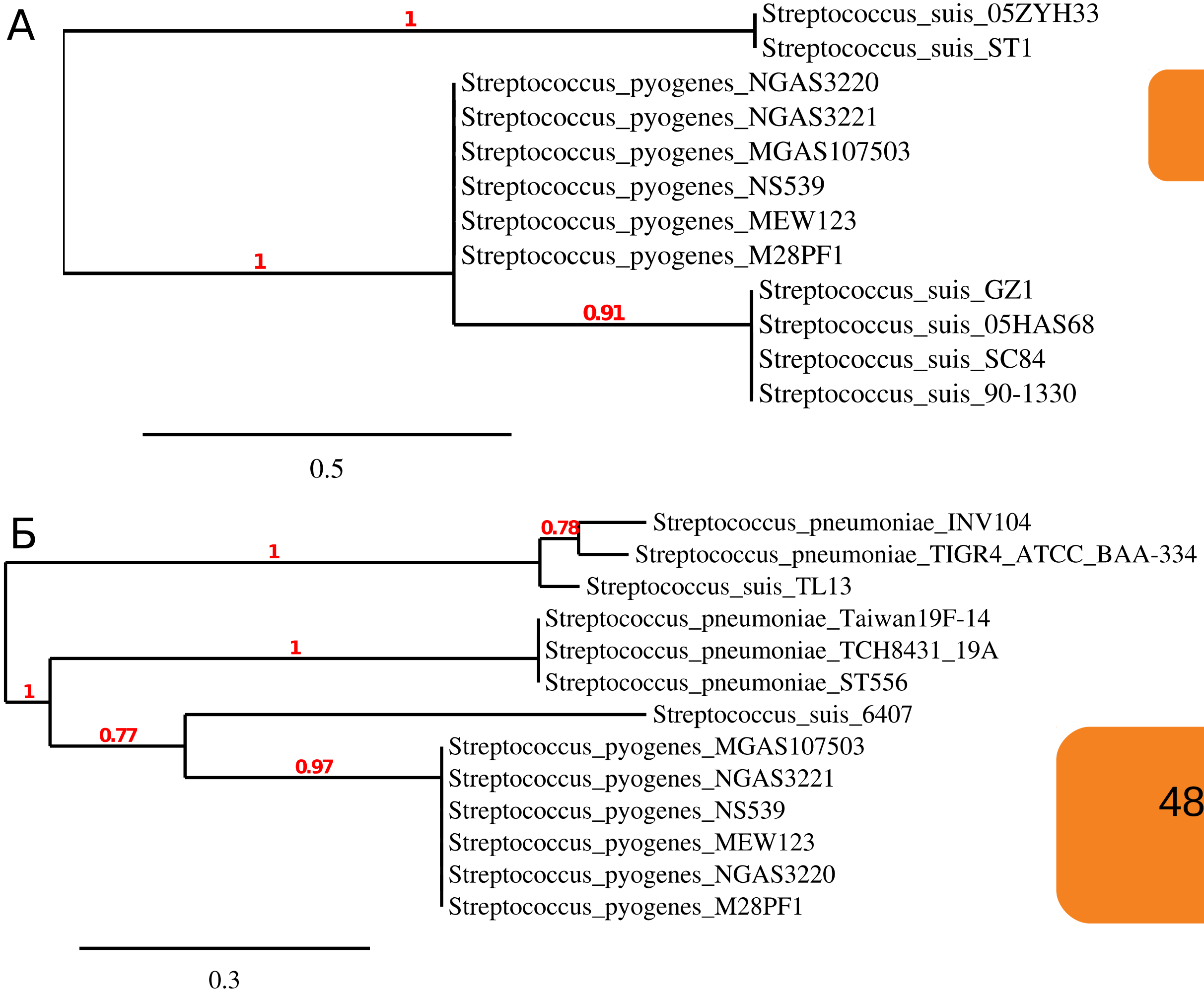
Oliveira, P.H., Touchon, M., Cury, J. et al. Nat Commun. 2017

Evolution of gene content



Ortologous groups in different breakpoint intervals are HT candidates

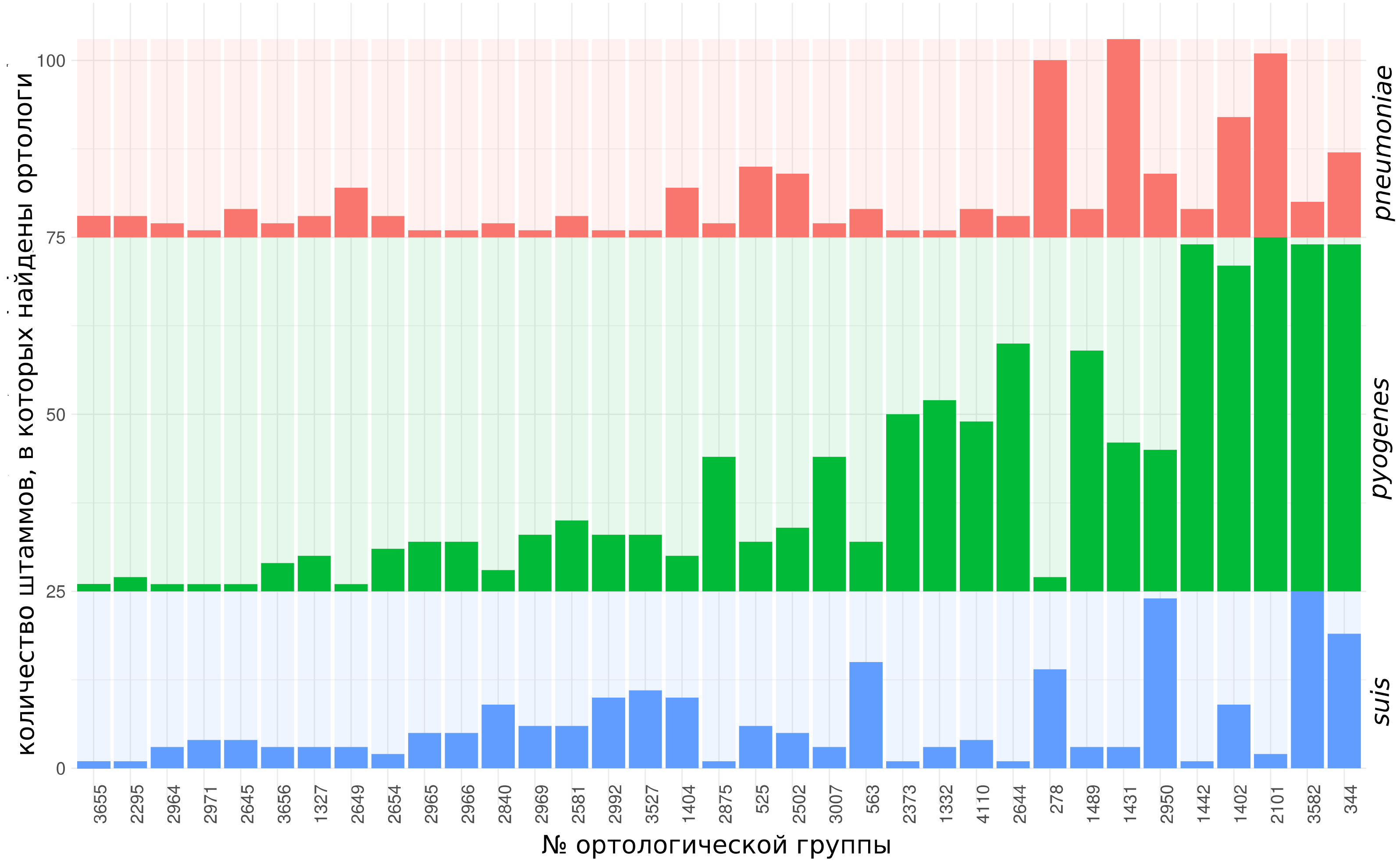
Evolution of gene content



176 ortologous groups

48 of them have inconsistent phylogenetic trees

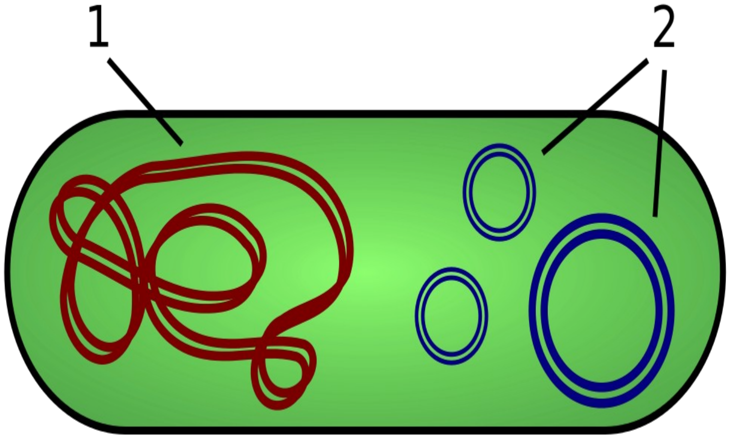
Evolution of gene content



Bacterial genome structure

1. Chromosome(-s)

- circular, double-stranded DNA molecule
- 1Mb – 6 Mb
- one origin of replication
- carry house-keeping genes and a lot of others



2. Plasmids

- circular, double-stranded DNA molecules
- 15 kb – 200 kb
- replicate independently
- carry genes that benefit the survival of the organism.

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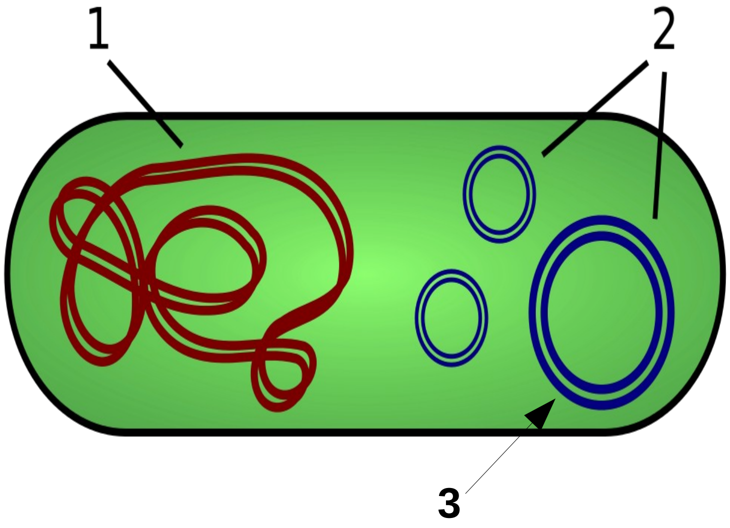

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3. Other secondary replicons

- circular, double-stranded DNA molecule
- 300 Mb – 3 Mb

- plasmid type origin of replication
- have small part of core genes
- is subjected to regulation by chromosomally encoded mechanisms

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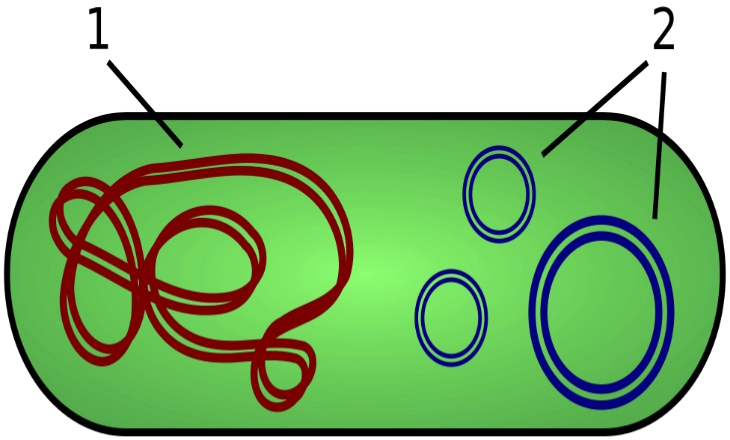

Chromosome **+** plas**mid = chromid**

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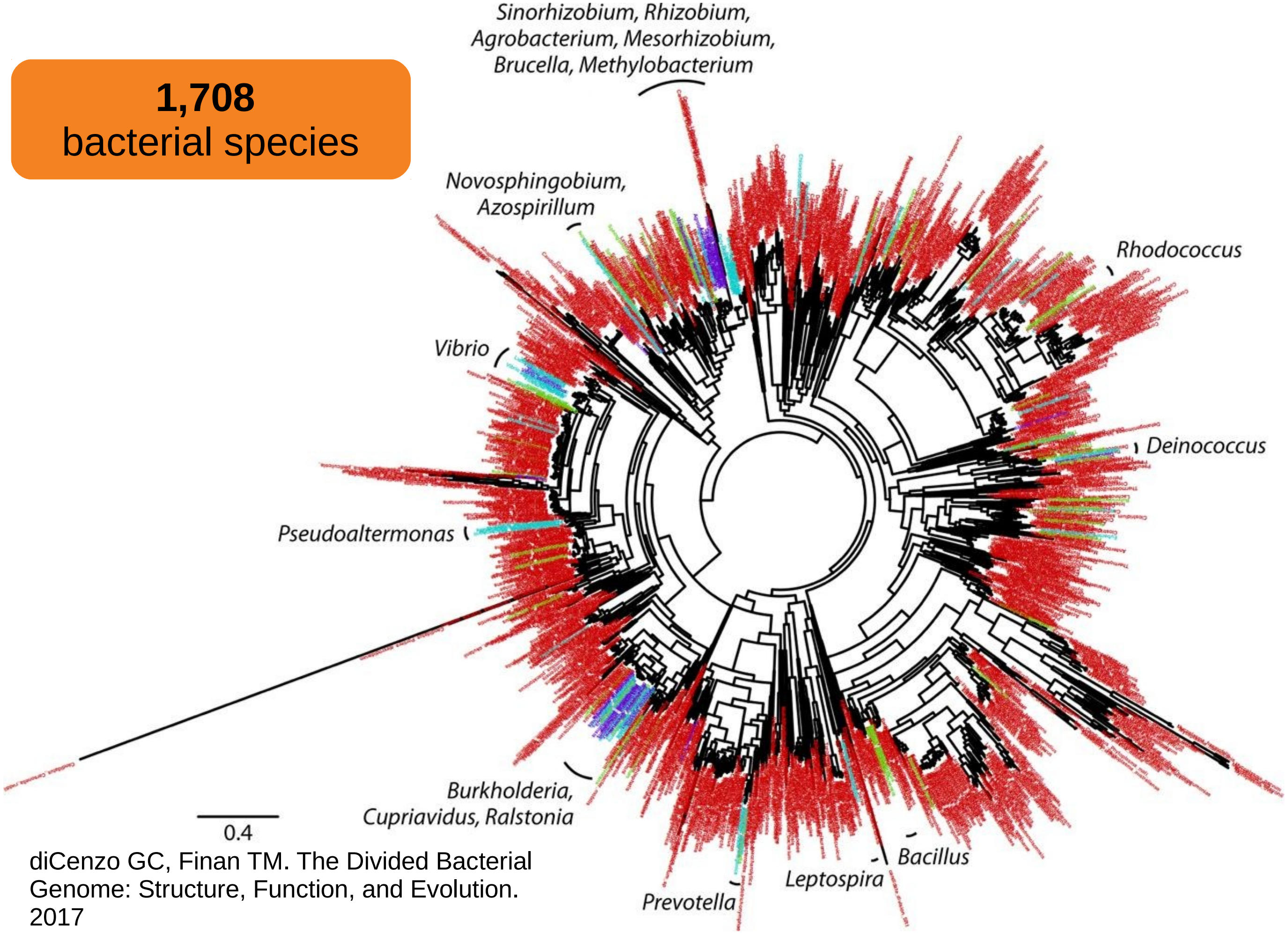
Bacterial tree of life

1,708
bacterial species



diCenzo GC, Finan TM. The Divided Bacterial Genome: Structure, Function, and Evolution. 2017

Colors:

red for species with no megaplasmid or chromid

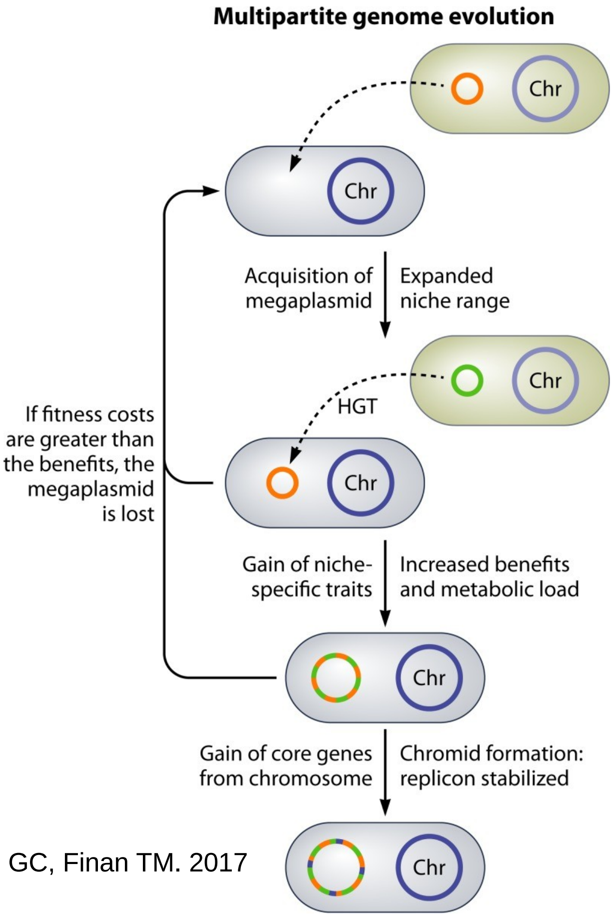
green for species with a megaplasmid(s) but no chromid

blue for species with a chromid(s) but no megaplasmid

purple for species with both a megaplasmid(s) and a chromid(s).

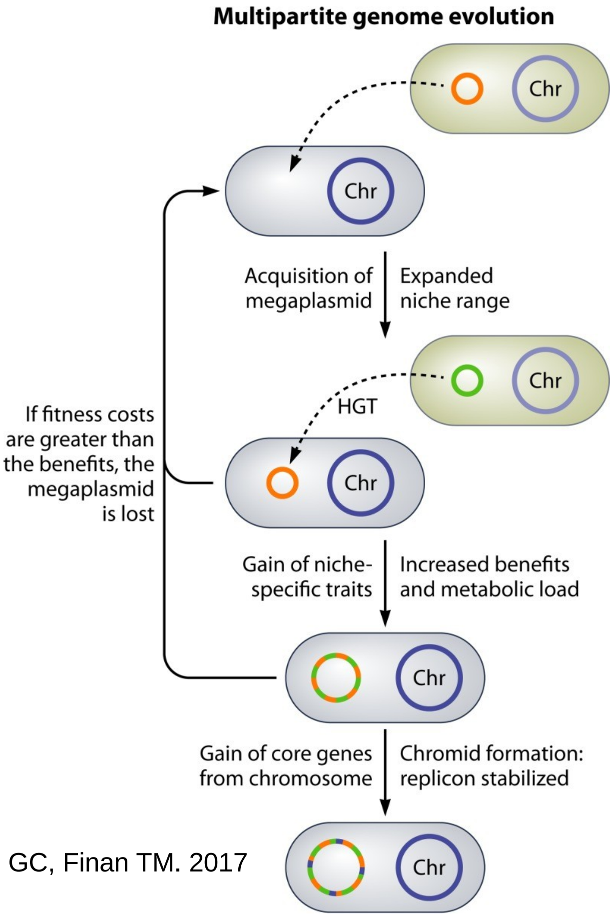
10% of bacterial genomes are split between two or more large DNA fragments

Chromid formation hypothesis



diCenzo GC, Finan TM. 2017

Chromid formation hypothesis



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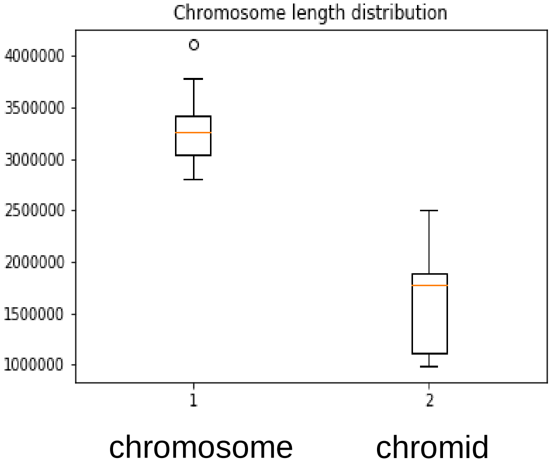

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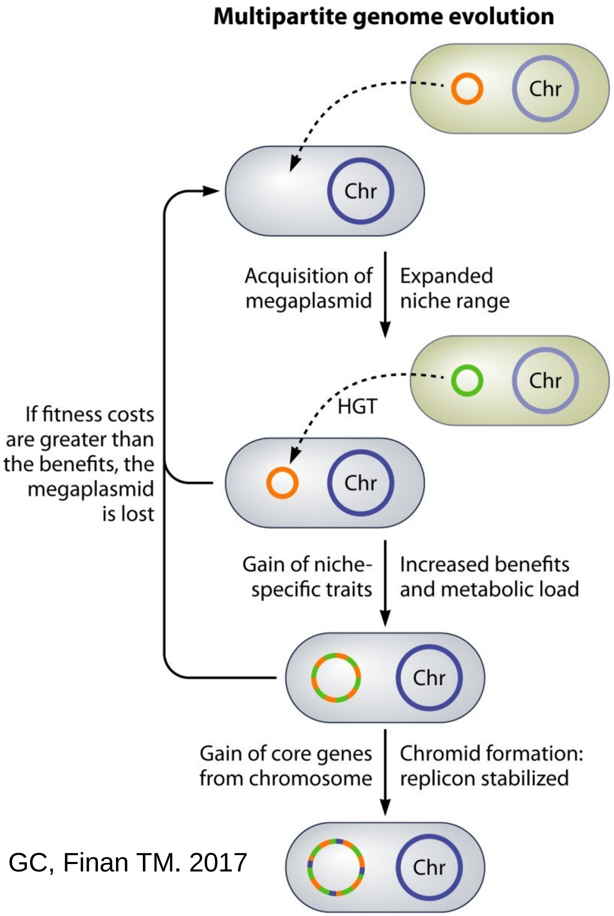

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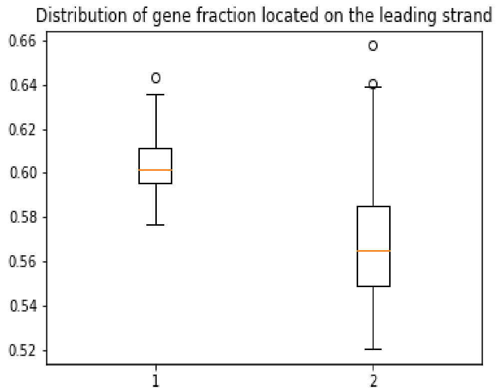
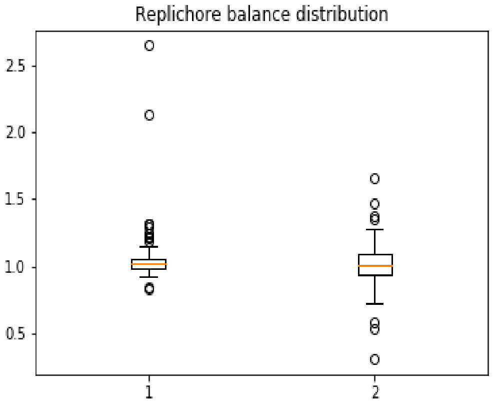
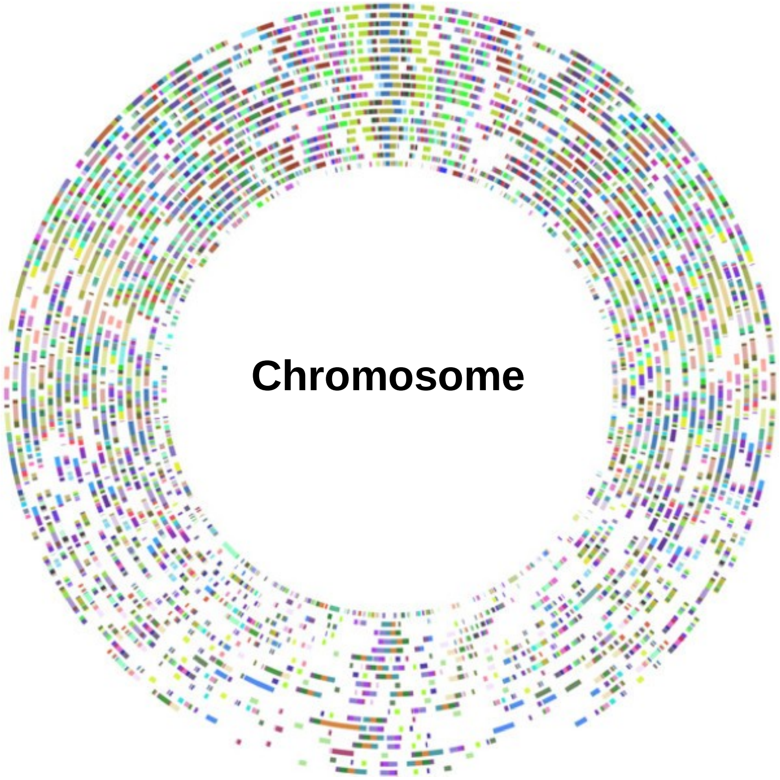


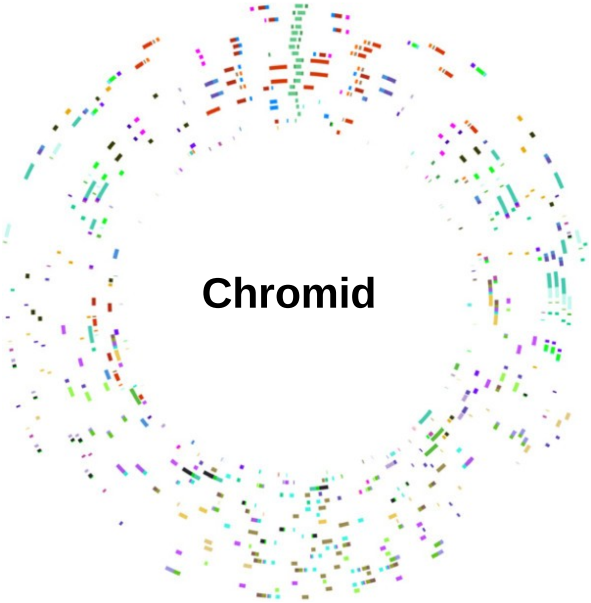
chromosome chromid



chromosome chromid

Chromosome and chromid structure





Dikow, Rebecca B, and William Leo Smith. "Genome-level homology and phylogeny of Vibrionaceae (Gammaproteobacteria: Vibrionales) with three new complete genome sequences." BMC Microbiology vol. 13 80. 11 Apr. 2013, doi:10.1186/1471-2180-13-80

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