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DNA Uptake by Transformable Bacteria

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Historical introduction

The first dim realization that hereditary material was transferred from male to female animals probably arose among early pastoralists some ten thousand years ago, if not before. However, it was not until 1944 that the chemical substance of heredity, DNA, was directly shown to effect genetic change by demonstration of its role in bacterial transformation (Avery, McCarty & McLeod, 1944). The work of Avery and colleagues indicated that cells of *Streptococcus pneumoniae* could take up naked DNA. In the next decade, conjugative transfer of genetic markers, requiring cellular contact, was observed in bacteria (Lederberg & Tatum, 1946), and the introduction of viral DNA was shown to accompany bacteriophage infection (Hershey & Chase, 1952).

By the time that the double-stranded, helical structure of DNA was proposed in 1953, a number of animal and plant viruses had been purified and analyzed and found to contain either DNA or RNA. It was realized that all viruses contain nucleic acid as their genetic material, and that the nucleic acid must be introduced into the cell to infect it. A natural ability to be transformed genetically by free DNA was discovered in additional bacterial species including *Haemophilus influenzae* and *Bacillus subtilis*. During the 1950's extrachromosomal DNA elements called plasmids were discovered in bacteria, and many plasmids were found to carry the ability to be transferred by conjugation. Thus, mechanisms for DNA transfer appeared to be widespread.

Beginning in the late 1950's, the use of isotopically labeled material showed that DNA was physically introduced into recipient cells during transformation (Fox, 1957; Lerman & Tolmach, 1957). It was shown that transforming DNA is converted

to single-stranded segments during entry (Lacks, 1962) and that these lengthy segments are incorporated into the chromosomal DNA of the recipient cell (Fox & Allen, 1964; Notani & Goodgal, 1966). This molecular processing of transforming DNA and the realization that the development of competence for DNA uptake was a transient property of the cell, itself under elaborate control (Tomasz & Hotchkiss, 1964), that required synthesis of a dozen proteins (Morrison & Baker, 1979) pointed to the complexity of the natural transformation systems. Meanwhile, conjugation was also shown to result in transfer of single-stranded DNA (Cohen *et al.*, 1968), and this process, too, required the function of at least a dozen genes (see review by Wilkins, 1995).

In the 1970's various methods for artificially introducing DNA into cells began to be elaborated. These artificial mechanisms will be discussed here only briefly. Also, the mechanisms of viral transfer and conjugation will not be presented in much detail. The emphasis of this review will be on DNA uptake by the natural mechanisms of bacterial transformation. Research up to the mid-1970's on this topic was previously reviewed (Lacks, 1977b). Several fine recent reviews cover DNA uptake more broadly or from different perspectives (Dreiseikelman, 1994; Dubnau, 1991, 1997; Sabelnikov, 1994; Lorenz & Wackernagel, 1994; Lunsford, 1998; Palmen, Driessen & Hellingwerf, 1994). In the case of transformation, discovery of the mechanisms of competence regulation during the past decade has facilitated the identification of genes involved in DNA uptake. Therefore, most of the components of the uptake systems are now known, although their arrangements and precise functions are not. No case of DNA uptake is yet understood in detail, but it should be instructive at this time to assess the state of our knowledge.

Overview of DNA uptake mechanisms

The various processes of DNA uptake by cells can be categorized as: viral DNA entry, conjugation, or transformation. Within each category, a variety of mechanisms have been found. However, considerable similarities occur among the different mechanisms of conjugation and, especially, transformation. All of these natural mechanisms of DNA transfer are quite elaborate and involve multiple protein components, as the case may be, of the virus, the donor cell, and the recipient cell. The mechanisms of viral infection and conjugation will be discussed mainly with respect to their relevance to transformation.

Infection by viruses

Introduction of DNA in viral infection always involves interaction of viral proteins with receptors on the cell surface. Some viruses have elaborate structures and appendages composed of multiple proteins. For example, *Escherichia coli* T4 phage contains a tail-like appendage implicated in DNA uptake. As illustrated in Figure 1A, tail fibers bind to surface lipopolysaccharide (Cerritelli *et al.*, 1996), after which the tail core penetrates the outer membrane, fusing it with the inner cell membrane of the Gram-negative bacterium, to allow passage of phage DNA into the cell (Tarahovsky *et al.*, 1991). The phage protein gp2 may serve as a "pilot" that attaches to an end of incoming DNA to protect it from cellular exonucleases (Lipinska *et al.*, 1989) and perhaps to assist its entry. Such pilot proteins have been proposed in various DNA uptake systems but with little direct evidence, possibly because a single protein molecule per viral genome is difficult to detect.

A simpler virus, such as the filamentous phage fd, contains only a few coat

proteins. This virus infects "male" cells of *E. coli*, that is cells which contain the sex-factor plasmid F and which, therefore, extrude fibrils, called pili, from their surface. A minor coat protein, gp3, located at one end of the filamentous virus, binds to a pilus (Gray, Brown & Marvin, 1981), and the virus is drawn to the cell surface as the pilus retracts. Oligomers of this same gp3 protein then form a transmembrane channel (Glaser-Wuttke, Keppner & Rasched, 1989) through which the single-stranded fd DNA enters the cell. In addition to the pilin proteins forming the pilus, entry may require other host proteins such as TolA, mutants of which cannot be infected by fd. (Sun & Webster, 1986). TolA is a membrane protein, and it may contribute to the entry channel (Levengood & Webster, 1989).

Viral transfer mechanisms can introduce either single- or double-stranded DNA. The other natural mechanisms of DNA transfer, however, introduce only single-stranded DNA. This may reflect their function, which is to transfer genetic information from one cell to another, unlike the virus which acts as an independent entity and takes over the cell machinery.

Conjugation — cell to cell transfer

The key feature of conjugative DNA transfer is its requirement for close contact between cells, so that the DNA passes directly from donor cell to recipient without external exposure. Close contact is achieved by the action of donor cell pili, which first bind to the recipient cell surface. Upon retraction of the pili, the two cells are juxtaposed, and a channel through which single-stranded DNA can pass is formed (reviewed in Wilkins, 1995).

Conjugative transfer systems are often present on plasmids in both Gram-positive and Gram-negative bacteria. They allow transmission of the plasmid to other

cells independent of gene transfer mechanisms in the host. Typically, up to two dozen *tra* genes in the plasmid may encode components of the transfer system (Wilkins, 1995). In addition to the pilins and proteins that process and export them, these genes encode proteins that make up the transmembrane channel, and proteins that act on the plasmid DNA prior to its transfer, and even, by accompanying the DNA, after its transfer to the recipient cell (Rees & Wilkins, 1991).

Once the cells are in contact, a bridgelike channel must be formed between them for passage of the DNA. Many of the *tra* genes presumably encode proteins for this structure. Recipient proteins, such as OmpA, may play roles in cell contact and channel formation (Manoil & Rosenbusch, 1982; Sugawara & Nikaido, 1992). Several *tra* gene products process the donor DNA. In the case of F-factor, the protein TraI, a DNA-dependent ATPase with helicase activity, makes a single-strand break at the *oriT* site on the plasmid, binds covalently to the newly formed 5'-end, and unwinds the strand (Matson, Nelson & Morton, 1993). It is not clear whether TraI leads the donor strand into the recipient cell, as depicted in Fig. 1B, or whether it binds to the intercellular pore so that donor DNA loops into the cell (Wilkins, 1995). A single-stranded DNA binding protein is encoded by the F-factor; it may bind to the complementary strand, which is used as a template to resynthesize in the donor cell the strand corresponding to the one transferred.

Related to conjugative transfer is the interkingdom transmission of bacterial plasmid DNA from *Agrobacterium tumefaciens* to plant cells to form crown gall tumors (for reviews, see Kado, 1991; Citovsky & Zambryski, 1993). In this case, the Ti plasmid, which is also capable of conjugative transfer between bacteria, carries a

set of approximately two dozen *vir* genes that when activated, remove a single-strand segment of plasmid DNA, called T-DNA and transfer it through a conjugative bridge structure through the membrane of a plant cell, where it finds its way into the nucleus and becomes incorporated into the plant genome. The *virD1* and *virD2* products form an endonuclease that cuts at the T-DNA borders to release the strand segment. The VirD2 protein is bound to the 5-end of T-DNA, probably covalently, where it may act as a pilot protein to shepherd the strand into the host cell nucleus, protecting it from exonucleolytic digestion, and/or conserving the original bond energy for ligation to plant DNA (Dürrenberger *et al.*, 1989). Some of the *vir* genes are homologous to *tra* genes, for example *virB2* and *traA*, the pilin-encoding gene of the F-factor (Shirasu & Kado, 1993). Another gene, *virB11*, shares sequence similarity with *comGA*, which is required for transformation (Albano, Breitling & Dubnau, 1989).

Genetic transformation by free DNA

Natural bacterial transformation

Genetic transformation by purified DNA has now been demonstrated in over 40 species of bacteria (Lorenz & Wackernagel, 1994), but it is by no means a universal capability. As in conjugation, many specific proteins are required for transformation. However, since donor DNA is not accompanied by proteins, probably even under natural conditions, the proteins required for DNA uptake are produced in the recipient cell, rather than in the donor cell, as is the case for conjugation. It is not known whether under natural circumstances donor DNA is extruded from or leaks out of the cell or is released on lysis of cells, but extracellular

DNA can be detected in cultures (reviewed by Lorenz & Wackernagel, 1994).

The process of natural transformation allows large amounts of DNA--as much as 10% of their DNA content--to be taken up by cells (for a review, see Lacks, 1988). Chromosomal DNA markers routinely transform more than 1% of the recipient population; homogeneous, plasmid DNA containing a chromosomal marker can transform more than half of the cells. In most species all of the cells become competent to take up DNA; in *B. subtilis*, however, only ~10% of the population becomes competent. The DNA that is taken up by the recipient cell can be integrated with very high efficiency, with estimates ranging between 0.5 and 1.0.

Artificial transformation--electroporation

In contrast to natural transformation, artificial methods introduce relatively small amounts of DNA into cells. Two types of methods have been used. A cell-DNA mixture is subjected to abrupt shifts in divalent cation concentration and temperature in one method (Mandel & Higa, 1970) and to high-voltage electrical pulses in the other (Harlander, 1987). The former was more important historically, but the latter method, called electroporation, has become the method of choice because of its simplicity and general applicability. Although the precise mechanisms by which these agents act are not known; it is presumed that they form transient pores in the cell membrane(s), through which DNA can pass (for reviews see Chang *et al.*, 1992; Sabelnikov, 1994).

Despite the small quantities of DNA introduced by artificial transformation, it has proven extremely useful in working with the many species that are not naturally transformable. The DNA is taken up in the form presented to the cells without degradative processing, which is advantageous for establishing a plasmid. This

compensates, in part, for the relatively poor uptake.

Molecular fate of DNA in transformation

Initial attachment of double-stranded DNA

In all known systems of natural transformation, DNA must be double-stranded, which is its native state, to be efficiently taken up. Although, denatured (Miao & Guild, 1970) or single-stranded (Barany & Boeke, 1983) DNA can enter cells, its ability to do so is less than 1% of double-stranded DNA. Kinetic studies, in which the concentration of donor DNA is varied, suggest the existence on the surface of Gram-positive bacteria of ~50 sites that can reversibly bind dsDNA. Very quickly, however, DNA becomes irreversibly bound, so that it can no longer be washed away, although its sensitivity to external agents, like DNase, shows it to be still outside the cell. With *S. pneumoniae*, donor DNA at this stage can be examined in mutants lacking the EndA nuclease required for entry (Lacks, Greenberg & Neuberger, 1974) or in wild-type cells treated with chelating agents (Seto & Tomasz, 1974), which block the nuclease action. With *B. subtilis*, the entry process is slower, and the external state of DNA can be investigated without inhibiting its entry. These Gram-positive species and others are able to take up DNA indiscriminantly with regard to its nucleotide sequence.

At least some Gram-negative species, typified by *H. influenzae*, require for binding a 9- to 11-nt sequence found specifically in their own DNA (Danner *et al.*, 1980). Cells of *Neisseria gonorrhoeae* also require a specific sequence, but one that is different from *H. influenzae* (Goodman & Scocca, 1988). In addition to the sequence requirement, DNA bound by these species becomes resistant to

extracellular agents. In the case of *H. influenzae* it has been shown that such bound DNA is protected by cell membranes in a vesicle (Kahn, Maul & Goodgal, 1982) called a transformasome. Within the transformasome, donor DNA remains double-stranded, but as in the case of Gram-positive cells, it is converted to single strands on entry into the cell proper (Barany, Kahn & Smith, 1983). According to one model (Sabelnikov, 1994), DNA binds to receptors on the outer membrane that recognize the specific sequence. This triggers curvature of the membrane, which envelopes the DNA to form a vesicle within the outer membrane. The vesicle, or transformasome, then contacts the inner membrane, fusing with it at the location of a competence-induced structure for DNA entry.

DNA degradation and entry of single strands

External strand breaks

It is likely that DNA binds initially to a cellular receptor in a reversible manner. However, in the transformation of *S. pneumoniae* and *B. subtilis*, a stage of irreversible binding in which the DNA is still external can be identified. Such binding is an active process with its own ionic and energy requirements. In *S. pneumoniae* it has been possible to isolate this stage in mutants lacking the membrane nuclease, EndA (Lacks *et al.*, 1974) and to show that concomitant with this binding is the appearance of single-strand breaks (nicks) in the DNA. These breaks apparently occur randomly along the DNA, every 2.5 kb on average, to give single-strand segments of 5 kb (weight average; Lacks & Greenberg, 1976); they may result from enzymatic action at entry sites. Proteins with strand nicking activity have been isolated from the cell surface of competent streptococci (Fujii *et al.*, 1987;

Lunsford, Nguyen & London, 1996), but they have not been well characterized. That the breaks are required for binding is indicated by the occurrence of at least one break on every molecule bound, as demonstrated for a covalently closed circular DNA donor (Lacks, 1979b). The reduction by half of DNA strand length upon uptake by cells (Morrison & Guild, 1972) also indicates that a strand break is required for DNA uptake.

In leaky mutants of *endA* that produce some nuclease, the nicks become double-strand breaks (Lacks & Greenberg, 1976); therefore, it can be presumed that in wild-type cells, the single-strand breaks are quickly converted to double-strand breaks, as the opposite strand is degraded and the initially nicked strand begins to enter the cell. In *B. subtilis*, donor DNA can be detected on the surface of wild-type cells, irreversibly bound, and nicked to give single-strand fragments of ~5kb (weight average; Dubnau & Cirigliano, 1972). Although the molecular processing of DNA during binding and entry has been investigated more fully in *S. pneumoniae*, these stages of uptake are considered to be similar in *B. subtilis* (Dubnau, 1991).

Binding is not sequence-specific in these Gram-positive species, but it is specific for unencumbered double-stranded DNA. Neither single-stranded DNA, RNA-DNA hybrids, nor glycosylated phage T4 DNA show appreciable binding or ability to compete with native DNA (Lacks, 1977a). Since the single-strand breaks render the binding irreversible, it is possible that a covalent link is formed with a surface protein during breakage. This protein might serve as a pilot, leading the DNA strand into the cell, or it might have another function, perhaps as the putative helicase proposed to assist DNA entry in *B. subtilis* (Londono-Vallejo & Dubnau,

1993). The TraI protein of the F-factor is reported to nick the transferred DNA, bind to it, and act as a helicase (Matson *et al.*, 1993). In the conjugative plasmid RP4, its TraI protein also accompanies single-stranded DNA into the recipient cell (Rees & Wilkins, 1990).

Single strand entry

Only single strands of donor DNA enter into *S. pneumoniae* cells (Lacks, Greenberg & Carlson, 1967). Similarly, newly entered DNA in *B. subtilis* is detectable as single strands (Piechowska & Fox, 1971). An amount of DNA approximately equal to the amount taken up is released in an acid-soluble form outside the cells (Lacks & Greenberg, 1973; Morrison & Guild, 1973). The released product consists of oligonucleotides of size distribution identical to that produced by the action of the EndA membrane nuclease of *S. pneumoniae* (Lacks *et al.*, 1974). It appears that one strand of DNA enters the cell as the complementary strand is degraded. Selective end-labeling of donor DNA showed that the 3'-end of the strand must enter first, whereas the opposite strand is degraded from the 5'-end (Mejean & Claverys, 1993). A reasonable view of events during entry is that a DNA strand with its 3'-end formed by the nick made on binding, enters the cell at the same time that the EndA nuclease makes an endonucleolytic break on the opposite strand and continues to degrade that strand from 5' to 3' as its complement enters 3' to 5'. A rate of 100 nt per sec was calculated for DNA entry in *S. pneumoniae* (Mejean & Claverys, 1993).

Null mutants of EndA are reduced in transformability to <0.1% of the normal level (Puyet, Greenberg & Lacks, 1990), and they are correspondingly reduced in

DNA uptake (Lacks, Greenberg & Neuberger, 1975). This accords with their role in DNA entry. The residual transformation, which is low but real, and the low level of transformation demonstrable with single-stranded DNA (Barany & Boeke, 1983) may result from an alternative mechanism for entry in the absence of EndA activity. A possible candidate for catalyzing such entry is the putative helicase encoded by *comFA* in *B. subtilis* (Londono-Vallejo & Dubnau, 1993) and its homologue, *cflA*, in *S. pneumoniae* (Table 1). An interesting set of mutants found in *S. pneumoniae* do not take up DNA into the cell but still bind DNA and degrade the same amount as wild-type cells (Morrison *et al.*, 1983). They are presumably normal for EndA but lack another factor necessary for entry, which might be the helicase, a pilot protein, or a protein forming the entry pore.

In Gram-negative species, DNA entry into the cell proper from the transformosome may occur by a mechanism similar to the Gram-positive species. DNA apparently enters the cell as a single strand, with its 3'-end entering first (Barany *et al.* 1983).

Ionic and energy requirements

Irreversible, external binding of DNA to *S. pneumoniae* cells requires an energy source (Lacks *et al.*, 1974) and potassium ions (Lacks, 1979a). The energy is required, possibly, for covalent linking of the DNA to a surface protein at the nick site. No divalent cations are necessary for binding. Potassium ions are necessary, perhaps for orienting the binding/entry complex in the membrane by maintaining the electrostatic potential across it.

When cells were preloaded with bound DNA in the presence of a chelating

agent, uptake into the cells was observed upon its removal, and that uptake was partially inhibited by a sugar analogue (Seto & Tomasz, 1974). So it appears that energy is needed for entry, too, perhaps to power a helicase that unwinds the entering DNA or a translocase that draws it into the cell. Calcium and magnesium ions are both required for entry (Seto & Tomasz, 1976; Lacks, 1977a). The role of calcium ions is unknown, but magnesium ions are required for the membrane nuclease activity (Lacks *et al.*, 1974).

The contribution to DNA uptake of the protonmotive force at the membrane, both with respect to electrostatic potential and pH gradient across the membrane, has been examined in both *S. pneumoniae* and *B. subtilis*. The data were reviewed recently (Palmen *et al.*, 1994), but no firm conclusions were drawn with respect to a requirement or function in uptake. However, some data with *S. pneumoniae* suggest that uptake depends on the ATP level in the cells (Clavé & Trombe, 1989). Possible roles for ATP are to activate a protein that is linked covalently to donor DNA during binding or to power helicase or translocase activity during entry.

Consequences of the entry mechanism

Nonhomologous DNA

DNA that enters into *S. pneumoniae* is coated with a single-stranded DNA binding protein that is induced during competence (Morrison, 1978). Nonhomologous DNA that is taken up persists in the cell with a half-life of ~30min at 30 C (Lacks *et al.*, 1967). It is apparently degraded slowly by exonucleases, and its breakdown products are reused for DNA synthesis.

Homologous recombination

DNA that is homologous to the recipient genome has a much shorter half-life as single strands, ~6 min at 30 C. This corresponds to the time required for integration of donor DNA into the chromosome (Ghei & Lacks, 1967). The single-stranded form of the donor DNA facilitates its interaction with the duplex DNA of the chromosome, and recombination occurs with an efficiency of at least 50% (Fox, 1957; Lerman & Tolmach, 1957).

Plasmid establishment

Because strand breaks occur on DNA binding and one strand is degraded during entry, the most plasmid material that can be introduced in a single entry event is a linearized single strand. Inasmuch as such a strand cannot circularize to form a replicon, establishment of a plasmid requires the interaction of complementary strand segments introduced in two separate events (Saunders & Guild, 1981)). However, if a plasmid carries a DNA segment homologous to the chromosome, pairing can occur in this segment between plasmid and chromosome to enable a single plasmid strand to establish the plasmid by a process called chromosomal facilitation (Lopez *et al.*, 1982).

Restriction of donor DNA

Restriction endonucleases generally do not act on either single-stranded or hemimethylated DNA. Therefore, chromosomal transformation by unmodified DNA is not affected by restriction enzymes in the host (Trautner *et al.*, 1974; Lacks & Springhorn, 1984). However, plasmid transfer requires interaction of two donor strands and is susceptible to restriction. In the case of *S. pneumoniae*, its DpnII restriction system circumvents the plasmid susceptibility by expressing an accessory methyltransferase, DpnA, that can methylate single-stranded DNA, so that plasmid

DNA is already methylated at potential restriction sites by the time that it becomes a double-stranded replicon (Cerritelli, Springhorn & Lacks, 1989).

Regulation of competence for DNA uptake

Streptococcal species

Competence-stimulating polypeptides

Early investigators of streptococcal transformation realized that the bacteria were not always transformable. They became competent for transformation only when grown in particular media and then only at a certain stage in the growth cycle, namely late logarithmic growth. Under these conditions an extracellular factor that stimulated competence in noncompetent cultures was isolated from cultures of *S. gordonii* (Pakula & Walczak, 1963) and *S. pneumoniae* (Tomasz & Hotchkiss, 1964). The factor from *S. pneumoniae* appeared to be a small protein (Tomasz & Mosser, 1966). This competence stimulating polypeptide (CSP) was recently shown to be a 17-mer polypeptide, EMRLSKFFRDFILQRKK (Háverstein, Coomaraswamy & Morrison, 1995). Other strains of *S. pneumoniae* and related streptococcal species have CSPs varying slightly in size and composition (Morrison, 1997).

Quorum-sensing mechanism

It was realized that a factor accumulating extracellularly could act as a signal of adequate bacterial culture density to render it likely that DNA leaking out of one cell would reach another cell of the species (Tomasz, 1965). The molecular mechanism of such quorum sensing is now understood (reviewed in Morrison, 1997). The precursor of CSP is encoded by *comC*, a small gene in an operon containing also *comD* and *comE*. (An operon is a cluster of genes transcribed on the same

messenger RNA.) Another operon contains *comA* and *comB*, the membrane-located products of which act to process the *comC* protein and export CSP out of the cell. When CSP accumulates, it signals ComD, which is a membrane-located histidine protein kinase, to phosphorylate ComE. The phosphorylated ComE activates transcription, possibly after another stage in the cascade, of competence-specific proteins.

Induction of competence genes

At least a dozen proteins are preferentially synthesized during the development of competence. Several operons encoding these proteins were found to have the "combox" sequence, TACGAATA (Campbell, Choi & Masure, 1998; Pestova & Morrison, 1998), in place of the typical pneumococcal SigA promoter (TTGACAN₁₂TNTGNTATAAT; Sabelnikov, Greenberg & Lacks, 1995). Thus, induction of these late competence genes may depend on a competence-specific sigma factor ultimately elicited by CSP. In a *trt* mutant strain of *S. pneumoniae*, which is transformable in the presence of trypsin and does not require CSP for competence (Lacks & Greenberg, 1973), combox genes are constitutively expressed (Lacks & Greenberg, unpublished data), perhaps because the putative sigma factor is no longer regulated.

Bacillus species

Competence-stimulating polypeptides

Cells of *B. subtilis* also become competent late in the culture cycle. In this species, two different polypeptides are released by the cell (reviewed by Solomon & Grossman, 1996). The ComX pheromone is a polypeptide of 9 or 10 aa, apparently

containing a modified tryptophan residue, that is processed from a 55-aa precursor. Similarly to CSP of *S. pneumoniae*, it acts on a histidine protein kinase (ComP) in the cell membrane, which in turn phosphorylates a transcription factor, ComA. Another competence-stimulating factor, which appears to be a small peptide, may act by blocking a phosphatase that restores ComA to an unphosphorylated and inactive state.

Regulation of gene expression

Phosphorylated ComA increases transcription of *srfA* (*comS*), which leads eventually to the accumulation of ComK (van Sinderen *et al.*, 1995). ComK acts to induce the late competence genes, not as a sigma factor, but as a transcription activator. Operons that are induced have a consensus SigA promoter, but they also have a characteristic pattern of A- and T-rich sequences upstream of the promoter, which apparently allow binding and activation by ComK (Hamoen *et al.*, 1998).

Gram-negative species

Regulated competence in H. influenzae

Competence appears in cells of *H. influenzae* when a culture is nutritionally depleted but can still carry on protein synthesis (Goodgal & Herriott, 1961). It appears to be mediated by the accumulation of cyclic AMP in the cell, which triggers the expression of a gene called *sxy* (Dorocicz, Williams & Redfield, 1993) or *tfoX* (Zulty & Barcak, 1995), the product of which, in turn, induces late competence genes (Karudapuram & Barcak, 1997). Null mutations in *sxy/tfoX* prevent competence, but certain missense mutants are constitutively competent, but at a lower level than normally attained (Redfield, 1991; Karudapuram & Barcak, 1997). The *sxy/tfoX*

product acts as a transcription activator for late competence genes, which generally have a 26-nt dyad symmetry element upstream from a SigA-like promoter (Karudapuram & Barcak, 1997). In the latter respect the induction system is more similar to *B. subtilis* than to *S. pneumoniae*.

Perpetual competence

A number of bacterial species, including the Gram-negative species *Neisseria gonorrhoeae*, *Acinetobacter calcoaceticus*, *Pseudomonas stutzeri*, the cyanobacterium *Synechococcus*, and the Gram-positive *Deionococcus radiodurans*, are competent throughout the culture cycle (see review by Lorenz & Wackernagel, 1994). This constitutive ability to take up DNA is mimicked by the *trt* mutant of *S. pneumoniae* (Lacks & Greenberg, 1973) and by some *sxy* mutants of *H. influenzae* (Redfield, 1991), which no longer regulate the late functions of competence.

Competence-inducible genes

Genes relating to competence have generally been classified as having early or late functions. Genes required for the *development* of competence, such as those involved in quorum sensing and signalling are the early genes. In *S. pneumoniae*, this class includes *comA,B,C,D*, and *E*. There may be additional genes mediating between these early genes and late genes. Late genes appear to constitute a regulon, that is, a set of coordinately induced operons. The late gene functions are needed both for DNA uptake and for allowing the introduced donor strands to persist in the cell and recombine with host DNA. The three best studied inducible systems, those of *S. pneumoniae*, *B. subtilis*, and *H. influenzae*, differ markedly in their early genes and their regulatory systems. However, their late genes show many similarities. The

fundamental mechanisms of uptake, therefore, may be quite alike.

Genes unique to the uptake mechanism

Inasmuch as the earliest and most complete characterization of late genes has been in *B. subtilis* (reviewed in Dubnau, 1997), the nomenclature originally used for them (*i.e.* *comGA*, *comGB*, etc.) will be taken to describe the general type. Their homologues in other species will derive their name from the *B. subtilis* gene, for example, comG-like: *cglA*, *cglB*, etc. Some exceptions based on the historical record, such as *cilC* for a *comC* homologue in *S. pneumoniae* (Campbell *et al.*, 1998), will be made. Since this review is centered on *S. pneumoniae*, reference will frequently be made to *cgl*, *cel* and *cfl* genes of this species.

The cgl family and cilC

The *comG* operon of *B. subtilis* contains seven genes, which encode proteins related to type IV pilins of Gram-negative bacteria (Albano *et al.*, 1989). Similar operons are found in other transformable species, and defects in any of the genes prevent binding and entry of DNA. The *cgl* operon of *S. pneumoniae* (Pestova & Morrison, 1998; see TIGR database for full sequence) also contains seven genes, which are homologous to those of *B. subtilis* (partly shown in Fig. 2). The *comG* proteins have been characterized with respect to their primary sequences, processing, and membrane location (Chung, Breidt & Dubnau, 1998). Based on those findings, the *cglA* and *cglB* products are larger proteins, 313 and 347 residues in length, respectively, an energy-transducing protein and a membrane-spanning protein responsible for transporting through the cell membrane the products of the five downstream *cgl* genes, which are all smaller polypeptides with hydrophobic segments

at their N-termini. In *B. subtilis*, ComGC, ComGD and ComGE contain the residues KGFT preceding the hydrophobic segment; in *S. pneumoniae*, a similar sequence, KAFT, precedes the segment in CglC, CglD and CglF (Fig.2). These N-terminal sequences are characteristic of prepilin-like proteins, typified by the type IV pilus protein of *Pseudomonas aeruginosa* (Sastry *et al.*, 1986). The earliest evidence connecting pilins to transformation was from *N. gonorrhoeae*, where strains unable to make pili were defective in transformation (Biswas *et al.*, 1977).

The *B. subtilis* *comC* gene (Dubnau, 1991) and its *S. pneumoniae* homologue, *cilC* (Campbell *et al.*, 1998; see TIGR database for full sequence), are both stand-alone genes unlinked to the *comG* or *cgl* locus. They encode a peptidase-methyltransferase that processes prepilins by cleaving the polypeptide at the F residue and methylating the new N-terminus (Strom, Nunn & Lory, 1993). In *H. influenzae*, the *cgl* locus contains only four genes. They encode proteins HI0299, HI0298, HI0297, and HI0296 (Fleischmann *et al.* 1995), which are homologues of the *P. aeruginosa* prepilin, ComGA, ComGB, and ComC, respectively.

In the three species with different patterns of competence regulation, the *cgl* operon is under late gene control. In *S. pneumoniae* the operon is preceded by the CATGAATA combox (Pestova & Morrison, 1998); in *B. subtilis* by the ComK recognition site (Hamoen *et al.*, 1998); in *H. influenzae* by the dyad symmetry element (Karudapuram & Barcak, 1997). *S. gordonii* uses a similar regulatory mechanism to *S. pneumoniae*, and a CATGAATA combox precedes its *comY* operon, which contains genes closely homologous to at least four *cgl* genes (Fig. 2; Lunsford & Roble, 1997). Although *S. gordonii* is transformable, *Streptococcus pyogenes* has

never been shown to be transformable, yet it has a homologous *cgl* locus (Fig. 2), preceded by a combox (Håverstein & Morrison, 1999). *Lactococcus lactis* also has a *cgl* operon (Fig. 2; sequence from Breunder, A. & Hammer, K., GenBank Acc. No. Y15043, 1997), but it is apparently transcribed from a typical SigA promoter. These observations raise the possibility that both species are transformable. Perhaps *S. pyogenes*, which lacks genes homologous to *comA-E* in *S. pneumoniae*, has a different system for signalling the development of competence than other streptococci, and maybe in *L. lactis* the entire regulatory mechanism is different, as in *B. subtilis*. Alternatively, the *cgl* pathway may have functions other than enabling DNA uptake; for example, in bacterial adhesion to surfaces.

How *cgl* products act in DNA uptake is unknown, but several possibilities can be envisioned (Chung *et al.*, 1998). By analogy to pilins, the products may form an appendage outside the cell membrane. This structure may act as a scaffold on which other proteins that bind and process DNA for entry are arranged. This scaffold may penetrate the peptidoglycan layer of the cell wall to form a passage for external DNA. In this connection some remodeling of the cell wall may occur, as discussed below. It is possible that *cgl* proteins are directly involved in binding or processing DNA, but no evidence for such functions have been adduced. An intriguing hypothesis, however, is that the *cgl* system, in a manner akin to pilus extrusion and retraction, serves as a motor for bringing DNA into the cell (Dubnau, 1997).

cel (comE-like) genes

Two genes, *comEA* and *comEC*, of the three in the *comE* operon of *B. subtilis* are essential for DNA uptake (Hahn *et al.*, 1993). Homologues of these two genes,

celA and *celB*, compose a late competence operon in *S. pneumoniae* (Pestova & Morrison, 1998). In *H. influenzae*, corresponding homologues, HI1008 (Fleischmann *et al.*, 1995) and *rec2* (Clifton, McCarthy & Roe, 1994), are transcribed separately, each under control of the dyad symmetry element. Relationships between products of these genes are shown in Fig. 3.

ComEA and CelA are proteins of ~20kDa with a long stretch of hydrophobic residues at the N-terminus. The 12-kDa *H. influenzae* homologue has a similar hydrophobic stretch but otherwise matches only the C-terminal half of the two other proteins. A resemblance between the C-terminus of ComEA and that of *E. coli* UvrC was previously noted (Dubnau, 1997). Mutations in *comEA* prevent binding of DNA to the cell, and it was shown recently that the ComEA protein *in vitro* binds tightly to DNA in a nonspecific fashion, but does not nick DNA (Provvedi & Dubnau, 1999). This protein, therefore, is very likely responsible for the initial, reversible binding of DNA to the cell.

ComEC, CelB, and Rec2 are 80-kDa proteins with multiple hydrophobic stretches that could be transmembrane segments. ComEC is not required for DNA binding, but it is necessary for DNA entry (Inamine & Dubnau, 1995). These proteins may form channels in the membrane for passage of DNA (Dubnau, 1997).

cfl (*comF*-like) genes

The *comF* operon of *B. subtilis* consists of three genes, two of which are essential for transformation and have counterparts in the two-gene *cfl* operon of *S. pneumoniae* (sequence from TIGR). ComFA mutants are reduced in transformability ~1000-fold (Londono-Vallejo & Dubnau, 1994). CflA mutations are

similarly defective, and they fail to take up DNA (D. Morrison, personal communication). These 50-kDa proteins show sequence similarity to ATP-dependent DNA helicases (Londono-Vallejo & Dubnau, 1993). Although they lack hydrophobic regions, ComFA was associated with the cytoplasmic face of the cell membrane (Londono-Vallejo & Dubnau, 1994).

With respect to function, it was suggested that ComFA acts as a helicase to help separate the DNA strands and propel one strand into the cell. It may also have a nicking activity, inasmuch as TraI of the F-factor conjugative system acts as a helicase after nicking the donor DNA (Matson *et al.*, 1993). Comparison of protein sequences indicates some resemblance of ComFA and CflA to UvrB of *E. coli* (Fig. 4A). UvrB contains a latent ATPase that is activated when it interacts with UvrC, and the UvrB-UvrC complex is able to nick DNA (Orren & Sancar, 1989). Conceivably, CflA, either by itself or together with CclA (which resembles UvrC), has the dual functions of nicking and unwinding donor DNA. If it binds covalently to the nicked DNA, as TraI is thought to do, it might also assist its entry into the cell.

ComFC, CflB, and the *com101A* (= *comF* [Tomb *et al.*, 1991]) gene product of *H. influenzae* (Larson & Goodgal, 1991) are homologous 25-kDa proteins. Mutations in *comFC* reduced transformation only ~10-fold, but the reduction was much greater in *comF*. Mutants in *comF* bound normal amounts of DNA, but whether these proteins function in entry or in a later stage of transformation is unknown. The proteins contain two putative zinc fingers at their N-termini (Fig. 4), which may enable them to bind other components of the entry complex.

Post-entry genes

Examination of their genomes indicates that both *S. pneumoniae* and *B. subtilis* harbor two *ssb* loci that encode proteins homologous to the single-stranded DNA binding protein of *E. coli*. One is expressed as a late competence gene, and the other is constitutively expressed and presumably functions in DNA replication. In *S. pneumoniae*, it is apparently the competence-induced protein that is found bound to newly entered donor strands (Morrison, 1978). Whether such binding assists the uptake process is unknown, inasmuch as no mutants in the competence induced *ssbB* gene (= *cilA* [Campbell *et al.*, 1998]) have been tested.

There is only a single *recA* gene in *S. pneumoniae*, but its expression is increased ~5-fold during competence (Martin *et al.*, 1995), as a result of the presence of a combox (Campbell *et al.*, 1998) preceding its upstream neighbor, *exp10* (Pearce *et al.*, 1995; = *cinA* [Martin *et al.*, 1995]). DNA appears to enter normally in *recA* mutants.

Genes of unknown or accessory function

Three late competence genes in *S. pneumoniae* of unknown significance for DNA uptake are *exp10/cinA*, *coiA*, and *cilB*. Mutations in the first two genes reduce transformation ~10-fold (Pearce *et al.*, 1995; Pestova & Morrison, 1998). Homologues of *exp10/cinA* are found in many bacteria, but aside from a hydrophobic N-terminal region indicating a membrane location, nothing is known about the function of its protein product. As deduced from the genomic sequence of *S. pneumoniae*, the *coiA* gene is the first in an operon containing four genes. The products of *coiA* and *coiB* both appear to be peptidases, *coiC* encodes a putative

methyltransferase, and *coiD* encodes a putative cell-wall serine proteinase. It may be speculated that these enzymes play a role in cell wall remodelling during the development of competence.

CilB is homologous to the *H. influenzae* gene, *dprA*, in which mutations reduce chromosomal transformation 10,000-fold, with no effect on plasmid transfer (Karudapuram, Zhao & Barcak, 1995). Mutations in *dprA* may affect only chromosomal DNA entry because plasmids enter *H. influenzae* cells by a different mechanism (Pifer, 1986). Otherwise, the gene may be required only for chromosomal integration, as appears to be the case for *recP* in *S. pneumoniae* (Morrison *et al.*, 1973).

The case of *dprA* is unusual in that it is regulated as a late competence gene (Lacks & Greenberg, in preparation), but it is not normally required for either chromosomal or plasmid transformation. It encodes a DNA methyltransferase that protects unmodified incoming plasmid DNA by methylating it while it is in a single-stranded form, thereby allowing plasmid establishment by unmodified donor DNA in a cell containing the *DpnII* restriction system (Cerritelli, Springhorn & Lacks, 1989).

Role of a membrane nuclease in DNA uptake

The *endA* gene

The only gene known to function in DNA uptake that is not induced during the development of competence is *endA* of *S. pneumoniae*. This constitutive gene is expressed from several upstream promoters, all with a SigA consensus sequence (Puyet *et al.*, 1990). The strongest promoter precedes the first gene of the operon

in which *endA* is the third and final gene. EndA is a 30-kDa polypeptide with a hydrophobic segment near its N-terminus (Puyet *et al.*, 1990), and it is located in the cell membrane from which it can be solubilized by mild detergents (Lacks & Neuberger, 1975). *In vitro*, it acts as a general endonuclease, producing oligonucleotide fragments from both single- and double-stranded DNA and from RNA (Rosenthal & Lacks, 1977). When isolated from membranes, EndA is found in a larger structure of ~250 kDa (Rosenthal & Lacks, 1980).

Mutants of *endA* that retain at least 5% of wild-type nuclease activity are fully transformable, but those with less than 1% activity are defective. Null mutants bind DNA but do not transport it into the cell; they are reduced in transformability more than 1000-fold (Lacks *et al.*, 1975; Puyet *et al.*, 1990). It is interesting that neither *endA* nor *cflA* null mutants reduce transformability as much as defects in *cgl* genes or those required for development of competence. Perhaps both EndA, which hydrolyses the complementary strand, and CflA, which may unwind donor DNA and/or translocate a donor strand into the cell, are required for efficient DNA strand entry, but in the absence of one, the other activity still manages to introduce some DNA.

No-entry degraders

Normally, one donor strand is degraded as the other enters the cell. In certain mutants, however, the expected amount of donor DNA is degraded and found outside the cell, but no DNA enters the cell (Morrison *et al.*, 1983). The single strand produced by EndA action presumably remains outside the cell. The mutations that give rise to these "no-entry degraders" occur in both the *cel* and *cfl* loci (D.

Morrison, personal communication). If CelB composes the pore for DNA entry through the cell membrane and CflA is needed for DNA passage through the pore, then defects in either could block entry without blocking degradation.

B. subtilis nucleases

Cells of *B. subtilis* contain at least ten enzymes with DNase activity (Rosenthal & Lacks, 1977). One of them, a 16-kDa protein encoded by *nucA*, is membrane-located (Smith *et al.*, 1983). This gene is under competence control, but mutations of it do not prevent transformation (van Sinderen, Kiewiet & Venema, 1995). However, the plethora of DNases in *B. subtilis* might allow redundancy of the entry nuclease. A possible candidate for this redundant function is the 30-kDa product of the gene *yurI* of *B. subtilis* (Kunst *et al.*, 1997), which has a potential membrane-binding segment and is homologous (28% identity; see Fig. 5) to the periplasmic nuclease, EndA of *E. coli*, a protein with enzymatic activities very similar to EndA of *S. pneumoniae*. A form of the *yurI* gene, called *bsn*, was cloned from a strain of *B. subtilis*, and its product was characterized as an RNase with no DNase activity (Nakamura *et al.*, 1992). However, only a truncated, extracellular form of the enzyme was examined, and that form may have lost its DNase activity. In addition, the nucleotide sequence of *bsn* was only 73% identical to the gene in the transformable strain 168 (shown in Fig. 5).

Is *S. pyogenes* transformable?

In addition to the *cgl* operon, many homologues of *S. pneumoniae* late competence genes are under combox control in *S. pyogenes* (Håverstein & Morrison, 1999). This suggests that bacteria of this species may be transformable, albeit with

a system different from *S. pneumoniae* for eliciting competence development. It was therefore of interest to look for the presence of *endA* in the *S. pyogenes* genomic sequence (SGSP database). A three-gene operon with the first two genes very closely homologous to those of *S. pneumoniae* (77% and 50% identity, respectively) is present. However, the *endA* homologue, although very similar to that of *S. pneumoniae* (61% identity, see Fig. 5), is truncated and missing 94 residues from its N-terminus. Because the hydrophobic segment of the protein is absent, the protein could not be bound to the membrane so as to function in DNA uptake. But *S. pyogenes* contains yet another nuclease gene, which we designate *endB*, unlinked to the first, and also encoding a product similar to *S. pneumoniae* EndA (29% identity), albeit less so than the *S. pyogenes endA* product (Fig. 5). The EndB protein, however, does contain a potential membrane-binding segment. It could support transformation in *S. pyogenes*.

Cell wall lysis and rebuilding

The first gene in the operon encoding EndA in *S. pneumoniae* is a *murA*-like gene that encodes UDP-N-acetylglucosamine 1-carboxyvinyltransferase, an enzyme required for cell wall synthesis. It is one of two *murA*-like genes in *S. pneumoniae*, and it may participate in cell wall synthesis and reconstruction during competence development. *B. subtilis* similarly contains two such genes, *murA* and *murZ*. Only one such gene is present in *E. coli* (Blattner *et al.*, 1997). The lytic fragility of cells of *S. pneumoniae* during competence and the ability of such cells to spontaneously form protoplasts have been reported (Lacks & Neuberger, 1975). The latter propensity was shown not to depend on the *cwl* (= *lytA*) gene that encodes the major

pneumococcal autolysin. It could depend on a competence-induced gene, which may be one of those with unknown function. *CoiA*, a putative peptidase, and *CoiD*, a putative cell-wall serine proteinase, are possible candidates. The purpose of such remodeling, would be to install into the cell wall an appendage, perhaps formed of *cgl*-encoded proteins, that could allow attachment of DNA and its transport through the peptidoglycan layer of the cell wall and the cell membrane.

Structure and function of the uptake machinery

A speculative scenario of how the late-competence gene products and other cell envelope components might interact to enable DNA uptake is depicted in Fig. 6. As a first step, *CglA* and *CglB* may act together to export *CglC*, *D*, *E*, *F*, and *G*, with *CilC* processing the N-termini of *CglC*, *D*, and *F*. The five downstream *cgl* products would form an appendage extending into the cell wall layer and anchored in the cell membrane. Prior action of *coi*-encoded peptidases and *MurA* might disrupt and rebuild the cell wall in the vicinity of the pilin-related appendage. The *Cgl* structure would act as a scaffold for other proteins involved in DNA uptake, such as *CelA*, *CelB*, *CflA*, *CflB* and *EndA*. The scaffold would essentially trap *CflA* and *CflB*, which are not directly bound to the membrane. This structure would allow access of donor DNA to *CelA*, which could bind it reversibly. Combined action of *CelA* and *CflA* might then nick the DNA in an ATP-driven reaction, which would leave the DNA irreversibly bound to either *CflA* or *CflB* and, hence, the cell. Under normal conditions, helicase activity of *CflA* would separate the donor strands, and *EndA* would degrade one strand, both of which actions facilitate entry of the other strand into the cell through a membrane pore formed by *CelB*. Presumably, *CflA* or *CflB*, attached to the incoming strand at its 3'-end, acts as a pilot protein to bring

it through the transmembrane pore. One or more of these proteins may be able to pass through the transmembrane pore in either direction.

Once inside the cell, the entering strand is covered by SsbB protein. This may or may not assist its entry into the cell. Analysis of mutants defective in SsbB should answer this question. If EndA is defective, only a small amount of DNA is internalized by action of CflA. Similarly, if CflA is defective, only a small amount is internalized by action of EndA. When EndA is functional and CeiB or CflA is defective, degradation of a donor strand could proceed, but the complementary strand would be unable to enter the cell, as found for mutants exhibiting degradation but no entry of DNA. Null mutants of CeiA would not bind DNA at all.

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FIGURE LEGENDS

Fig. 1. Modes of DNA uptake. A. Viral infection: gp2, phage-encoded protein; r, cell membrane receptor; tf, phage tail fiber. B. Conjugation: d, TraD, i, TraI, and t, other plasmid *tra* gene products; om, OmpA, and x, unknown, host proteins; h, donor cell helicase; s and ts, single-stranded DNA binding proteins. C. Transformation: End, membrane-bound endonuclease releases oligonucleotides (Oligos); other proteins, EA, EB, FA, FB, and G, are induced during competence development and have structural and functional roles in uptake; ts is a competence-induced single-stranded DNA binding protein. The mechanisms shown are in part hypothetical.

Fig. 2. Comparison of homologous ComG-like (Cgl) proteins related to type IV pilins. A. ComGC-like (CglC) proteins. B. *H. influenzae* HI0299 (PilA) compared to PaePilA, the type IV prepilin from *P. aeruginosa*. C. ComGD-like (CglD) proteins. Only the N-terminal half of SgoComYD was cloned. LlaCglD was translated from the reported sequence data after insertion of single nucleotide before position 1509. D. ComGF-like (CglF) proteins. Key to species: Spn, *S. pneumoniae*; Sgo, *S. gordonii*; Spy, *S. pyogenes*; Lla, *L. lactis*; Bsu, *B. subtilis*. Key to symbols indicating similarity of residues: *, identical; :, very similar; ., similar. This Figure and Figs. 3, 4 and 5 were constructed with the aid of the CLUSTAL W program (Thompson, Higgins & Gibson, 1994).

Fig. 3. Comparison of *S. pneumoniae* CelA and *B. subtilis* ComEA to each other and to the carboxyl half of *E. coli* UvrC. Symbols as in Fig. 2.

Fig. 4. Comparison of homologous ComF-like (Cfl) proteins. A. *S. pneumoniae* CflA and *B. subtilis* ComFA proteins compared to each other and to *E. coli* UvrB. B. Comparison of *S. pneumoniae* CflB, *B. subtilis* ComFB, and *H. influenzae* HI0434 proteins. Symbols as in Fig. 2.

Fig. 5. Comparison of homologous endonucleases. A. *S. pneumoniae* EndA compared to putative *S. pyogenes* nucleases SpyEndA and SpyEndB. B. Comparison of *E. coli* and *B. subtilis* EndA nucleases. Symbols as in Fig. 2.

Fig. 6. Proposed mechanism for DNA uptake in *Streptococcus pneumoniae*. A. DNA binding. All components except EndA, a membrane nuclease, and MurA, a cell wall synthetic enzyme are induced during competence development. CeiA, a peptidase, and MurA reconstruct the cell wall for insertion of the DNA pore structure. CglA and CglB are responsible for export of CglC-G, prepilin like components of the uptake structure. The latter are processed by CeiC; their final arrangement in the cell envelope is unknown and arbitrarily drawn in the Figure. CeiA binds to donor DNA, and in conjunction with CflA makes a single strand break in it, possibly attaching the new 3'-end covalently to CflA or CflB. B. DNA entry. CflB may act as a pilot protein bringing the single strand through a membrane pore formed by CeiB. Entry of the donor strand may be facilitated by degradation of the complementary strand by EndA and helicase action of CflA. A competence-induced protein, Ssb, binds to the incoming donor strand. Potassium ions are needed for binding, and calcium and magnesium ions for entry.

Table 1. *Genes implicated in DNA uptake*^a

<i>B. subtilis</i>	<i>S. pneumoniae</i>	<i>H. influenzae</i> ^b	Possible functions
	<i>coiA</i>		Cell wall degradation
	<i>murA</i> ^c		Cell wall resynthesis
<i>comGA</i>	<i>cglA</i>	[HI0298] <i>pilB</i>	Prepilin membrane transport pore
<i>comGB</i>	<i>cglB</i>	[HI0297] <i>pilC</i>	Prepilin transport ATPase
<i>comGC</i>	<i>cglC</i>	[HI0299] <i>pilA</i>	Pilin-like wall structure
<i>comGD</i>	<i>cglD</i>		Pilin-like wall structure
<i>comGE</i>	<i>cglE</i>		Pilin-like wall structure
<i>comGF</i>	<i>cglF</i>		Pilin-like wall structure
<i>comGG</i>	<i>cglG</i>		Pilin-like wall structure
<i>comC</i>	<i>cilC</i>	[HI0296] <i>pilD</i>	Prepilin processing
<i>comEA</i>	<i>celA</i>	[HI1018] ^c	Donor dsDNA binding
<i>comEC</i>	<i>celB</i>	[HI0061] <i>rec2</i>	DNA membrane transport pore
<i>comFA</i>	<i>cflA</i>		Nickase, translocase, helicase?
<i>comFC</i>	<i>cflB</i>	[HI0434] <i>com101A (comF)</i>	Pilot protein?
<i>bsn</i> ^c (<i>endA</i>)	<i>endA</i>		Degrades donor DNA strand
<i>nucA</i> ^c	-		Alternative degradative nuclease
<i>ssbB</i> ^c	<i>cilA</i> ^c		ssDNA binding protein
	<i>cilB</i> ^c	[HI0985] <i>dprA</i>	Late DNA processing

^a See text for references. All genes except *murA*, *bsn* and *endA* are competence-inducible.

^b Genome designations in brackets; additional gene names in parentheses.

^c No experimental evidence for uptake.

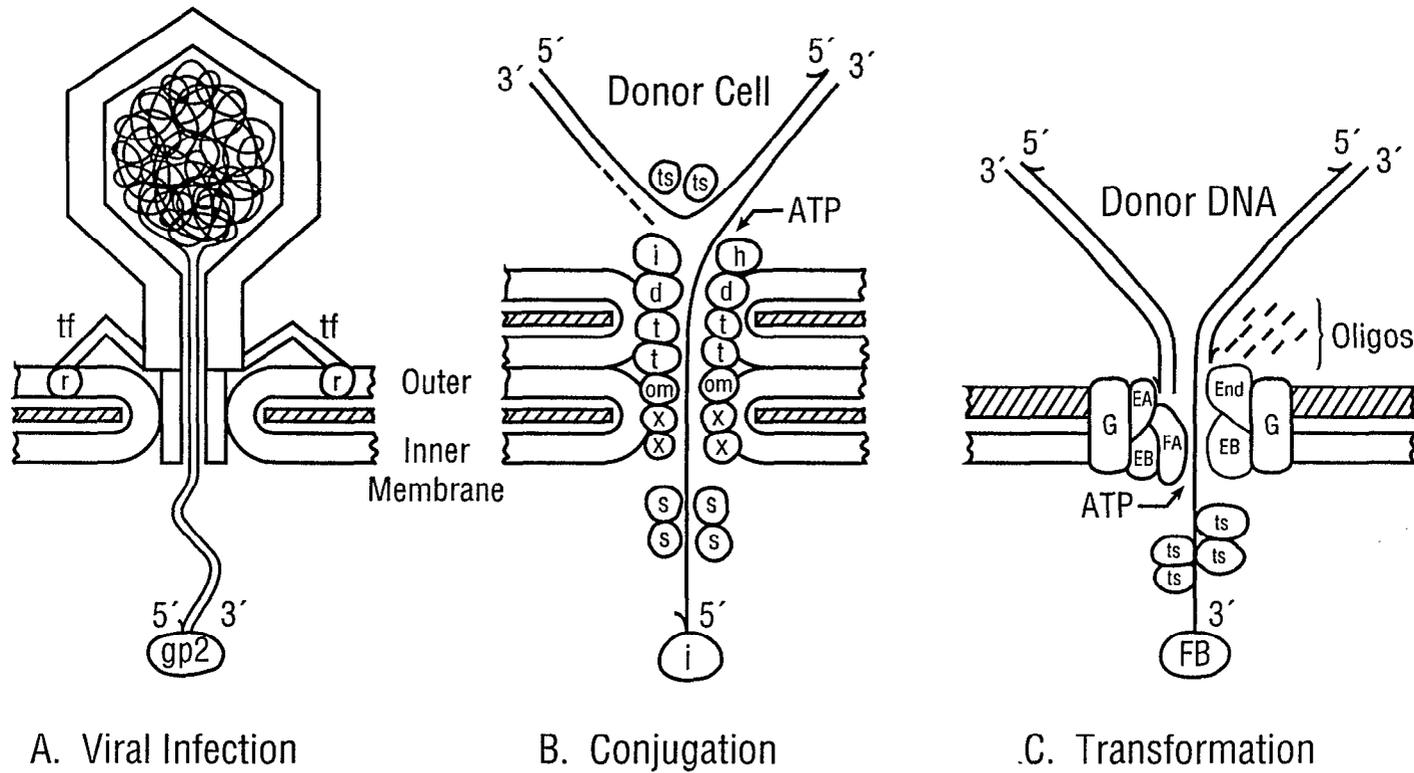


Fig. 1


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SpnCela  MEAIEKIKEYKIIIVICTGLGLLVGGFFLLKPAQTPVKETNLQAEVAA---VSKDLVSEKEVNKEEKEEPLEQDL 73
BsuComEA MNWLNQHKKA--IILAAASAAVFTAIMIFLATGKNKEPVKQA-----VPT---ETENTVVKQEANNDESNE-----T 61
EcoUvrC  KLPEVKRMECPDISHTMGEQTVASCVVFDANGPLRAEYRRYNTGITPGDDYAAMNQVLRRRYKKAIDDSKIP-DV 462
      : * . . * : . . : * : : : : :
      : * : : : : : : : : : : : : : :

SpnCela  ITVD-VKGAVKSPGIYDLPVGSRINDAVQKAGLTEQADSKSLNLAQKVSDEA--LVYVPTKGEEAVSQQTGLGTA 146
BsuComEA  IVID-IKGAVQHGPVYEMRTGDRVSOAIEKAGGTSEQADEAQVNLAIEILQDGT--VVYIPKKGEETAVQQGGGGSV 134
Hin1008  -----MKTLFTSVVLCCGALVVSSSFABEK--ATXQTAQSVVTTQAEAQVAPA 45
EcoUvrC  ILIDGGKQLAQAKNVFAELDVSWDKNHPLLGVAKGADRKAGLETLFFEPEGEGFSLPPDSPALHVIQHIRDESH 538
      * : * ** : : . . . . . : : : : . . . . .

SpnCela  SSIS-KEKKVNLNKASLEELQ-VKGLGGKRAQDIIDHR--EANGKPKSVDELKQVSGIGGKTIEKLKDYVTVD 216
BsuComEA  QSDGGKALVNINTATLEELQ-ISGVGPSKAEAIAYR--EENGRFQTIEDITKVSIGIGKSFEEKSSITVK 205
Hin1008  VVSD---KLNINTATASEIQKSLTGIGAKKAEIVQYR--EKHGNFXNAEQLELVQGIGKATLEKNRDRRIIF- 112
EcoUvrC  DHAIGGHRKKRAKVNTSSLET-IEGVGPKRRQMLLKVMGGLQGLRNASVEEIAKVPGISQGLAEKIPWSLKH- 610
      . : . . . : : * * : : : : : . . : : * ** . ** :

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Fig. 3

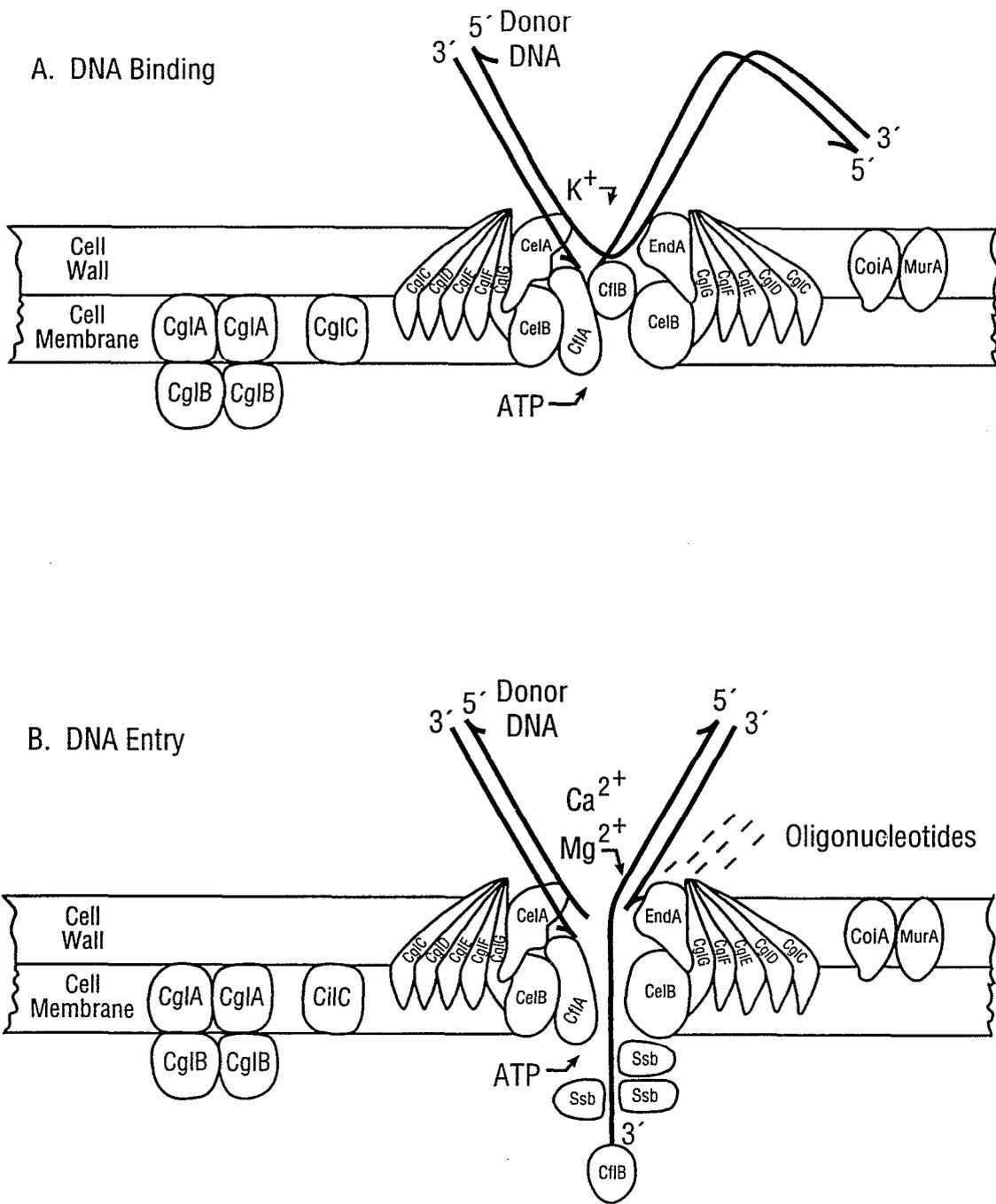


Fig. 6