

Mechanisms of Infectious Disease • Fall 2008

Lecture 1

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Genetic Basis of Variation in Bacteria

- I. Organization of genetic material in bacteria
 - a. chromosomes
 - b. plasmids
- II. Genetic variation: Source
 - a. point mutations
 - b. DNA rearrangements
- III. Genetic variation: Transmission
 - a. transformation
 - b. transduction
 - c. conjugation
- IV. Genetic variation: Implications for pathogenesis

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Genetic basis of variation: Griffiths (1928)

There are two strains of *Streptococcus pneumoniae*.

ROUGH COLONY (R)

SMOOTH COLONY (S)

R strain is benign
(Lacking a protective capsule, it is recognized and destroyed by host's immune system)

S strain is virulent
(Polysaccharide capsule prevents detection by host's immune system)

Genetic basis of variation: Hershey and Chase (1952)

Radioactive protein capsule (³⁵S)

Labelled phages infect bacteria. Blender separates phages outside the bacteria from the cells and their contents. Cells and Phages are separated by centrifugation. Most ³⁵S found in supernatant. Most ³²P found in pellet.

Radioactive DNA (³²P)

Most ³⁵S found in supernatant. Most ³²P found in pellet.

Genetic basis of variation: Griffiths (1928)

The controls:

The experiment:

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Genetic basis of variation: Avery et al. (1944)

DNA as the transforming principle

DNA/RNA mix from S strain

Treat w/ DNase → DNA only → **S transformants Recovered**

Treat w/ RNase → RNA only → **NO S transformants**

Live nonvirulent bacteria

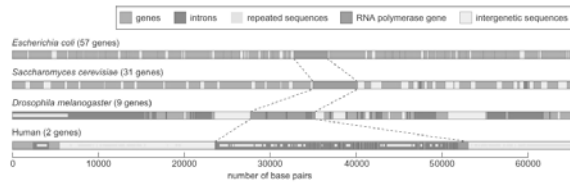
transformed with **DNA isolated from heat-killed virulent bacteria**

→ Encapsulated virulent bacteria → **Mouse dies**

Organization of genetic material in bacteria: chromosomes

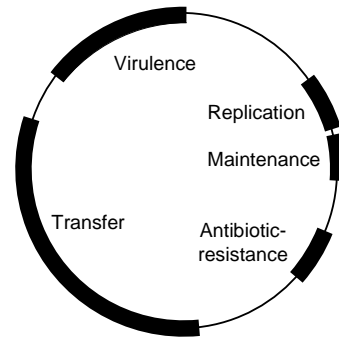
- **Most** bacteria contain a single chromosome (+ extrachromosomal elements)
- **Some** bacteria have been found also to contain 2-3 replicons which can be considered either megaplasmids or minichromosomes e.g. 3.0 Mb and 0.9 Mb replicons in *Rhodobacter sphaeroides*
- A **few** bacterial genera contain >1 chromosome e.g. 2.1 Mb and 1.2 Mb chromosomes in *Brucella*
- **Some** bacteria harbour large replicons essential for survival in a specific ecological niche but not under laboratory conditions e.g. 1.4 Mb and 1.7 Mb replicons in *Rhizobium meliloti* are required for plant symbiosis

Organization of genetic material in bacteria: chromosomes



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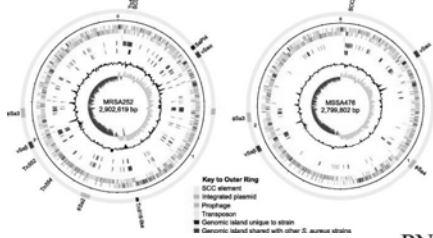
Organization of genetic material in bacteria: plasmids



Organization of genetic material in bacteria: chromosomes

Complete genomes of two clinical *Staphylococcus aureus* strains: Evidence for the rapid evolution of virulence and drug resistance

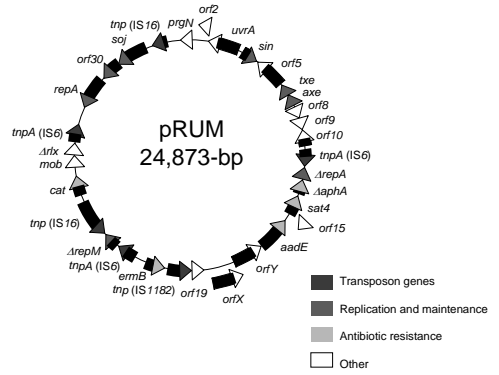
Matthew T. G. Mitchell¹, Edward J. Fair¹, Subh A. Lindley¹, Sharon I. Peacock¹, Nicholas P. J. Day¹, Mark C. England¹, Tim J. Foster¹, Corin L. Moore¹, Laurence Hunt¹, Rebecca Allen¹, Andrew Warren¹, Nicholas Barton¹, Stephen G. Bentley¹, Carol Collingworth¹, Tracy Chillingworth¹, Carol Chew¹, Louise Clark¹, Craig Cotter¹, Alex Coombes¹, Jim Duggan¹, Linda Dowd¹, Theresa Farrell¹, Zhen Han¹, Barbara Harlin¹, Heidi Hauser¹, Simon Hooper¹, Ana Ignatyeva¹, Keith D. James¹, Nicola Kenyon¹, Alan Leslie-Love¹, Rebecca Mayes¹, Sharon Meade¹, Karen Murray¹, Douglas Ormond¹, Michael A. Quail¹, Einar Rødvaldsen¹, Kim Rutherford¹, Mandy Sanders¹, Sarah Sharp¹, Mark Simmonds¹, Kim Stevens¹, Sally Struelens¹, Bart G. van den Berg¹, Brian G. Young¹, and Julian Parkhill^{1,2*}



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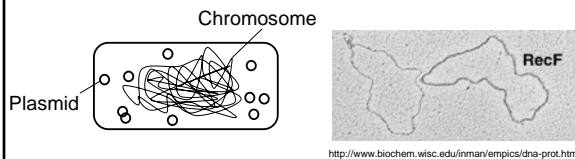
PNAS

Organization of genetic material in bacteria: plasmids



Organization of genetic material in bacteria: plasmids

- Extrachromosomal
- Circular or linear
- 2 kb to hundreds of kb in size
- Non-essential
- May carry 'supplemental' genetic information or may be cryptic
- Employ host functions for most of DNA metabolism



Organization of genetic material in bacteria: plasmids

Examples of naturally-occurring plasmids and relevant features

Plasmid	Host	Plasmid size (kb)	Relevant feature
pT181	<i>Staphylococcus aureus</i>	4.4	Tetracycline resistance
ColE1	<i>Escherichia coli</i>	6.6	Colicin production and immunity
pGKL2	<i>Kluyveromyces fragilis</i>	13.5	Killer plasmid
pAM91	<i>Enterococcus faecalis</i>	26.0	Erythromycin resistance
pSK41	<i>Staphylococcus aureus</i>	46.4	Multidrug resistance
pBM4000	<i>Bacillus megaterium</i>	53.0	rRNA operon
pI258	<i>Staphylococcus aureus</i>	28.0	Metal ion resistance
pSLT	<i>Salmonella enterica</i> subsp. <i>typhimurium</i>	93.9	Virulence determinants
pMT1	<i>Yersinia pestis</i>	101.0	Virulence determinants
pADP-1	<i>Pseudomonas</i> sp.	108.8	Atrazine (herbicide) catabolism
pWW0	<i>Pseudomonas putida</i>	117.0	Aromatic hydrocarbon degradation
pBtoxis	<i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>	137.0	Mosquito larval toxicity
pX01	<i>Bacillus anthracis</i>	181.7	Exotoxin production
pSOL1	<i>Clostridium acetobutylicum</i>	192.0	Solvent production
pSymB	<i>Sinorhizobium meliloti</i>	1683.3	Functions associated with plant symbiosis

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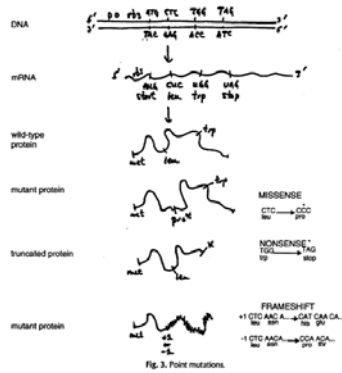
- IV. Genetic variation: Implications for pathogenesis

Sources of genetic variation: point mutations

Mutation phenotypes

- Silent mutation (synonymous), no change in amino acid
 $AGG \rightarrow AGA$, both codons specify Arginine
- Missense mutation (replacement; nonsynonymous), change in amino acid
 - Nonsynonymous missense (or radical replacement)
 UUU (Phe) \rightarrow UCU (Ser); Phe is hydrophobic and Ser is polar
- Nonsense mutation, premature termination of translation
 CAG (Gln) \rightarrow UAG (Stop)
- Frameshift, addition or deletion of base pairs, not in a multiple of three, within the coding region of a gene.

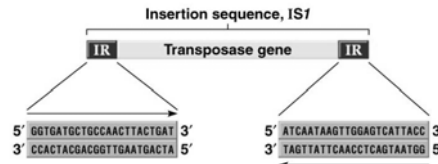
Sources of genetic variation: point mutations



Sources of genetic variation: DNA rearrangements

Insertion sequence (IS) elements:

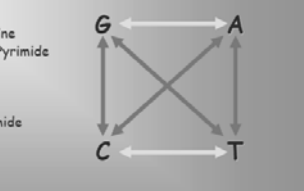
1. Simplest type of transposable element found in bacterial chromosomes and plasmids.
2. Encode only genes for mobilization and insertion.
3. Range in size from 768 bp to 5 kb.
4. IS1 first identified in *E. coli*'s galactose operon is 768 bp long and is present with 4-19 copies in the *E. coli* chromosome.
5. Ends of all known IS elements show **inverted terminal repeats (ITRs)**.



Sources of genetic variation: point mutations

Point Mutations

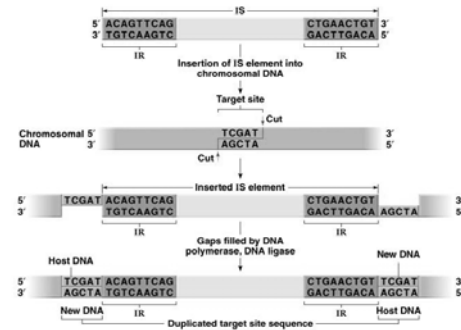
- Transitions
 - Purine \leftrightarrow Purine
 - Pyrimide \leftrightarrow Pyrimide
 - A \leftrightarrow G
 - C \leftrightarrow T
- Transversions
 - Purine \leftrightarrow Pyrimide
 - A \leftrightarrow C
 - A \leftrightarrow T
 - G \leftrightarrow C
 - G \leftrightarrow T



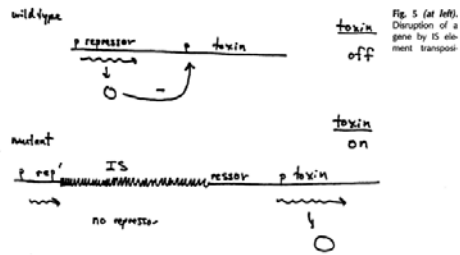
There are four types of transitions.
 There are eight types of transversions

Sources of genetic variation: DNA rearrangements

Integration of IS element in chromosomal DNA.



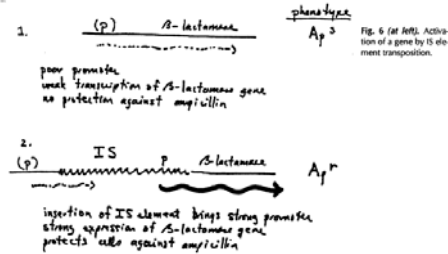
Sources of genetic variation: DNA rearrangements



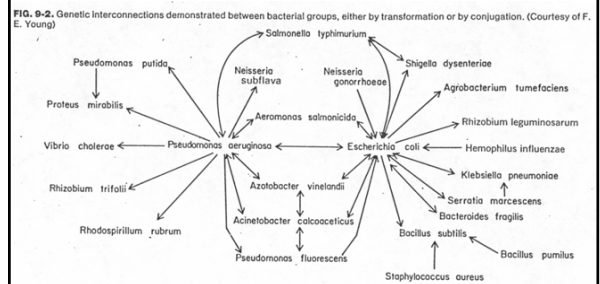
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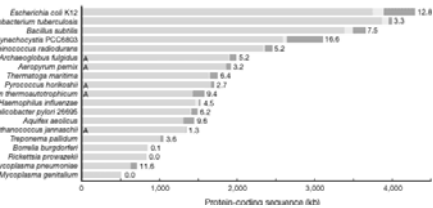
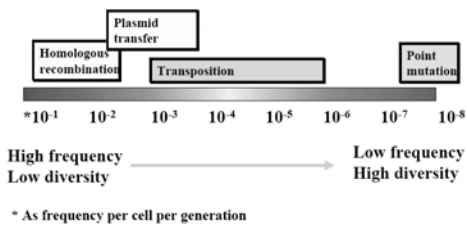
Sources of genetic variation: DNA rearrangements



Transmission of genetic variation



Sources of genetic variation: frequency of occurrence



Lengths of bars denote the amount of protein-coding DNA. For each bar, the native DNA is blue; foreign DNA identifiable as mobile elements, including transposons and bacteriophages, is yellow, and other foreign DNA is red. The percentage of foreign DNA is noted to the right of each bar. 'A' denotes an Archaeal genome.

Transmission of genetic variation: antibiotic resistance

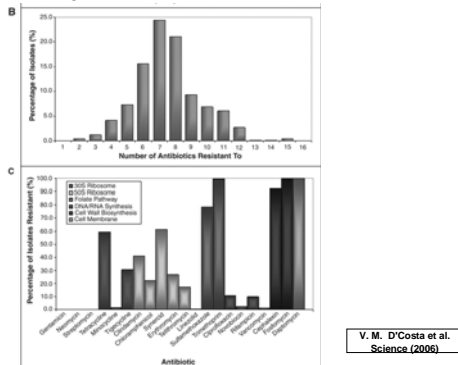


Fig. 1. Antibiotic resistance profiling of 480 soil-derived bacterial isolates

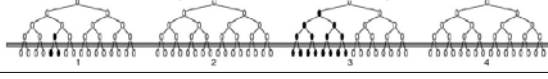
V. M. D'Costa et al. Science (2006)

Transmission of genetic variation: Luria-Delbruck test

1. Resistance by mutation is a physiological response

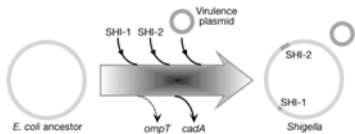


2. Resistance by mutation arises randomly in time



Time of exposure to selective agent

Transmission of genetic variation: pathogenesis



Transmission of genetic variation: Luria-Delbruck test

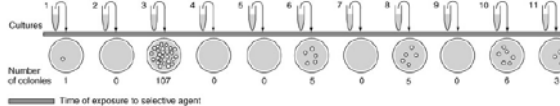
1. Resistance by mutation is a physiological response



2. Resistance by mutation arises randomly in time



(b) Fluctuation test results



Results fit with expectations if random mutation occur at random.

Transmission of genetic variation: Luria-Delbruck test

1. Resistance by mutation is a physiological response



Time of exposure to selective agent

Linear transmission of genetic variation

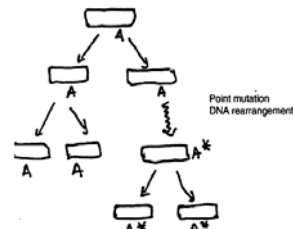
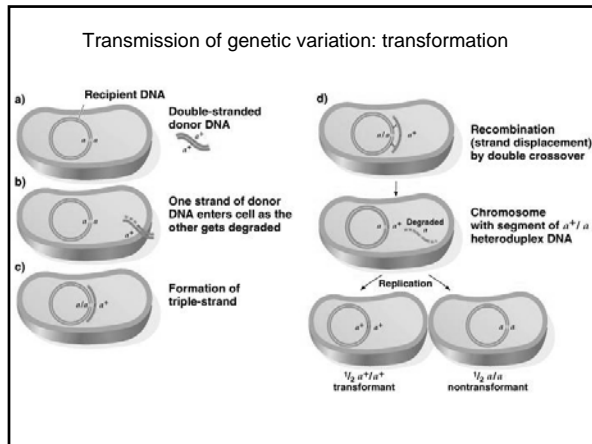
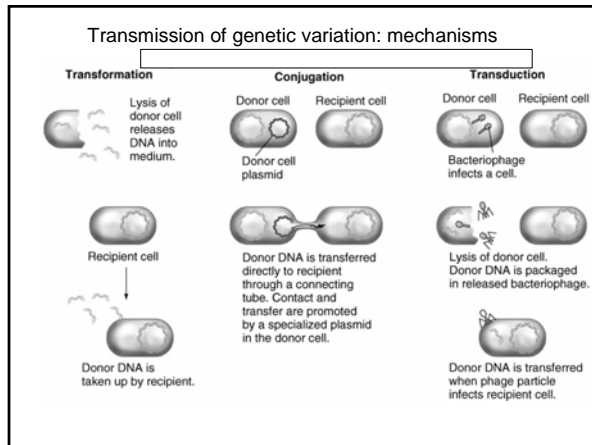


Fig. 1. Clonal variation.



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