

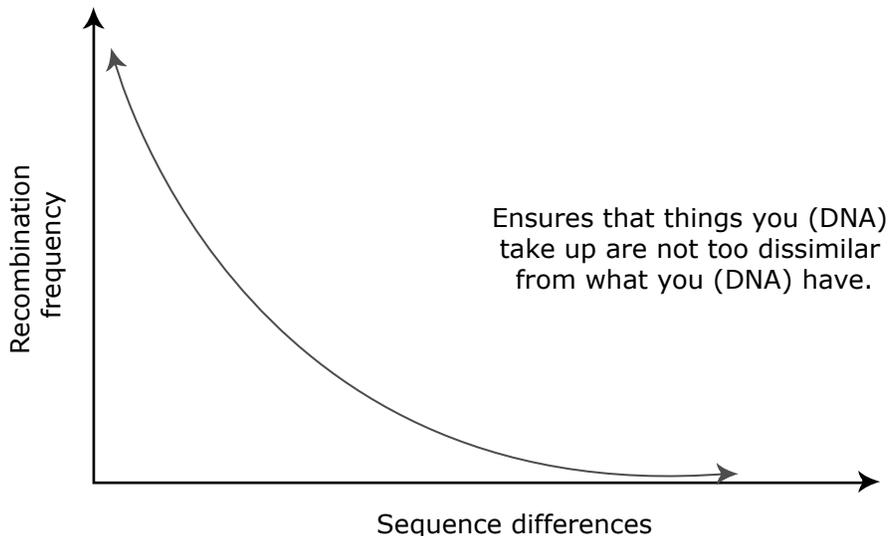
1.89, Environmental Microbiology
Prof. Martin Polz
Lecture 6

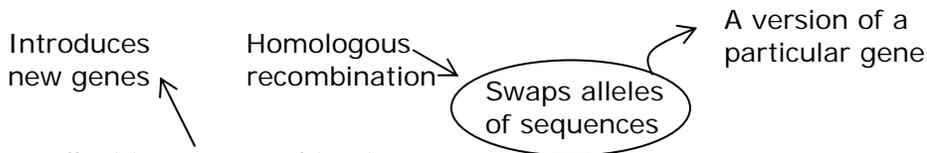
Figure 9.14: Gram[⊖] can detect density of surroundings: sense other bacteria → send out/catch DNA via transformation

- Transformation (cont.)
 - G[⊖]: either always competent or can be induced by physiological state or environmental conditions.
- Transduction
 - Consequence of errors in development of phages
 - Generalized transduction
 - Specialized transduction (lysogenic/temperate phage)
- Conjugation
 - Transfer of plasmids
 - F plasmids (fertility)
 - ↳ tra genes → transfer: sex pilus
 - Hfr (High Frequency of Recombination) plasmids
 - Plasmids can insert into chromosome → can transfer large pieces of host chromosome between cells while being transferred itself.

Fate of Transferred DNA

- Degradation by nucleases (example: restriction nucleases)
- Stabilization by circularization
- Homologous recombination (into chromosome)
 - Rec A (homologous recombination)
 - ↳ Results in patched or spliced DNA

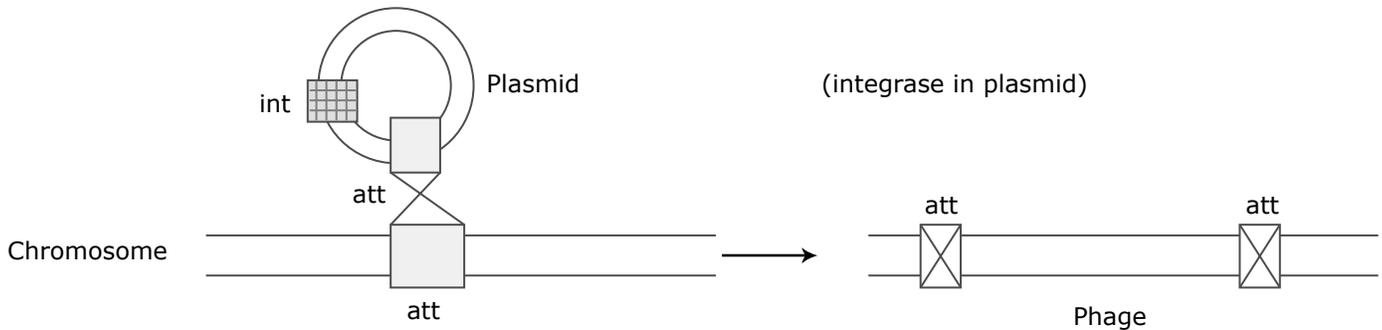




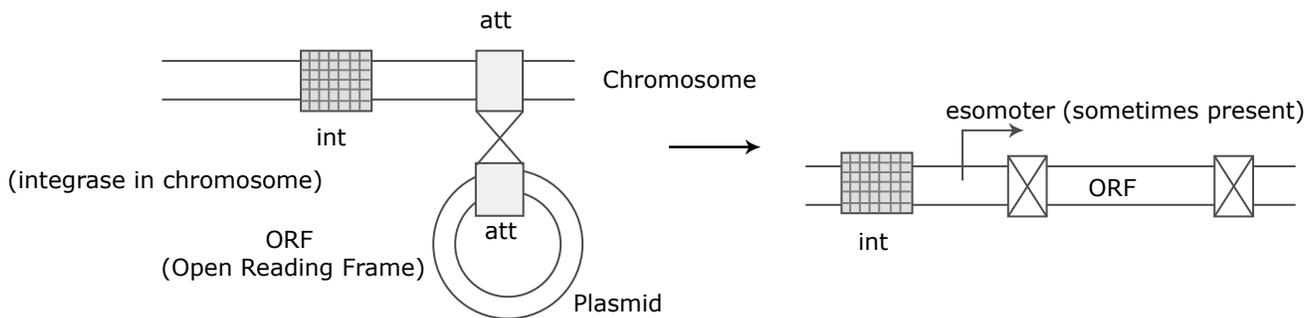
▪ **Illegitimate recombination**

↳ mediated by integrases. Important because can be expressed if promoter available.

a) **Phage:**



b) **Integrans:**



- **Point Mutation Rate:** 1.5×10^{-10} mistakes/bp/generation (mistakes that escape repair mechanism)
- **Gene transfer between phages:** 1 in 10^8 infections will lead to gene transfer
 Note: there are 20 million billion gene transfers per second in the ocean
 10^6 cells/mL sea water

Taxonomy: reliable classification with the goal of identification.

Phylogeny: uses evolutionary relationships to classify.

↓
 DNA sequences serve as evolutionary chronometers: can show relationship

- Genes: must be universally distributed, functionally conserved.

To be used as phylogenetic classifiers,
genes must fit these conditions

Phylogeny: genes must be universally distributed functionally conserved, & have an appropriate rate of change (point mutations)

Example: universal genes:

- 16 S rRNA genes
- RNA polymerases
- RecA
- ATPases

Traced back to one ancestor ↙ Can't have length variation

- 16 S rRNA – prominent role in phylogeny

Genes have three regions:

- a) universally conserved
- b) length is conserved
- c) neither length nor sequence are conserved

Alignment: Regions number 1 & 2

Evolutionary distance = % difference nucleotides

Example:

