



# Biofilm (III)

# Bacterial structure

- ◆ **Three architectural regions:**
  - **appendages** (proteins attached to the cell surface) in the form of flagella and fimbriae
  - **cell envelope** consisting of a capsule, cell wall and plasma membrane
  - **cytoplasmic region** that contains the cell genome (DNA) and ribosomes and various sorts of inclusions.
  - **The surface components of a bacterium are the constituents of its cell envelope and appendages.**

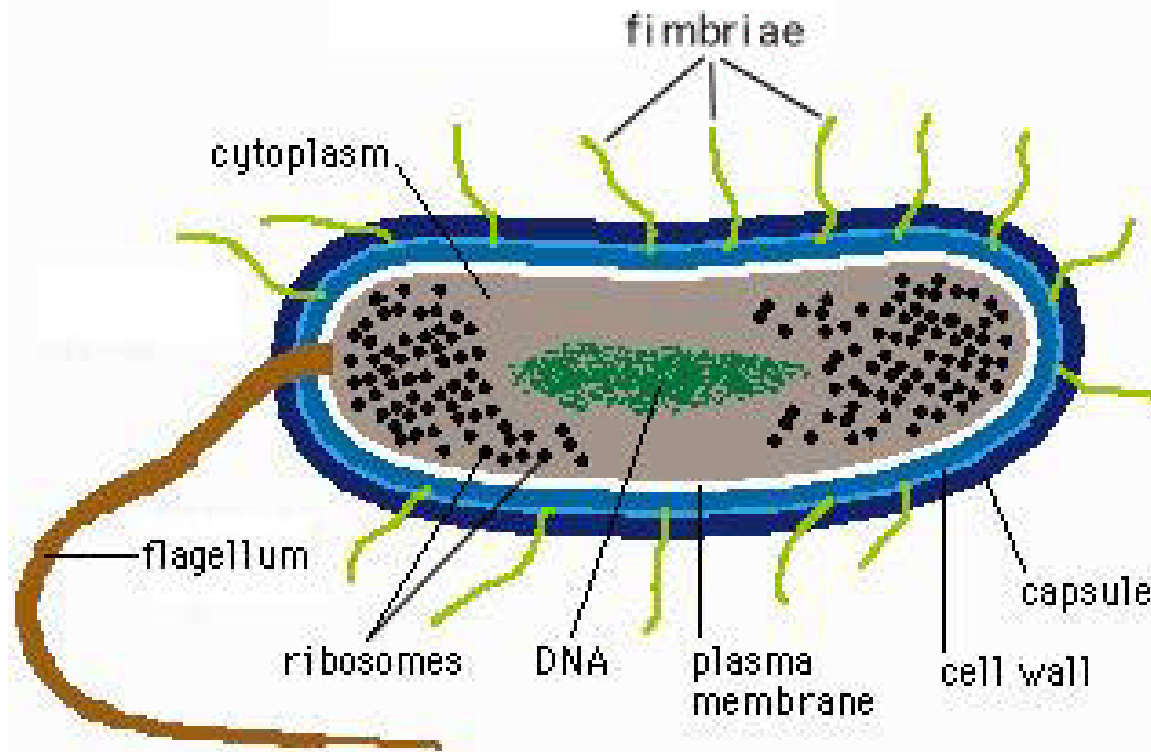
# Appendages

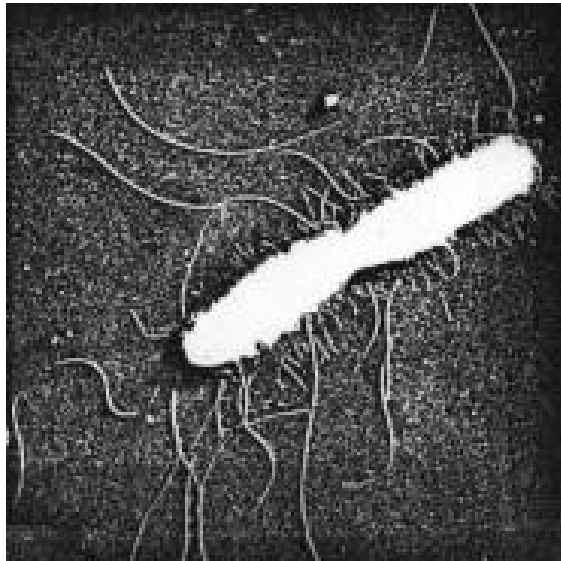
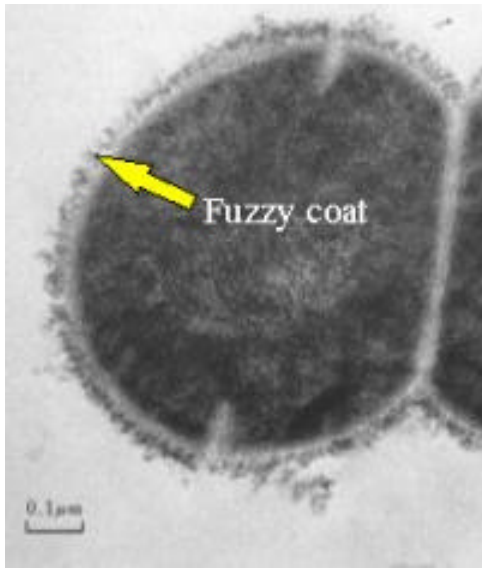
- ◆ **Flagella** are filamentous protein structures attached to the cell surface that provide swimming movement for most motile bacterial cells.
  - The diameter ~ 20 nm, well-below the resolving power of the light microscope.
  - The flagellar filament rotated by a motor apparatus in the plasma membrane allowing the cell to swim in fluid environments.
  - Powered by proton motive force (chemiosmotic potential) established on the bacterial membrane.

# Appendages

- ◆ Fimbriae are thin, hair-like, projections made of protein sub-units. A number of different types have been described (about 7 at the last count, labelled Types I-VII) which can be distinguished by their size (length and diameter) and the type of antigens they carry (G-, Duguid, 1960).
- ◆ **Fimbriae** and **Pili** are interchangeable terms used to designate short, hair-like structures on the surfaces of bacterial cells. Fimbriae are shorter and stiffer than flagella, and slightly smaller in diameter.

# Bacterial Cells





# Coaggregation

- ◆ Concept derived from oral bacteria (streptococci) study
  - 1970's, *Streptococcus mutans* or *S. sanguis* mix with *Actinomyces viscosus*
- ◆ Recognition between surface molecules on two different bacterial cell types so that a mixed-cell aggregate is formed.
- ◆ Bacterial cell clumping and aggregation.

# Clumping, aggregation and coaggregation

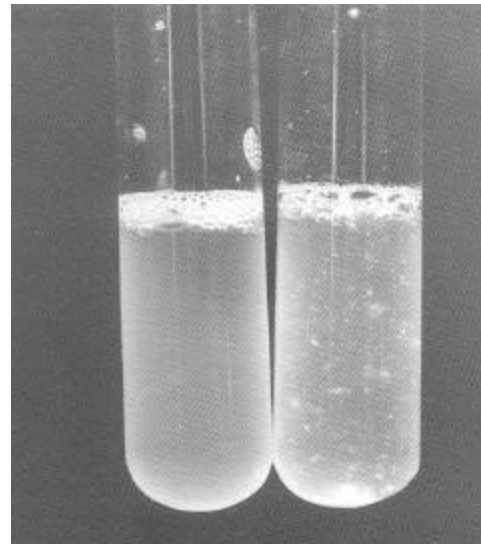


Fig. 2. Phenotype of *L. lactis* cell aggregation. Left: clumping negative (Clu<sup>-</sup>); right, clumping positive (Clu<sup>+</sup>). (65)

# Factors affecting coaggregation

- ◆ Visibly strongest when equal number of partners are present
- ◆ Cell age and culture medium do not seem to be factors
- ◆ Sensitive to heating (85C for 30C) or protease digestion
- ◆ Within pH 5.0-9.0 no distinct pH optimum
- ◆ pH4.5  $\text{Ca}^{++}$  positive effect
- ◆ EDTA and EGTA inhibit many coaggregation

# Mediating surface components

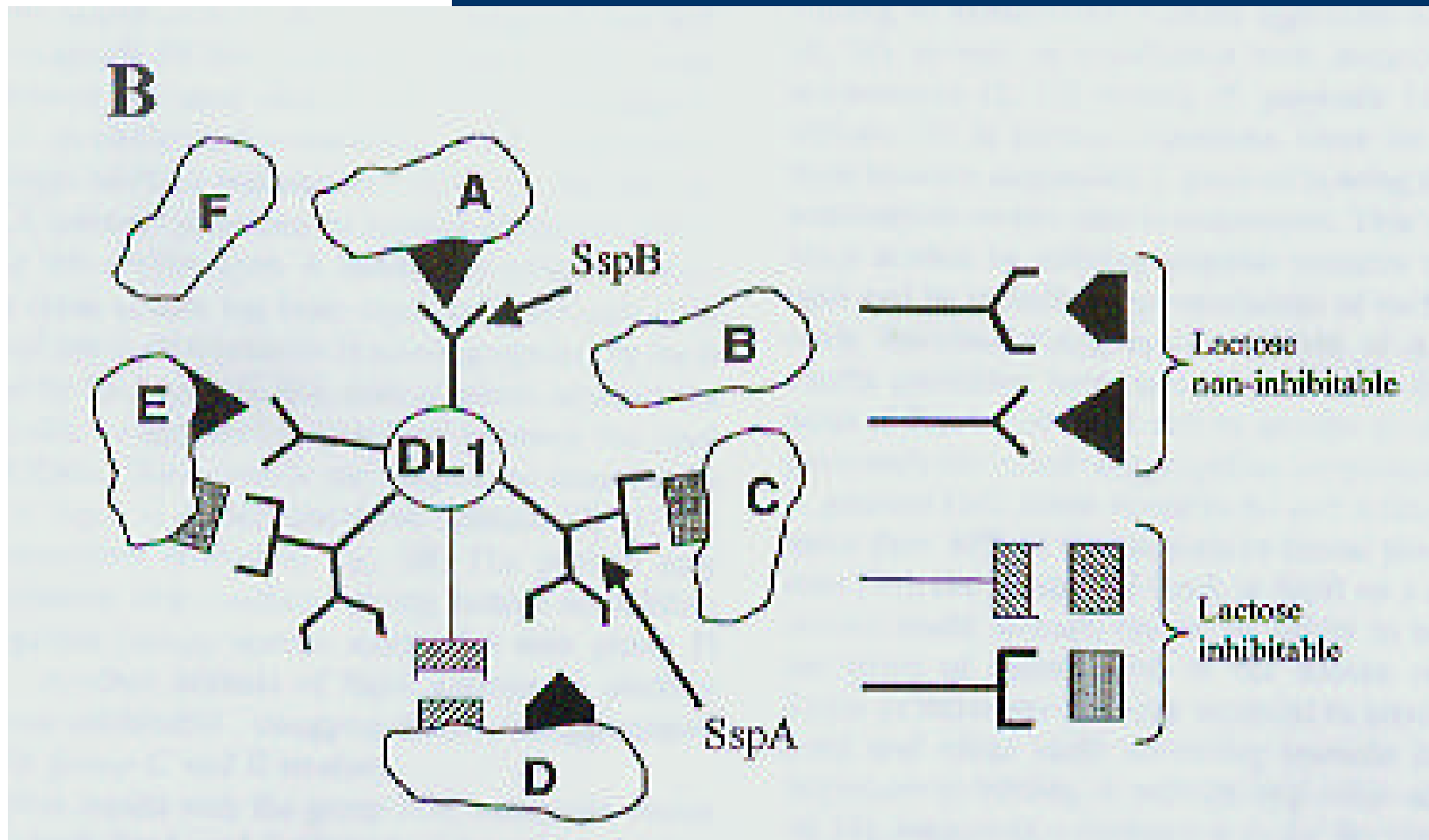
## ◆ Fimbriae

- Fuzzy coats, fuzzy components, fibrillar structures, delicate fibrils, threadlike structures
- Fibrous-appearing surface layer
- Fuzzy coats, fibrils, or fimbriae
- Fimbriae: nonflagellar bacterial appendages other than those clearly involved in the transfer of nucleic acid transfer-pili (Ottow, 1975)

# Mediating surface components

- ◆ Outer membrane
  - Type 1 receptor: loosely bound surface protein that binds lipoteichoic acid
  - Type 1 receptor: protein firmly anchored in the outer membrane
- ◆ Carbohydrate
  - Polysaccharide receptor in *S. sanguis*, bind to the lactose-sensitive lectin on type 2 fimbriae of *A. viscosus*

# Surface adhesin-receptor interaction



# Mixed culture interaction

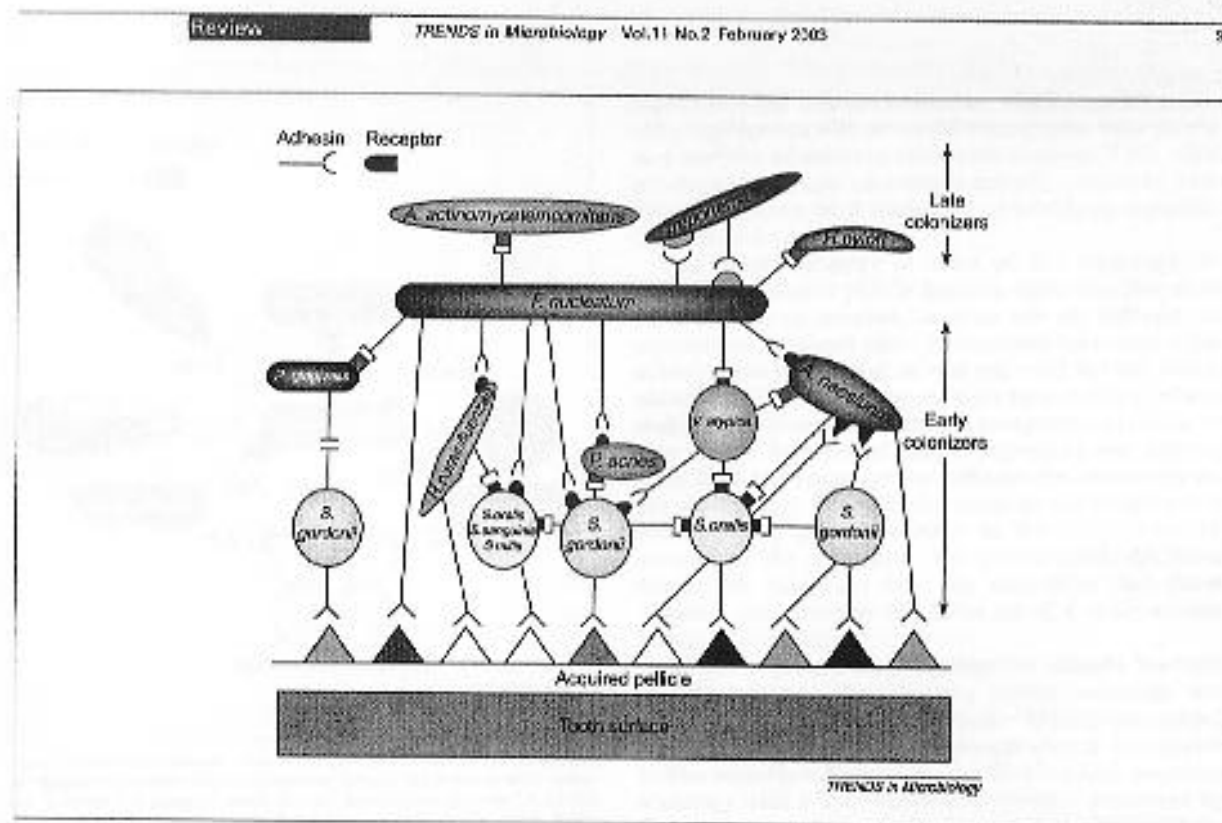
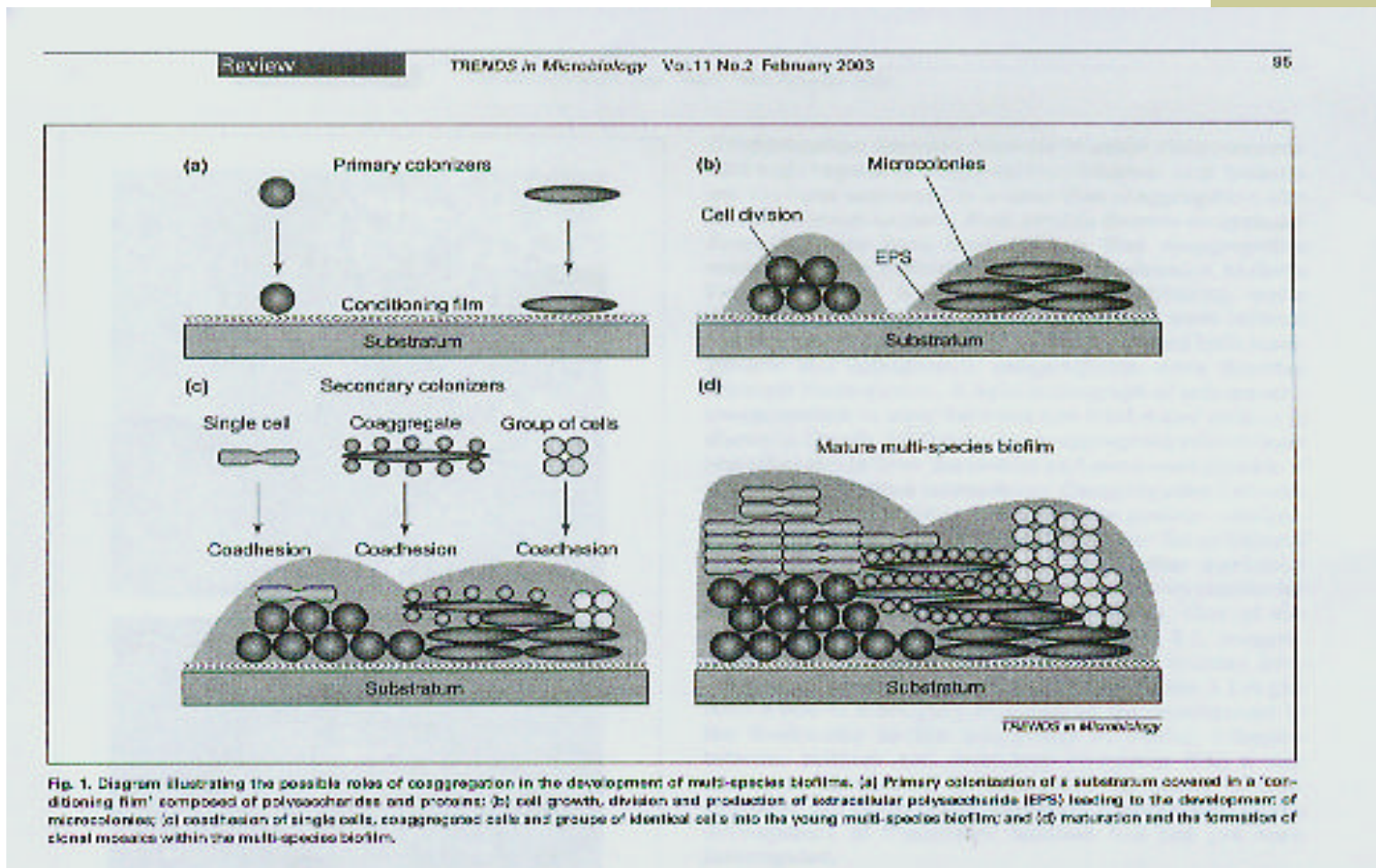


Fig. 3. Diagrammatic representation of the proposed temporal nature of human oral bacterial adhesion on the tooth surface. The species represented here are *Streptococcus gordonii*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus sanguinis*, *Haemophilus parainfluenzae*, *Prevotella bacteroides*, *Veillonella atypica*, *Actinomyces naeslundii*, *Fusobacterium nucleatum*, *Actinobaculum actinomycetemcomitans*, *Helicobacter pylori*, *Tropaeolum* spp. and *Porphyromonas gingivalis*. The complementary sets of adhesin-receptor symbols (an example is shown at the top) represent different specific coaggregations or adhesions to the acquired pellicle. Coaggregation between *P. gingivalis* and *S. gordonii* is mediated by protein adhesins expressed on the surface of both cell types. Identical symbols are not intended to indicate identical molecules, but they are related functionally. The rectangular symbols represent lactose-amine coaggregations, other symbols represent lactose-insensitive coaggregations.

is not known whether coaggregation is those species... (text is partially obscured)

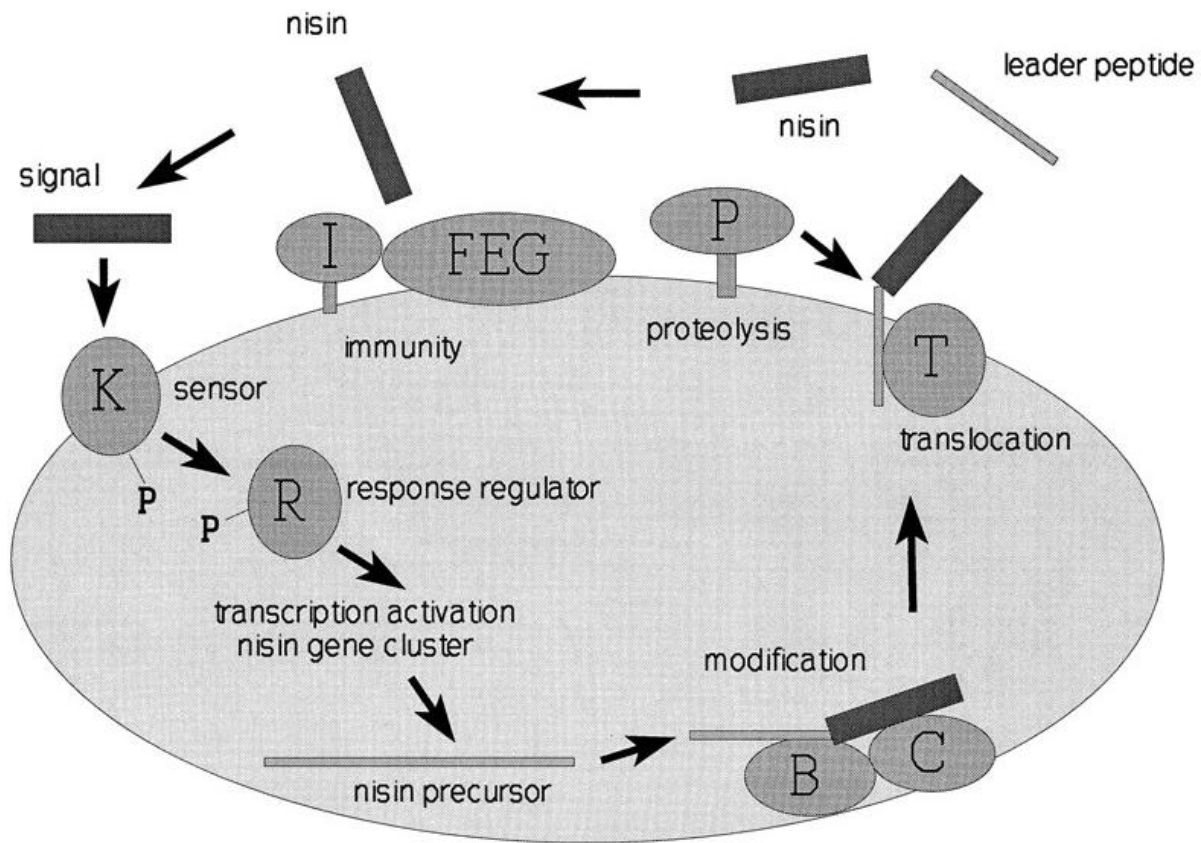
# Ecosystem Assembly





# Cell-cell communication in Gram+ bacteria

- ◆ Peptides
  - Nisin production
  - Natural competence
- ◆ Others?



**Figure 4:** Model for nisin biosynthesis and regulation. In Step 1, NisK senses the presence of nisin in the medium and autophosphorylates. In Step 2, the phosphate group is transferred to NisR, which acts as a transcriptional activator, followed by mRNA synthesis and ribosomal synthesis of unmodified precursor nisin and of biosynthetic proteins. In Step 3, the precursor is modified by the putative enzymes NisB and NisC(7, 9) . In Step 4, the fully modified precursor peptide is translocated across the membrane by the putative ABC transporter NisT(7, 9) . In Step 5, fully modified precursor nisin is extracellularly processed by NisP(8) , resulting in the release of active nisin. NisI(9) , together with NisF, NisE, and NisG(11) , protects the cell from the bacteriocidal action of nisin by a thus far unknown mechanism.