Folded DNA in Action: Hairpin Formation and Biological Functions in Prokaryotes

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INTRODUCTION

The B-helix form of DNA proposed by Watson and Crick accounts for most of DNA's behavior in the cell. Nevertheless, it is now obvious that DNA isn't always present in this canonical structure, but can also form alternative structures such as Z-DNA, cruciforms, triple-helix H-DNA, quadruplex G4-DNA and slipped-strand DNA (147). This review focuses on DNA hairpins, i.e. DNA with intrastrand base pairing, their functions and properties, in light of the specific behavior of DNA in horizontal gene transfer between bacterial cells.

Hairpin structures can be formed by sequences with inverted repeats (IRs), also termed palindromes, following two main mechanisms. Firstly, in several cellular processes, DNA is single-stranded (ssDNA); for instance, on the lagging strand of replication, during DNA repair or, more importantly, during rolling circle replication, bacterial conjugation, natural transformation and virus infection. ssDNA is not simply a transient inert state of DNA, but can fold into secondary structures recognized by proteins, notably involved in site-specific recombination, transcription and replication. A second mechanism is the formation of hairpins from double-stranded DNA (dsDNA) as a cruciform, i.e. two opposite hairpins extruding through intrastrand base pairing from a palindromic sequence. The existence of cruciforms was already hypothesized soon after Watson and Crick's discovery (119): negative supercoiling of double-stranded DNA (dsDNA) could provide free energy to stabilize cruciforms that would otherwise be unstable. Cruciforms then attracted much attention in the 1980's when their existence was experimentally assessed in vitro under natural superhelical densities (117). But most studies at that time rejected their possible implication in cellular processes because of the slow kinetics of cruciform formation, which made them theoretically very unlikely to occur in vivo (25, 130). Nonetheless, this point of view was revised when techniques revealing cruciforms in vivo were developed and biological functions involving DNA secondary structures were discovered.

There are three ways in which DNA hairpins can interact with proteins and impact cell physiology. (i) Cruciform formation modifies the coiling state of DNA (143), which is known to affect the binding of

regulatory proteins for transcription, recombination and replication (26)(54); (ii) the DNA-protein interaction can be inhibited if a hairpin overlaps a protein recognition site (65). (iii) Proteins can directly recognize and bind DNA hairpins (8, 48, 97, 100, 139).

We describe here the cellular processes leading to DNA hairpin formation, biological functions involving hairpins, and the mechanisms of protein-hairpin recognition. Finally, we try to shed light on the evolution of folded DNA with biological functions and their cognate proteins.

DNA HAIRPIN FORMATION

Hairpin formation from ssDNA

The production of a large amount of single-stranded DNA (ssDNA) in the cell occurs mainly during the entry of exogenous DNA, macromolecular synthesis and repair. The three mechanisms of DNA uptake, namely, natural transformation, conjugation and, occasionally, bacteriophage infection, involve the production of ssDNA (Figure 1). The processes of replication and transcription also involve the unwinding of duplex DNA; finally, DNA repair can lead to the production of large quantities of ssDNA. The amount of single strand available, its lifetime and the bound proteins are different properties of these processes that may affect the possibility of hairpins to fold.

Formation of ssDNA through horizontal gene transfer.

(i) Conjugation. Conjugation is the process by which one bacterium can actively transfer DNA to a neighboring cell (Figure 1). The mechanism of conjugation is conserved across all described systems. A protein called relaxase binds and nicks a cognate origin-of-transfer site (*oriT*). This reaction results in a complex between the relaxed plasmid and the relaxase (together with accessory factors), called the relaxosome. Only the strand that is covalently bound by the relaxase is transferred to the recipient cell as ssDNA. The transferred strand (T-strand) is excreted from the donor cell through the type IV secretion

system and the relaxase then directs recircularization of the T-strand in the recipient cell (for a comprehensive review, see (4)). Two main families of conjugative elements have been described: self-transmissible plasmids and "integrative and conjugative elements" (ICEs). ICEs cannot autonomously replicate and are thus carried by chromosomes or other replicons. These elements are able to excise themselves as circular intermediates through the action of a recombinase/excisionase and are then transferred following the same mechanism. In the recipient cell, they can be integrated through homologous recombination or through the action of a site-specific recombinase (14, 70). The length of the DNA molecule that is transferred is usually the size of the whole conjugative element (usually <200kb).

Occasionally, chromosomal DNA can be transferred. This happens when conjugative plasmids are integrated into the chromosome, a famous example being the plasmid F/Hfr system (96, 137). Alternatively, the conjugation functions carried by ICEs can also promote transfer of chromosomal or plasmid DNA, as demonstrated for the SXT element in *Vibrio cholerae* (60). In this case, the length of the transferred strand is limited by the conjugation bridge strength and the contact time between the bacteria. Since the time of early genetic mapping trough Hfr conjugation of the *Escherichia coli* chromosome by Nelson, we have learned that it takes about 100 min to transfer the whole *E.coli* chromosome (4.6 Mb) (111). Although very long DNA fragments can be transferred, the average length of ssDNA region is unknown. Indeed, the ssDNA length and its lifetime depend on the speed of complementary strand synthesis in the recipient strain. The only direct data available comes from microscopy experiments enabling visualization of complementary strand synthesis and showing that synthesis already starts within 5 min after the donor and recipient cells are mixed (6). Nevertheless, the number of ssDNA replication origins is unknown in most cases. Single-stranded origins of replication have been studied in the case of rolling-circle replication, which is discussed later (II.1). The fact that specific origins of replication have evolved for initiation of complementary strand synthesis suggests that this process does not happen easily at random sequences. It is therefore unlikely that complementary strand synthesis is initiated at numerous loci. Conjugation thus massively produces ssDNA and conjugative plasmids are probably a place of choice for the evolution of functions where hairpins are involved. Indeed, the very process of conjugation, for instance, implies DNA secondary structures (48) (see

"Hairpin and conjugation").

(ii) Transformation. Bacterial competence for natural transformation is a physiological state that permits uptake and incorporation of naked exogenous DNA (Figure 1). Many Gram-negative bacteria (species of *Haemophilus, Neisseria, Helicobacter, Vibrio* and *Acinetobacter*) as well as Gram-positive bacteria (species of *Bacillus, Mycobacterium* and *Streptomyces*) are capable of natural competence. In all cases, one strand of the transformed DNA is degraded, providing the energy for transport of the complementary strand across the cytoplasmic membrane (20). Some bacteria have been shown to fragment exogenous DNA so that they take only small bits, while others can take up long DNA molecules (37). Monitoring of ssDNA fate during transformation in *Streptoccocus pneumoniae* revealed that ssDNA does not subsist in the cell more than 15 min (104). Globally, the length of the incoming DNA and the lifetime of ssDNA in the recipient cell are probably shorter than for conjugation. The entering single strand is protected from the action of nucleases essentially by the binding of SSB (22), whereas, during conjugation, the relaxase is covalently bound to the T-strand, effectively protecting it from exonucleases. However, in some bacteria including *B.subtilis* and *S.pneumoniae*, a protein named DprA has been found to bind the incoming ssDNA, protecting it from both endo- and exonucleases and facilitating further homologous recombination (108). All in all, during transformation, ssDNA is not long-lived in the cell; it is either quickly integrated into the chromosome through homologous recombination or it is degraded.

(iii) Phage infection. Single-stranded phages encapsidate their genome and deliver it to newly infected cells in this form (Figure 1). The maximum amount of DNA that can be transferred is equivalent to the size of the phage genome (generally <10 kb), but here again, little is known about the timing of complementary strand synthesis. Nevertheless, hairpins have been found to play important roles at all steps of ssDNA phage life cycles, from synthesis of the complementary strand (88, 144) to phage DNA encapsidation (125) (see the part "DNA hairpin biological functions").

Macromolecule synthesis and repair.

(i) Transcription. RNA synthesis requires the opening of the DNA duplex. The size of the

transcription bubble ranges between 12 and 25 bp, covered by the transcription complex (44). This small opening leaves very little room for secondary structure formation, and transcription is thus unlikely to foster hairpin formation. On the contrary, the transcription bubble needs to unfold hairpins that it may encounter so as to enable production of the correct transcripts by the RNA polymerase (RNAP).

(ii) Replication. In contrast to transcription, DNA synthesis produces large amounts of ssDNA. Firstly, the replication initiation step often requires melting of a large DNA region around the origin of replication. Multiple hairpins have been found to play important roles at replication origins (16, 99) (see the part "Hairpins and replication origins"). Secondly, lagging strand replication is not continuous and an ssDNA loop is formed to place the DNA in the correct orientation for DNA polymerase. Half of the replication loop consists of nascent Okazaki fragment and the other half of ssDNA extruded by the helicase (Figure 2). In E.coli, Okazaki fragments are 1 kb to 2 kb nucleotides long, and the replication fork speed is about 1 kb.s-1 in optimal conditions (78). The lifetime of ssDNA should thus be on the order of a second. Evidence that inverted repeats (IRs) can fold into stable hairpins in vivo during replication came from the observation that large and perfect IRs are genetically unstable on plasmids in E.coli. Indeed, they are the cause of mismatched alignment or slippage during replication (91, 131). In particular, deletions of IRs occur preferentially on the lagging strand (138).

Finally, a special mode of replication, called rolling circle replication (RCR), involves unwinding of the full lagging strand into ssDNA (75). Multiple hairpins have been found to play important roles in RCR (82, 83, 85, 113) (see Figure 5).

(iii) DNA repair. A major source of ssDNA in the cell is through DNA repair. Double-strand breaks are processed by the RecBCD enzyme which produces ssDNA tails through its exonuclease activity. These ssDNA tails can then be bound by RecA and may be involved in homologous strand invasion and replication-dependent repair (79, 80, 86). Double-strand breaks can be caused by many agents, including ionizing radiation, UV light and oxygen radicals, but in normally growing cells as well, double-strand breaks are formed in almost every cell cycle as a consequence of replication through imperfect DNA templates (for a

comprehensive review, see (36)).

It has also been shown that when replication forks encounter a lesion, the replication of the lagging and leading strands can be uncoupled in order to bypass the lesion, leaving ssDNA gaps on the damaged strand (55, 90, 116). These gaps are around 1 kb in length and can be processed by RecA-mediated recombinational repair (Figure 2).

Single-strand binding proteins. In all these processes, ssDNA in the cell is not left naked. Several proteins bind ssDNA without sequence specificity. The most important ones are the RecA and single-strand binding (SSB) protein. SSB coats any ssDNA present in the cell and prevents intrastrand pairing, i.e. hairpin formation. The RecA protein also binds ssDNA forming a straight nucleoproteic filament. RecA can then promote strand invasion of homologous dsDNA and catalyze recombination (79). Furthermore, SSB directs RecA binding to ssDNA (81, 122). Recent single molecule studies have shown how tetrameric SSB can spontaneously migrate along ssDNA, melting unstable hairpins while stimulating RecA filament elongation (124).

Although ssDNA is present on many occasions in the cell, hairpin formation is strongly constrained by SSB and RecA binding. Proteins that ensure their function through hairpin binding are thus in competition with SSB and RecA for substrate availability. Hairpins that are formed need to be stable enough to resist SSB melting and coating. For instance, it was demonstrated that SSB can inhibit the activity of the plasmid pT181 RepC protein at secondary cleavage sites on ssDNA, but not at its primary binding site (76) (see the part "Rolling Circle Replication").

Cruciform extrusion

Mechanism of cruciform extrusion. The formation of DNA hairpins in the cell does not necessarily require the production of ssDNA. Extrusion of cruciforms occurs through the opening of the

DNA double helix to allow intrastrand base pairing. Base opening in relaxed DNA is both infrequent and transient. However, negatively supercoiled DNA molecules are much more active, because their topology facilitates both large- and small-scale opening of the double helix (42). Two main mechanisms for cruciform extrusion have been proposed (Figure 3)(92). The first (type S) implies small-scale melting of the double helix at the dyad of the IR (~10bp). This small opening allows a few bases to pair with their cognate base in the repeat. The stem can then be elongated through branch migration, which is also facilitated by negative supercoiling. The other mechanism (type C) involves the melting of a large region, which is favored by nearby AT-rich sequences. This large melting would allow hairpins to fold on both strands leading to cruciform formation (Figure 3). The S-type mechanism is highly dependent on the IR sequence (it is favored by the AT-rich sequence at the dyad), and works in physiological ionic conditions (133). On the other hand, C-type extrusion takes place in low-salt solutions and is highly dependent on the presence of AT-rich neighbor sequences, but should theoretically be suppressed at physiological ion concentrations (110). Nevertheless, this mechanism could possibly take place in DNA regions with propensities to undergo substantial denaturation, such as replication origins.

Regulation of cruciform extrusion. Cruciforms were extensively studied in the 1980's when techniques enabling their observation *in vitro* were developed, such as S1 sensitivity and 2D electrophoresis. Although cruciform extrusion can be energetically favorable under moderate superhelical densities, the slow kinetics of cruciform extrusion raises questions as to their relevance *in vivo* (25). However, several techniques later developed led to the demonstration of cruciform formation *in vivo* under natural superhelical densities (33, 34, 64, 112). In particular, cruciforms that were tuned to fold stably at different superhelical densities have even been used to measure the natural superhelix densities of plasmids. *In vivo* cross-linking with psoralen demonstrated that the propensity of an IR to fold into a cruciform strongly depends on its sequence and context, and that some IRs can exist as cruciforms at levels as high as 50% in plasmids in living *E.coli* cells (148, 149).

Nevertheless, most reported cruciform detection involved artificial conditions favoring hairpin extrusion: small loops, IR in AT-rich regions, perfect palindromes with AT-rich centers and GC-rich stems, *topA* background or salt shock to increase supercoiling (131, 149, 150). Random IRs do not seem to fold cruciforms at significant rates under average *in vivo* supercoiling. However, many factors may transiently increase local superhelical density to a critical level sufficient for cruciform extrusion (see review (118)). Biological processes such as transcription and replication may generate local and temporal domains of supercoiling on circular DNA (34, 93, 128). Indeed, during replication and transcription, enzymes alter the structure of DNA, such that additional twists are added (positive supercoiling) or subtracted (negative supercoiling). Negative supercoiling favors the unwinding of the DNA double helix, which is required for initiation of transcription and replication processes (59, 120). As transcription proceeds, DNA in front of the transcription machinery becomes positively supercoiled, and DNA behind becomes negatively supercoiled. Similarly, during replication, strand separation by the helicase leads to positive supercoiling of the duplex ahead of the fork (see review (128)).

Changes in supercoiling in response to external and/or internal stimuli could also play a significant role in the formation and stability of cruciforms. In *E.coli,* superhelicity has been shown to vary considerably during cell growth and to change under different growth conditions (7, 68). Moreover, topology analysis of reporter plasmids isolated from strains where the SOS stress response regulon is constitutively expressed revealed higher levels of negative supercoiling (98). Finally, the level of superhelicity is known to be variable between bacterial strains. For instance, the average supercoiling density of a pBR322 reporter plasmid extracted from mid-log cultures of WT *Salmonella* is 13% lower (σ=-0.060) than that from *E.coli* (σ=-0.069) (18).

Effect of cruciform extrusion on DNA topology dynamics. The positioning of IRs within topological domains appears to be another parameter that influences cruciform extrusion. Studies involving visualization of the cruciform on supercoiled plasmids through atomic force microscopy have shown that extrusion is favored when IRs are positioned at the apex of a plectonemic supercoil (115). Furthermore,

cruciforms can exist in two distinct conformations, an X-type conformation and a planar conformation. In the X-type conformation, the cruciform arms form an acute angle and the main DNA strand is sharply bent, whereas in the planar conformation, the arms are present at an angle of 180°C (129). It has been shown that the rest of the DNA molecule is deeply affected by the conformation adopted by the cruciform. X-type cruciforms tend to localize at the apex of the plectonemic supercoil and restrict slithering of the molecule, i.e. they reduce the possibility of distant sites coming into contact. Environmental conditions, such as salt concentration and protein binding, are factors influencing the conformation choice. For instance, the RuvA protein tetramer which binds to the Holliday junction at the base of cruciforms forces them into a planar conformation in which the constraints upon DNA movements are relieved (129). It has thus been proposed that cruciform extrusion may act as a molecular switch that can control DNA transactions between distant sites. Such long-range contacts are known to be essential in many cellular processes, including site-specific recombination, transposition or control of gene expression through DNA-loop formation (1, 46, 94, 127).

Genetic instability of inverted repeats

It was quickly noticed that long palindromes are impossible to maintain in vivo (for a review, see (91)), either because they are not genetically stable and will be partially mutated or deleted, or because they are not viable, i.e. the molecule carrying them cannot be replicated (24). It is assumed that instability and inviability are caused by the inability of the replication fork to process secondary structures that are too stable, and by the presence of proteins destroying these structures. In particular, the SbcCD enzyme can cleave hairpins forming on ssDNA, leading to double-strand breaks that are then repaired by recombination (17, 27). This leads to constraints on the size and perfection of the inverted repeats that can be maintained in vivo. Typically, a size of 150-200 bp is a limit for IRs, although the presence of mismatches and spacers between the repeats strongly improves their maintenance. However, a mutation mechanism was identified, which tends to restore perfection to quasi-palindromes during chromosomal replication (38). The model proposes

that during replication, the nascent DNA strand dissociates from its template strand, forming a partial hairpin loop structure. The nascent strand is then extended by DNA synthesis from the hairpin template, forming a more fully paired hairpin. IRs are thus balanced between a mechanism than tends to perfection and the fact that perfect IRs are not genetically stable.

DNA HAIRPIN BIOLOGICAL FUNCTION

Hairpins and replication origins

Hairpins play an essential and common role in replication initiation. Indeed, they have been found to be indispensable for initiation of complementary strand synthesis on single-stranded phages as well as for replication of dsDNA replicons, in particular, during rolling circle replication.

Priming on single strand. The first evidence for the role of DNA hairpins in a biological function came from the early studies of the primosome. The inability of DNA polymerases to initiate *de novo* replication makes the independent generation of a primer necessary (78). The primosome is a complex of proteins which carries out this priming through *de novo* synthesis of a small RNA whose 3' end can be used by the DNA polymerase as a starting point. The role of RNA in priming DNA replication was discovered primarily through studies of single-stranded phages, notably G4 and ϕX174 (88, 144). Single-stranded phages are delivered to the infected cells and have evolved diverse mechanism for priming synthesis of the complementary strand, but all the strategies described to date involve DNA hairpins.

(i) G4 type priming. Phage G4 carries, in the region of replication initiation, three hairpins with stems of 5 to 19 bp and loops of 4 to 8 bases. Early models invoked these structures as recognition sites for the primase, DnaG (88). However, it was later shown that none of these hairpins are required for DnaG to initiate primer synthesis in the absence of SSB in *E.coli* (135). The hairpins seem, in fact, to direct the binding of SSB so that primase recognition site 5'-CTG-3' is exposed (134). This mechanism is likely to be at stake for a

large number of G4-like phages, including a3, St-1 and ϕK. This is an illustration of how hairpins can direct protein binding and structure an ssDNA region (Figure 4).

(ii) ϕX174-type priming. Although ϕX174 is a close relative of G4, the priming mechanism leading to complementation of ssDNA cannot be realized by DnaG alone. The PriA protein, which is now known to play a major role in stalled replication fork restart, was first identified as an essential component of the ϕX174 primosome (144). It catalyzes priming from a specific primosome assembly site (PAS) which can adopt a stable secondary structure (5). However, it is now clear that the main PriA substrates are not PAS sites but D-loops and R-loops encountered during replication, DNA repair and recombination events. It has thus been proposed that PAS sequences have evolved to mimic the natural targets of PriA (103). A stem-loop formed on a single strand can indeed be viewed as a branched structure between a double strand and two single-strand components (a Y-fork). PriA was recently shown to bind Y-forks (136). This is an illustration of hairpins that have evolved to be recognized by a host protein, to direct primosome assembly (Figure 4).

(iii) Filamentous phage type priming. In the case of the M13 phage and other filamentous phages (f1 and fd), synthesis of the complementary strand is primed neither by DnaG nor PriA, but by the host RNA polymerase (RNAP) holoenzyme containing the sigma70 subunit which synthesizes a 20 nt long RNA primer (57, 71). The RNAP recognizes a double hairpin structure mimicking a promoter with a -35 and a -10 box (56) (Figure 4). Here again, hairpins have evolved to be recognized by a host protein. Hairpins recognized by the RNAP have now been associated with several functions (see 2.a).

Double-strand DNA replication. The first step in dsDNA replication is the melting of a region where the replication priming complex can load. This melting event is favored, with some exceptions, by a complex of proteins (DnaA for the chromosome, or Rep for plasmids), which binds the DNA (usually at direct repeats: DnaA boxes or iterons) and bends it (72, 77, 109). This bending promotes DNA melting, but also formation of alternative DNA structures.

A common feature of many origins of replication is the presence of inverted repeats (IRs). The

extrusion of IRs as cruciforms is energetically more favorable than the simple DNA melting and is thus very likely to occur, absorbing a part of the strain generated. Furthermore, when DNA melting actually occurs (which is favored by AT- rich regions present in most *oris*) IRs are free to fold into hairpins. There is thus ample opportunity at origins of replication for a DNA structure to arise and interact with proteins.

As a matter of fact, hairpins have also been shown to play essential roles in primosome assembly in dsDNA replication. The generation of a primer occurs in two major ways: opening of the DNA double helix followed by RNA priming (chromosomal, theta and strand displacement replications) or cleavage of one of the DNA strands to generate a 3'-OH end (rolling-circle replication (RCR)) (35, 75). In both mechanisms, cases where hairpins play essential roles have been described.

(i) Chromosomal and theta replication. The DnaA protein plays a central role in the replication of the bacterial chromosome and of several plasmids. It is involved in the control of replication initiation, unwinding of the helix and recruitment of the priming complex (for a review see (109)). It has been proposed that in some replication origins, a hairpin structure carrying a DnaA box folds in the region unwound by DnaA itself. This hairpin, named M13-A, is at the core of the ABC priming mechanism first described for the R6K plasmid (101). M13-A is specifically bound by DnaA, which then recruits DnaB, DnaC and finally initiates RNA priming. This mechanism was later proposed to occur at the *E.coli* origin of replication (16), and putative M13-A hairpins are present in a large number of theta-replicating plasmids.

Inverted repeats other than M13-A and called single-stranded initiators (*ssi*) are often present at replication origins and can be involved in RNA priming. In the same way that filamentous phages prime complementary strand synthesis, the F plasmid origin of replication has a hairpin (*ssiD* or *Frpo*) recognized by *E.coli* RNAP which synthesizes an RNA primer (100). Other *ssi* have been isolated from a variety of plasmids and shown to use a ϕX174 type priming involving PriA (for a review, see (99)).

(ii) Strand displacement replication. The best described example of strand displacement replication is plasmid RSF1010. The plasmid-encoded RepC protein binds to iterons and unwinds the DNA in a region carrying two single-stranded initiators (*ssiA* & *ssiB*). These sequences are IRs which fold into hairpins. The

secondary structures of these hairpins and parts of their sequences have been shown to be essential for replication (106). The current model states that plasmid-encoded RepB primase specifically recognizes *ssiA* and *ssiB* and primes continuous replication from these sequences (61-63). However, it is not clear whether *ssiA* and *ssiB* fold when the region is largely single-stranded or whether they extrude as a cruciform, thanks to the action of RepC.

(iii)Rolling circle replication (RCR). RCR is widely present among plasmids and viruses (including the filamentous phages previously mentioned), with the model being plasmid pT181 (for a review see, (75)). The plasmid-encoded Rep protein binds to the double-stranded origin of replication (*dso*) and bends the DNA, producing a strain leading to the extrusion of a hairpin carrying the Rep nicking site. This structure was among the first cruciforms probed in vivo (113). Rep nicks DNA in the hairpin and becomes covalently attached to the 5' phosphate (Figure 5). The free 3'-OH end serves as the primer for leading strand synthesis. No synthesis occurs on the lagging strand until it is completely unwound by the helicase and released as ssDNA. The synthesis of the complementary strand is then initiated at the single-strand origin (*sso*). Four classes of *sso* have been described (*ssoA*, *ssoW*, *ssoT* and *ssoU*). These classes have little nucleotide sequence homology, but share structural features (82) necessary for their recognition by the host RNA polymerase which primes complementary strand synthesis (82, 84, 85).

Hairpins and transcription

There are essentially three ways in which hairpins and cruciforms can affect transcription. (i) The extrusion of a cruciform dramatically reduces the local supercoiling of DNA. Since superhelical density is known to affect the activity of promoters, cruciform extrusions in promoter regions could reduce their activity (142). (ii) A cruciform could prevent proteins from binding to their cognate site if it overlaps the extruding sequence. (iii) RNA polymerases or transcription factors could recognize hairpins present on ssDNA or extruded from dsDNA. Since there is as yet no documented case for the first possibility, only the two other mechanisms are discussed here.

Hairpin promoters. We have already discussed how the RNAP can recognize hairpin promoters to

prime DNA replication (rolling circle replication / filamentous phage type priming / F plasmid replication). The RNAP primes F plasmid replication through recognition of the F*rpo* hairpin, but under certain conditions, it can produce transcripts longer than the one needed for priming and express the downstream genes (100).

Accordingly, transcription from a structured single-stranded promoter was suggested to occur during conjugative DNA transfer for several *oriT*-associated genes of enterobacterial conjugative plasmids, namely *ssb*, *psiB* and sometimes *ardA*. Considering that conjugation consists of ssDNA entry into the recipient cell, the product of these genes - respectively single-strand binding, anti-SOS and anti-restriction - could be needed for maintaining the plasmid in the recipient. Indeed, the transcriptional orientation of these genes, always on the leading strand, means that the transferred strand is destined to be the transcribed strand (21). Moreover, conjugative induction of these first loci so as to enter the recipient bacterium was shown to be transfer-dependent (69). The burst of activity observed shortly after initiation of conjugation led to the proposal that this early transcription could be mediated by the presence of a secondary structure in the transferred ssDNA (3, 114)that mimics an RNA polymerase promoter recognized by the F*rpo* sigma factor (100).

Other hairpin promoters which are not involved in priming have been described. Notably, the N4 virion carries three hairpin promoters specifically recognized by the virion RNA polymerase (vRNAP) and used to direct the transcription of the phage early genes (Figure 6). Upon infection of *E.coli*, the N4 double-stranded DNA injected into the cell is supercoiled by the host DNA gyrase, which leads to the extrusion of hairpin promoters as cruciforms (28, 29).

Promoter inhibition through cruciform extrusion. Early studies have shown how an artificial IR overlapping a promoter can regulate transcription by superhelix-induced cruciform formation (64). Although promoters usually have higher activity with increasing superhelix density, such a promoter has a lower expression level at high superhelix density because of the extrusion of the IR as a cruciform preventing RNAP binding. It has also been shown that the N4 hairpin placed between the -10 and -35 boxes of the *rrnB*

P1 promoter can repress its activity in a supercoil-dependent manner (28). DNA cruciform extrusion seems likely to be a mechanism for the regulation of genes repressed by supercoiling. However, it is not clear how common this mechanism of regulation is, since no compelling natural example has been reported. The *bgl* operon promoter, which presents a 13bp IR, was first though to be a natural example of such regulation (132). However, it was later shown that no cruciform is required to account for its supercoiling-dependent repression (15).

Hairpins and conjugation

IRs are present in a majority of origins of transfers (*oriT*) (40). The best described is the origin of transfer of R388, where an IR named IR2 located 5' to the nicking site plays an essential role (49). Conjugation occurs as follow: DNA is nicked at the *oriT* and bound covalently by the plasmid-encoded relaxase protein TrwC. The T-strand is then unwound through rolling circle replication and transferred to the recipient cell. Although the folding of IR2 into a hairpin is not required for the initial nicking of the *oriT*, the recircularization of the T-strand requires folding of IR2 into a hairpin specifically recognized by the relaxase (48).

In addition to IR2, other IRs important for transfer efficiency are present in R388 *oriT* (95), but their exact role remains to be elucidated. It is not yet known whether their sequence or structure is important. They probably help adapt *oriT* into a potentially active state through cruciform formation.

Two relaxases other than TrwC have been crystallized: the F plasmid relaxase TraI (31) and the R1162 plasmid relaxase MobA (107). Although they show poor sequence homology to TrwC, the 3D structure of all this relaxases is very similar. These enzymes are evolutionarily homologous to certain identical mechanisms of action.

Hairpins and recombination

To date, there are three compelling examples of recombination systems using DNA hairpins as substrates: the CTX phage recombination site, the IS*200*/IS*605* insertion sequence family, and integron *attC*

recombination sites.

The single-stranded CTX phage of Vibrio cholerae. CTX is a single-stranded phage involved in *V. cholerae* virulence. In lysogenic phase, it integrates the *V. cholerae* chromosome I or II at its respective *dif1* and *dif2* sites. Chromosomal *dif* sites are recombination sites recognized by the XerCD protein complex which solves concatemers and allows proper chromosome segregation. CTX enters the infected cells as ssDNA, and the single-stranded form is directly integrated into one of the chromosomes (140). The *attP* recombination site of CTX carries a ~150 bp forked hairpin, which is homologous to *dif* sites (Figure 7). The phage uses this hairpin to hijack the host XerCD protein complex which catalyzes a strand exchange between *attP* and the *dif* site (30).

The IS200/IS605 insertion sequence family. The mechanism of transposition of the recently discovered IS200/IS605 insertion sequence family greatly differs from systems already described, in particular those using DDE transposase catalysis (50). The best studied representative of this family, IS*608,* was originally identified in *H*. pylori (74). It presents at its ends short palindromes recognized as hairpins by the TnpA transposase. “Top strands” of the two IS ends are nicked and joined together by TnpA a few base pairs away from the hairpins (19 nt upstream from the left hairpin and 10 nt downstream from the right hairpin) (8, 53). TnpA then catalyzes the formation of a single-stranded transposon circle intermediate which is then inserted specifically into a single-stranded target. This target site is not recognized directly by TnpA, but by four bases at the foot of the hairpin in the transposition circle (Figure 8 and (52)) that realize unconventional base pairing with the ssDNA target sequence.

The IS91 insertion sequence. IS*91* is a member of an insertion sequence family displaying a unique mechanism of transposition. The IS*91* transposase is related to replication proteins of RCR plasmids. IS*91* transposition involves an ssDNA intermediate generated in a rolling circle fashion (105). Short palindromes have been identified in the regions essential for transposition just a few base pairs away from the recombination sites. Their exact functions have not been studied. Nevertheless, striking similarities between these regions, RCR plasmids *dso* and conjugation *oriT*s suggest that these palindromes might fold into

hairpins recognized by the IS91 transposase.

Integrons. Integrons are natural recombination platforms able to stockpile, shuffle and differentially express gene cassettes. Discovered by virtue of their importance in multiple antibiotic resistances, they were later identified in 10% of sequenced bacterial chromosomes, where they can contain hundreds of cassettes (11). The cassettes are generally single ORFs framed by *attC* recombination sites (121). When expressed, the integron integrase can recombine *attC* sites leading to excision of a circular cassette. Such a cassette can then be integrated at a primary recombination site named *attI*. *attC* recombination sites have been shown to be recognized and recombined by the integrase only as hairpins (Figure 9) (12, 102). A surprising feature of *attC* hairpins is their huge polymorphism. Their stem length ranges from 54 to 80 bp and their loop length from 3 to 80 bp. Highly conserved mismatches known to be involved in hairpin recognition by the integrase are also present (12, 13) (see the part "Strand selectivity").

Other hairpin DNA: phage packaging, retrons, etc.

Single-stranded phage packaging. The single-stranded filamentous phages (f1, fd, M13, Ike) contain IRs that can fold into hairpins. We have already described the hairpins involved in complementary strand synthesis, but the largest hairpin identified on these genomes is the packaging signal (PS) recognized in translocation of ssDNA into the virion capsid. This hairpin is probably recognized by the phage transmembrane protein pI and determines the orientation of DNA within the particle (125). Both the structure and sequence determinants of the PS-hairpin are required for its function (126).

Retrons. Retrons are DNA sequences found in the genomes of a wide variety of bacteria (89). They code for a reverse transcriptase similar to that produced by retroviruses and other types of retro-elements. They are responsible for synthesis of an unusual satellite DNA called msDNA (multicopy single-stranded DNA). msDNA is a complex of DNA, RNA and probably protein. It is composed of a small single-stranded DNA linked to a small single-stranded RNA molecule folded together into a secondary structure. msDNA is produced in many hundreds of copies per cell (89). Whether msDNA are selfish elements or play a role in the cell remains to be discovered.

HAIRPIN FORMATION: CRUCIFORM EXTRUSION VS. SINGLE-STRANDED HAIRPIN

Under what conditions do DNA hairpins fold? Do they extrude from the double helix as cruciforms or do they fold from ssDNA during replication, repair or horizontal gene transfer? Both the single-stranded phage hairpins and the *sso* of RCR plasmids obviously fold from ssDNA. On the other hand, there is consistent evidence that the N4 hairpin promoters and the hairpin of the RCR plasmids *dso* fold as cruciforms (28, 113). However, there are only a few cases of successful cruciform detection of natural IR *in vivo*. Indeed, most reported *in vivo* cruciform detection involved artificial conditions favoring hairpin extrusion: small loops, IR in AT-rich regions, perfect palindromes with AT-rich centers and GC-rich stems, topoisomerase mutants or salt shock to increase supercoiling (131, 149, 150).

We recently investigated the conditions that can lead to integron *attC* site folding (Loot et al., 2010). These recombination sites are extremely good candidates for studying hairpin formation *in vivo.* Recombination events can only happen with folded *attC* sites and can be detected at very low frequencies. Furthermore, only the bottom strand of the *attC* site is recognized by the integrase (12, 41). This enables distinguishing recombination events occurring with hairpins formed on the lagging strand of replication from events occurring with hairpins extruding as cruciforms, or during other processes such as repair. Apparently, *attC* hairpins fold much more frequently on the lagging strand of replication than through other processes. It is nevertheless important to note that *attC* sites are imperfect IRs with at least 2 extrahelical bases, a bulge of 4-5 bp and a spacer sequence between the IRs (the loop of the hairpin, called the variable terminal sequence) of up to 80 bp. Such imperfections are known to hinder cruciform formation, and extrusion of imperfect IRs has only been detected in very AT-rich IRs (10). Nevertheless, transformation of non-replicative plasmids carrying *attC* sites into cells where they could only be maintained after a recombination event enabled us to show that *attC* sites can extrude cruciforms at low frequencies (<10-3). Most surprisingly, *attC* sites with

large spacer sequences (80 bp) between the repeats were also able to fold cruciform structures. Interestingly, it was noted that the recombinogenic strand of *attC* sites is always found on the leading strand of replication in natural integrons. Under such conditions, the most probable pathways for *attC* hairpin formation are through ssDNA generated by repair or cruciform extrusion. It has been observed that integron cassettes are particularly AT-rich (102), which could favor *attC* site extrusion following a C-type mechanism. Although it is not yet known whether the SOS response triggers IS608 movements, we know that this is the case for other classes of insertion sequences such as IS10 (2, 39).

To summarize, large perfect IRs can presumably fold into cruciforms but are genetically unstable because of their propensity to hinder replication and be cleaved by SbcCD. Small perfect (or almost-perfect) IRs can fold into cruciforms only when their sequence and context allow it. The N4 promoters and pT181 plasmid origin of replication are examples of such IRs with biological functions. Imperfect IRs are genetically more stable regardless of their size, but fold into cruciforms only rarely. They could still be involved in biological functions that take place at low frequencies such as integrons or IS608 recombination. Alternatively, imperfect IRs present in topologically constrained regions such as replication origins could also fold into cruciforms, which might be the case for the M13-A hairpin and for the *ssi* present in some origins of replication. Note that these hairpins are specifically bound by cognate proteins that could stabilize cruciforms.

PROTEIN / HAIRPIN RECOGNITION

Mimicry: subverting the host proteins

Some of the hairpins described in the literature have evolved to mimic the "natural" target of the protein they interact with. The PAS sequences of single-stranded phages mimic Y-forks that are recognized by PriA. The *sso* of RCR plasmids, the F*rpo* hairpin and the filamentous phages priming hairpins all mimic promoters recognized by the host RNAP. The M13-A hairpin mimics a natural *dnaA* box and the CTX *attP*

recombination site mimics the *V. cholerae dif* sites recognized by XerCD.

There is a noteworthy difference between hairpins like the CTX *attP* site, where mimicry is clear-cut, and the variety of hairpins recognized by RNAP. The latter indeed display an impressive diversity of structures and sequences. Although elements of the *ssoA* class present a large hairpin with near-consensus -35/-10 boxes (85), other *sso* classes like *ssoU* present much more complex structures with several hairpins and -35/-10 boxes harder to recognize (82). Another structural variation is that used by the filamentous phages. Here, a double hairpin acts as the recognition site with the -35 box on one stem-loop and the -10 box on the other (56). The fact that they are all recognized by RNAP suggests poor specificity of RNAP binding to hairpin DNA. The few common features of all these sequences are the widespread presence of mismatches in the hairpins and the fact that they do not work as promoters in dsDNA form, but bind RNAP very strongly when single-stranded (in some cases even more strongly than strong double-stranded promoters (56). These observations are consistent with the fact that the sigmaA and sigma70 of *B. subtilis* and *E.coli,* respectively, bind strongly to ssDNA containing promoter -10 sequences (66). The mismatches that often span the -10 box could be there to ease access for RNAP and increase hairpin-promoter activity. High activity might be required by single-stranded molecules which need to synthesize their complementary strand promptly before triggering the SOS response of the host, as was observed for phages defective in complementary strand synthesis (58).

In all these cases, mimicry of dsDNA is not perfect: to different extents, mismatches are present in the hairpins. These mismatches are probably, in some cases, necessary for maintenance of long IR *in vivo,* as discussed above. But do they have a role in and an impact upon hairpin recognition? CTX might be the only mimicry case in which imperfection has a clear function: mismatches are essential for the irreversibility of single-stranded phage integration (140).

Protein recognition of hairpin features

Other systems have evolved proteins recognizing special features of hairpin DNA. This is the case for

integron integrase IntI, for IS200/IS605 family transposase TnpA, for mobilizable plasmid relaxases (TrwC etc.), for N4 virion RNAP and probably for strand displacement replication proteins RepB. The features that make a hairpin structurally different from dsDNA are essentially: (1) the bottom of the stem, which can be either a Y-fork or a Holliday junction depending on whether the hairpin forms on ssDNA or as a cruciform; (2) the loop which is single-stranded; and (3) extrahelical bases and bulges produced by mismatches between the IRs.

The crystal structure of the interaction between IntI, N4 vRNAP, TnpA, TrwC and their cognate hairpins has been obtained (47, 49, 97, 123). All four highlight different mechanisms of recognition. IntI binds as a dimer to the stem of the hairpin and specifically recognizes two extrahelical bases. A central bulge in the stem also seems to be important for formation of a recombination synapse involving 4 IntI monomers. N4 vRNAP presents a base-specific interaction with the single-stranded loop of the hairpin and fits the stem structure through interaction with the phosphate and sugar backbone. TnpA binds the stem primarily through contact with the phosphate backbone, but also shows a base-specific interaction with the bases of the loop and, importantly, with an extrahelical T in the middle of the stem. Finally, the TrwC interaction is somewhat different from the others, since it binds not only to the hairpin structure, but also to the ssDNA 3' to the stem-loop, where the nicking site is present. The binding to the ssDNA part is base-specific, whereas the interaction with the hairpin occurs essentially through contact with the DNA backbone (49).

Strand selectivity

Whether it be during phage complementary strand synthesis, at the sso of RCR plasmids or during conjugation, only one DNA strand is available. In these cases, the question of strand selectivity is not physiologically relevant. However, when both DNA strands are free to fold into hairpins, erroneous recognition of one strand over the other may be problematic. Indeed, an inverted repeat, once folded, generates the same hairpins on the top and bottom strands, except for the loop and eventual bulges and extrahelical bases. Still, in all the processes in which a protein recognizes hairpin features, strand selectivity

has been observed: the protein recognizes one strand and not the other. In light of the hairpin/protein interactions described above, it is easy to understand how proteins discriminate between the two strands. They all show base-specific interactions with bases either in the loop, at the single-stranded base of the stem or with extrahelical bases. Any of these interactions can account for strand selectivity. Some of these systems appear to have good reason to process one strand and not the other. The N4 virion needs to initiate transcription in the right direction. Recombination of the wrong strand for integron cassettes would lead to their integration in the wrong direction, where they could not be transcribed. Finally, if a different strand of IS*608* is recognized at each end of the transposon, this would lead to the junction of the top strand with the bottom strand, a configuration that cannot be processed further and is likely to be lethal. Therefore, one strand had to be chosen and the other strongly discriminated against.

EVOLUTION OF HAIRPINS WITH BIOLOGICAL FUNCTIONS

A variety of hairpins have been selected to be recognized by host proteins, especially in single-stranded phages and plasmids. The single-stranded nature of DNA during transfer of mobile elements drove the evolution of secondary structures able to hijack the host cell machinery. The use of host priming proteins, host RNAP or even host recombinases incites single-stranded phages not to bring additional proteins with them and still be processed into a replicative form. Similarly, when a quick reaction is required upon transfer, ssDNA hairpins are the best elements for driving the response, as exemplified by the hairpin promoters present on several conjugative plasmids. We first discuss how horizontal gene transfer, the presence of ssDNA in the cell and the SOS response are interrelated. Secondly, we briefly review the origin of those proteins that have evolved to specifically use hairpin DNA as their substrate.

Single-stranded DNA, stress and horizontal transfer

We have seen that hairpin formation in the cell is most likely to occur in the presence of ssDNA in the

cell. Intracellular single-stranded DNA triggers the SOS response (Figure 10). ssDNA is the substrate for RecA polymerization. The formation of a RecA nucleofilament on ssDNA stimulates self-cleavage of the general repressor LexA, leading to its inactivation. Promoters from the SOS regulon, controlling mostly DNA repair, recombination and mutagenic polymerases, are than de-repressed (Figure 10).

SOS is thus induced when an abnormal amount of ssDNA is present in the cell. The formation of hairpins from ssDNA is thus likely to occur in a context where the SOS response is activated. Induction of the SOS response is often synonymous with stress. This happens, for example, when the cell tries to replicate damaged DNA, causing replication forks to stall (141). Another source of ssDNA comes from DNA intake by horizontal gene transfer and phage infection. For instance, conjugative transfer of R plasmids - conjugative plasmids carrying multiple resistances - has been shown to induce the SOS stress response in the recipient cell, except when an anti-SOS factor is encoded by the plasmid (*psiB*, already mentioned in the part "Hairpins and transcription") (Z. Baharoglu, D. Bikard, D. Mazel, submitted for publication). Interestingly, the expression of these anti-SOS genes is under control of ssDNA promoters, i.e. of hairpin substrates.

Furthermore, in the case of integrons, expression of the integrase (*intI*) has recently been shown to be controlled by SOS (51). Some antibiotics are known to induce the SOS response in Gram-negative and Gram-positive bacteria (73). These antibiotics, such as quinolones, trimethoprim and beta-lactams, were tested and found to be inducers of expression of the *intI* promoter. This is certainly a way for integrons to "know" when potential substrates are present in the cell and to recombine them. Indeed, the induction of SOS during conjugative transfer of R plasmids results in induction of the integrase, allowing genome rearrangements in the recipient bacterium (Z. Baharoglu, D. Bikard, D. Mazel, submitted for publication). Furthermore, integrons are often found on conjugative plasmids and may well take advantage of the single-stranded transfer to acquire cassettes and spread horizontally. Similarly, for IS*608*, specific integration into the ssDNA substrate has been proposed as a mechanism for targeting mobile elements and ensuring interbacterial spread (53).

Not only does the SOS response promote genetic rearrangments, but it also induces horizontal gene

transfer. It is known, for instance, that stress can induce competence in some bacteria (23) (Figure 10). Another effect of SOS induction is the derepression of genes involved in the single-stranded transfer of integrating conjugative elements (ICEs), such as SXT from *V.cholerae*, which is a ~100 kb ICE that transfers and integrates the recipient bacteria's genome, conferring resistance to several antibiotics (9). Moreover, different ICEs are able to combine and create their own diversity in a RecA-dependent manner (i.e. using homologous recombination, which is also induced by SOS) (45, 145). As for R plasmids, SXT transfer was observed to induce SOS in *V.cholerae*. Finally, some lysogenic phages are also known to induce their lytic phase under stressful conditions (43). One might thus see the use of ssDNA by integrons and other recombination systems as a mechanism for evolving: diversity is generated under stressful conditions.

On the origins of folded DNA binding proteins

While, in many examples described above, one can see that hairpins evolved to subvert the host machinery, in other instances, proteins evolved to specifically and sometimes exclusively recognize hairpin structures. This is the case for the RCR Rep proteins, the relaxases of conjugative elements, the transposase of IS608, the integron integrases and phage N4 vRNAP. Where do these proteins come from and what pushed them to recognize ssDNA rather than dsDNA?

RCR Rep proteins, relaxases and IS608 transposase. Interestingly, the IS608 transposase as well as conjugative relaxases have been found to be structurally similar to RCR Rep proteins (123). All of these proteins have in common the use of a tyrosine residue to covalently bind DNA. The Rep proteins belong to a vast superfamily spanning eubacteria, archae and eukaryotes (67). The superfamily is characterized by two sequence motifs: an HUH motif (histidine-hydrophobic residue-histidine) presumed to ligate a Mg2+ ion and required for nicking, and a YxxxY motif where the tyrosines (Y) bind the DNA covalently, with one of the tyrosine being optional. All these proteins thus probably have a common ancestor, ancient enough to account for the diversity of their functions and their spread among the kingdoms of life. The ability to bind hairpin DNA might have been an important feature in early stages of life when single-

stranded DNA might have been more widely present. In this instance, the relaxases of conjugative plasmids obviously need to recognize ssDNA features to process the ssDNA in the recipient cell. Recombination of ssDNA by the IS608 transposase is probably a way to target mobile elements and to ensure their spread. Finally, the reason why RCR plasmid Rep proteins would recognize hairpins rather than the more stable dsDNA is probably that origins of replications need to be strongly negatively coiled to unwind the double helix, and under these conditions, hairpins can be the most stable conformation of DNA.

Integron integrases. Integron integrases (IntI) are also tyrosine recombinases covalently binding DNA. However, they are not related to the Rep protein superfamily. The closest relatives to integron integrases are the XerCD proteins. However, IntI proteins carry an additional domain, compared to XerCD. This domain is involved in binding of the extrahelical bases of the *attC* hairpins that are essential for strand selectivity (13, 97). It would be tempting to speculate that integrons diverged from a single-stranded CTX-like phage which already used XerCD to recombine hairpin DNA. This special feature of ssDNA recombination would then have been selected to form an evolving recombination platform, thanks to its ability to sense both stressful conditions and the occurrence of horizontal gene transfer.

N4 vRNAP. N4 vRNAP is an evolutionarily highly divergent member of the T7 family of RNAPs (32). N4 vRNAP and T7 RNAP recognize their promoter with similar domains and motifs. However, N4 vRNAP recognizes a hairpin, whereas T7 RNAP recognizes dsDNA. The difference lies in the domain interacting with the hairpin loop. It displays substantial architectural complexity and base-specific interactions for N4 vRNAP, whereas the same domain in its counterpart just fits an AT-rich DNA sequence without base recognition (19). The reason why the N4 phage has evolved to transcribe several genes only from cruciform promoters is unclear. It is likely a way for the virion to sense the coiling state of DNA in the cell, which is known to be modified during the cell cycle and is particularly negative during the SOS stress response (98).

CONCLUSION

The use of DNA hairpins in biological processes is ubiquitous in prokaryotes and their viruses. How do these hairpins arise from duplex DNA? Numerous cellular processes lead to the formation of ssDNA, notably replication and the mechanisms of horizontal gene transfer, but also DNA damage and repair. Furthermore, the implication of cruciform DNA has been demonstrated at the RCR *dso* and for N4 phage promoters. Nevertheless, functions associated with cruciforms do not seem to be widely spread due to the slow kinetics of cruciform formation. However, cruciforms might play a role in special cases, but the difficulty of probing them in vivo makes these events underestimated. In eukaryotes, cruciform binding proteins have recently been identified and are suggested to play a major role in genome translocation (87) and replication initiation (146).

Not surprisingly, single-stranded phages have been found to use DNA hairpins at almost every step of their life cycle: complementary strand synthesis, replication, integration into the host chromosome and packaging. But hairpins play a role in the replication of a much larger number of elements, probably including the origin of replication of *E.coli*.

A striking feature is the opportunism of single-stranded DNA in subverting host machinery. The three different mechanisms of complementary strand synthesis have evolved hairpins directing priming by three different host proteins (DnaG, PriA, RNAP) in three different ways. Another example of opportunistic use of host machinery is the CTX phage which integrates *V. cholerae* chromosome I through a hairpin mimicking the XerCD recombination site. Also, the variety of hairpins recognized by the RNAP, either for replication priming or for transcription leads to the perception of ssDNA as evolutionarily very flexible.

Finally, the evolution of functions involving ssDNA is deeply intertwined with horizontal gene transfer, response to stress and genome plasticity. Horizontal gene transfers lead to ssDNA production and involve functions requiring hairpins. Together with stresses that also generate ssDNA, they activate the SOS response and trigger systems involved in genome plasticity, some of which use hairpin DNA, such as IS608 or integrons. To close the loop, the SOS response can trigger more horizontal transfer, notably through

activation of natural transformation, ICE conjugation and lysogenic phages.

The cases discussed above illustrate at least three different families of proteins in which specific hairpin binding activities have independently evolved. It thus seems quite easy both for proteins to evolve hairpin binding activity and for hairpins to evolve in such a way that they can exploit host proteins. Hairpin recognition can be seen as a way for living systems to expand the repertoire of information storage in DNA beyond the primary base sequence. These hairpin recognition examples illustrate how DNA can carry information via its conformation. Finally, this review is probably not exhaustive, as new functions in which folded DNA plays a role most likely remain to be discovered.

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FIGURES LEGENDS

Figure 1. DNA uptake and production of ssDNA in the cell. The three mechanisms: conjugation, natural transformation and infection by ssDNA phage lead the production of large amount of ssDNA in the cell.

Figure 2. Hairpin formation during replication. Hairpins can fold on the ssDNA formed by the discontinuous replication of the lagging strand, or on ssDNA gaps remaining after lesion bypass.

Figure 3. Mechanisms of cruciform extrusion. In the C-type pathway, a substantial region of dbDNA is denatured allowing the folding of the whole hairpins on both strands in one step. In the S-type pathway, a small region is denatured (~10bp) allowing the folding of a small hairpin that can then be elongated through branch migration.

Figure 4. Priming of replication on ssDNA hairpins. G4-type priming: hairpins structure the region, directing the binding of SSB and allowing access to the dnaG primase. Phi174-type priming: a ssDNA hairpin forms a Y-fork recognized by PriA which directs the formation of a primosome. Filamentous phage type priming: an hairpin mimicking a promoter is recognized by the RNA polymerase (RNAP), which synthesizes an RNA primer for replication.

Figure 5. Rolling Circle Replication. A)The Rep protein binds an hairpin formed by double-stranded origin (dso) and extruded from dbDNA as a cruciform. Rep nicks DNA and covalently binds the 5'-end, leaving a 3'-end for replication to proceed. The leading strand is replicated while the lagging strand is

extruded and remains single-stranded until the single-stranded origin (sso) is reached. The RNA polymerase (RNAP) binds the sso hairpin and synthesizes an RNA primer for replication. B) The pT181 dso in cruciform conformation. C) The pT181 sso as folded by the mFOLD software.

Figure 6. N4 virion hairpin promoters. The three promoters of N4 controlling the expression of the early genes as cruciform structures.

Figure 7. The *V. cholerae* chromosome I dif site and the CTX phage hairpin. The CTX *attP* region folds into a forked hairpin mimicking the *V. cholerae dif*1. This enables the CTX phage to use the host XerC/D recombinase to catalyze its integration into the chromosome.

Figure 8. Organization of IS608 and Overall Transposition Pathway (adapted from Guynet, 2009 (52)). (A) Organization. *tnpA* and *tnpB* open reading frames (light and dark arrows, respectively). Left end (LE) and right end (RE) (red and blue boxes, respectively).(B) Sequence of LE and RE. Sequence and secondary structures, IP_L and IP_R, at the LE and RE IS*608* are shown. Left and right tetranucleotide cleavage sites are boxed in black (C_L) and underlined in blue (C_R). C_R forms part of IS*608*, whereas C_L does not. B_L and B_R are shown on a red and blue background, respectively. Position of cleavage and of formation of the 5′ phosphotyrosine TnpA-DNA intermediate (vertical arrows).(C) Transposition pathway. (i) Schematized IS*608* with IP_L and IP_R, left (TTAC; C_L) and right (TCAA; C_R) cleavage sites. (ii) Formation of a single-strand transposon circle intermediate with abutted left and right ends. The transposon junction (TCAA) and donor joint (TTAC) are shown. (iii) Pairing with the target (TTAC) and cleavage (vertical arrows). (iv) Inserted transposon with new left and right flanks (dotted black lines).

Figure 9. Recombination between an attC site hairpin of an integron cassette and a

double-stranded attI site. The first recombination steps (a-c) between the folded attC site and the dsDNA attI site are identical to classical recombination steps catalyzed by other tyrosine recombinases. (b) Four integrase monomers bind to the core sites (the proper strand of the attC site being recognized through a specific binding with the extrahelical G). Binding to structural determinants makes the pink monomers inactive, leaving to the green monomers the possibility to realize the first strand exchange (c). The pseudo-holliday junction formed cannot be resolved by a second strand exchange as occurs with classical tyrosine recombinases. The current model is that replication is involved to solve the junction in a process that remains to be understood (d).

Figure 10. ssDNA: at the crossroads of horizontal gene transfer, the SOS response and genetic rearrangements. 1) Conjugation, transformation, phage infection and environmental stress lead to the production of ssDNA in the cell. 2) The RecA proteins binds ssDNA and triggers the self-cleavage of LexA (brown circles). 3) The SOS regulon is derepressed, recombinases are expressed (orange triangles), and DNA coiling is modified. 4) Increased supercoiling leads to cruciform formation. 5) Induction of IS transposition and integron recombination.6) ICE conjugation, lysogenic phages and natural competence are induced.

SUMMARY

Structured forms of DNA with intrastrand pairing are generated in several cellular processes and are involved in biological functions. These structures may arise on single-stranded DNA (ssDNA) produced during replication, bacterial conjugation, natural transformation or during viral infections. Furthermore, negatively supercoiled DNA can extrude inverted repeats as hairpins in structures called cruciforms. Whether they are on ssDNA or as cruciforms, hairpins can modify the access of proteins to DNA and, in some cases, they can be directly recognized by proteins. Folded DNA has been found to play an important role in replication, transcription regulation and recognition of the origins of transfer in conjugative elements. More recently, they were shown to be used as recombination sites. Many of these functions are found on mobile genetic elements likely to be single-stranded, including viruses, plasmids, transposons and integrons, thus giving some clues as to the manner in which they might have evolved. We review here, with special focus on prokaryotes, the functions in which DNA secondary structures play a role and the cellular processes giving rise to them. Finally, we attempt to shed light on the selective pressures leading to the acquisition of functions for DNA secondary structures.

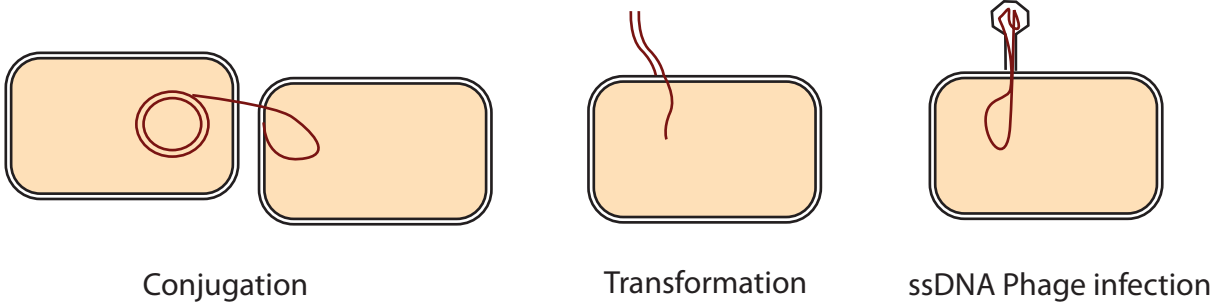


Figure 1. DNA uptake and production of ssDNA in the cell. The three mechanisms: conjugation, natural transformation and infection by ssDNA phage lead the production of large amount of ssDNA in the cell.

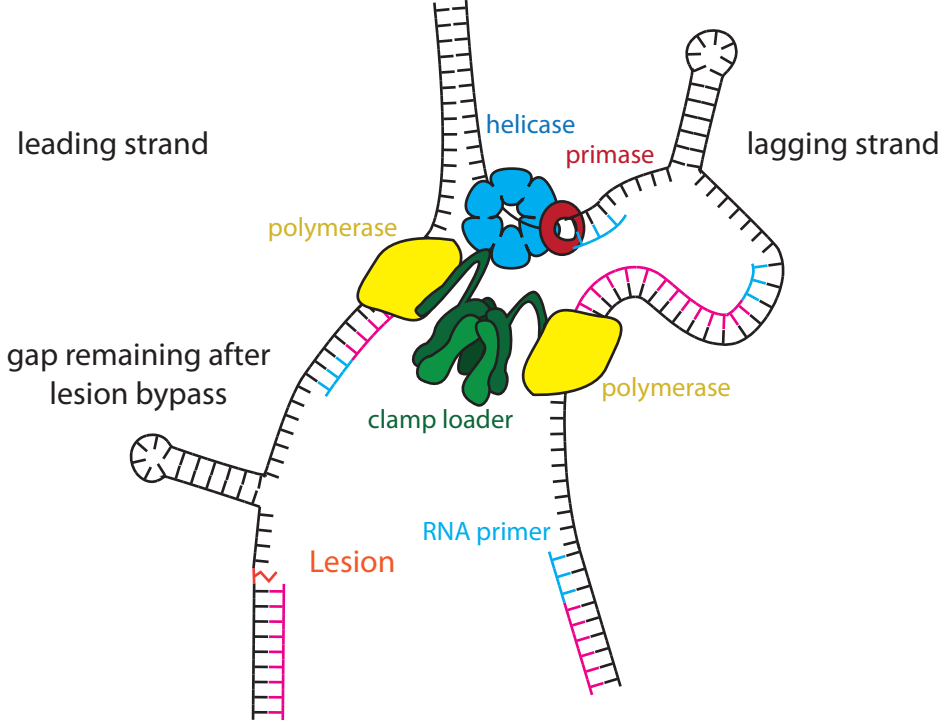


Figure 2. Hairpin formation during replication. Hairpins can fold on the ssDNA formed by the discontinuous replication of the lagging strand, or on ssDNA gaps remaining after lesion bypass.

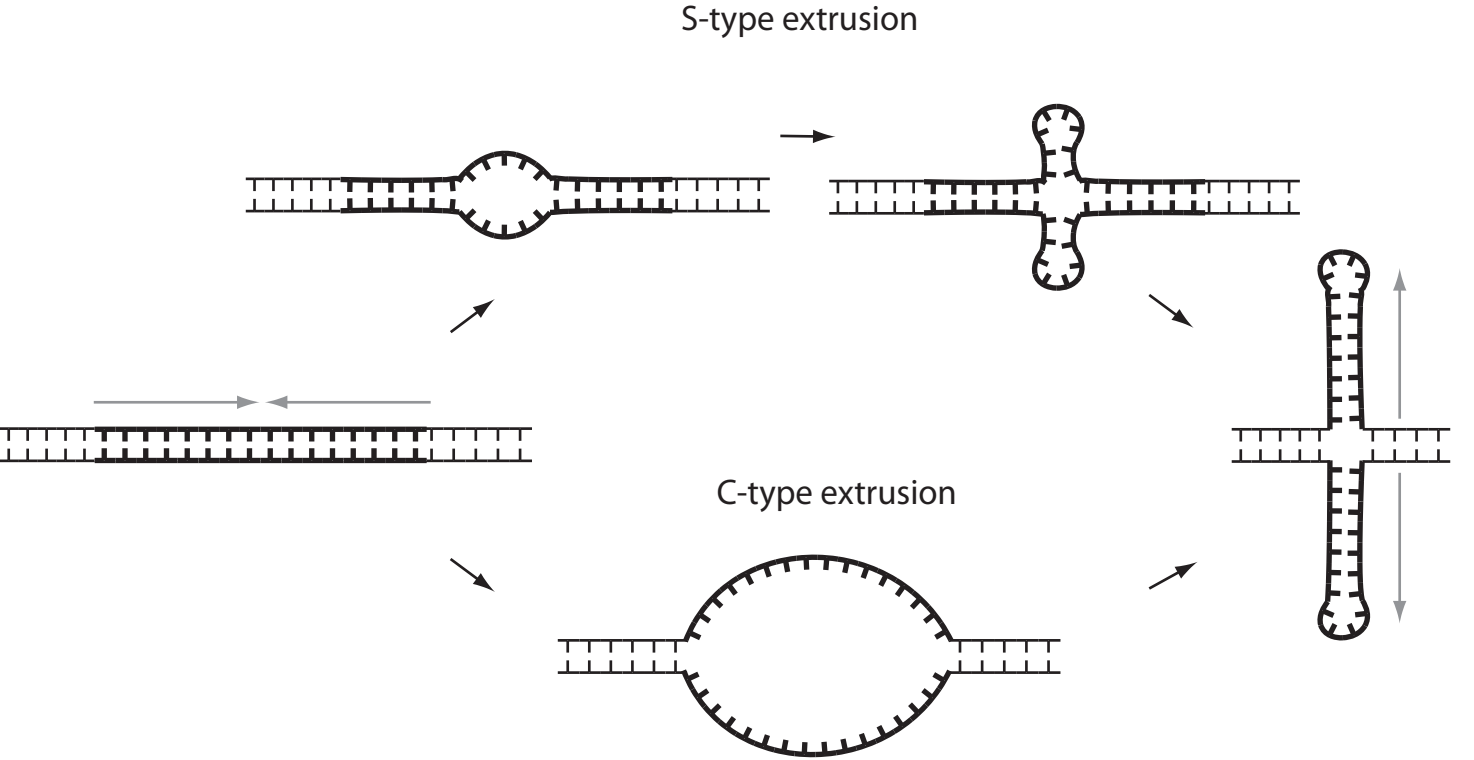


Figure 3. Mechanisms of cruciform extrusion. In the C-type pathway, a substantial region of dbDNA is denatured allowing the folding of the whole hairpins on both strands in one step. In the S-type pathway, a small region is denatured (~10bp) allowing the folding of a small hairpin that can then be elongated through branch migration.

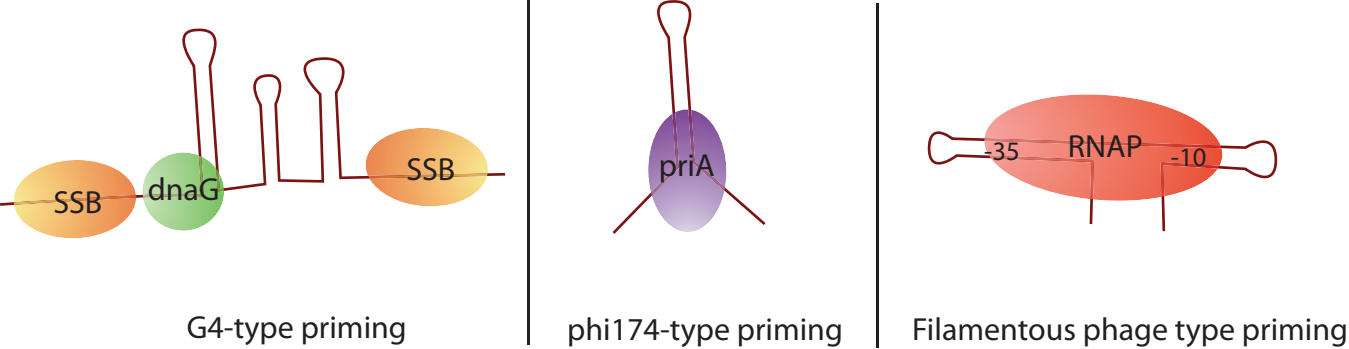


Figure 4. Priming of replication on ssDNA hairpins. G4-type priming: hairpins structure the region, directing the binding of SSB and allowing access to the dnaG primase. Phi174-type priming: a ssDNA hairpin forms a Y-fork recognized by PriA which directs the formation of a primosome. Filamentous phage type priming: an hairpin mimicking a promoter folds and is recognized by the RNA polymerase (RNAP), which synthesizes an RNA primer for replication.

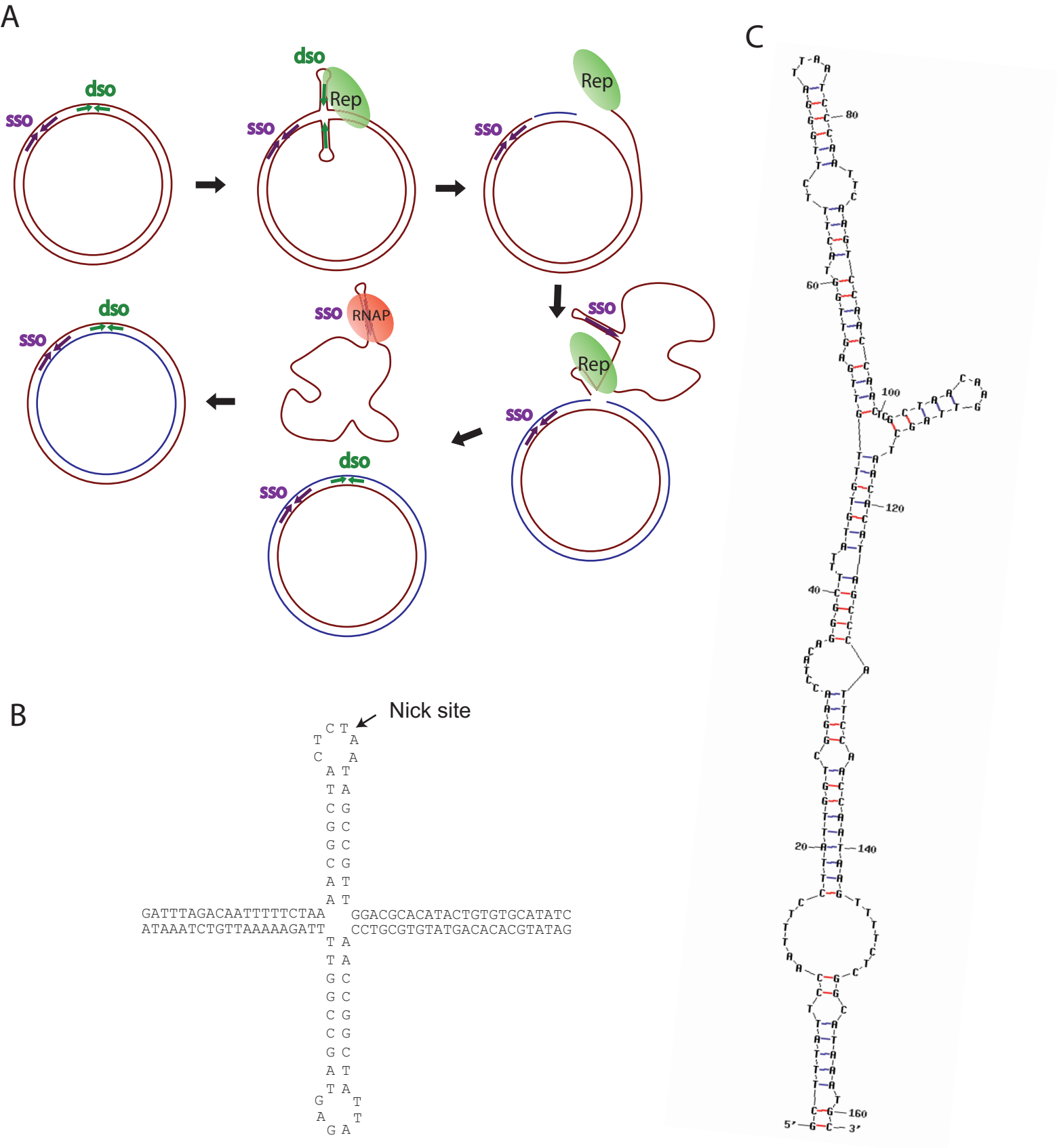


Figure 5. Rolling Circle Replication. A)The Rep protein binds an hairpin formed by double-stranded origin (dso) and extruded from dbDNA as a cruciform. Rep nicks DNA and covalently binds the 5′-end, leaving a 3′-end for replication to proceed. The leading strand is replicated while the lagging strand is extruded and remains single-stranded until the single-stranded origin (sso) is reached. The RNA polymerase (RNAP) binds the sso hairpin and synthesizes an RNA primer for replication. B) The pT181 dso in cruciform conformation. C) The pT181 sso as folded by the mFOLD software.

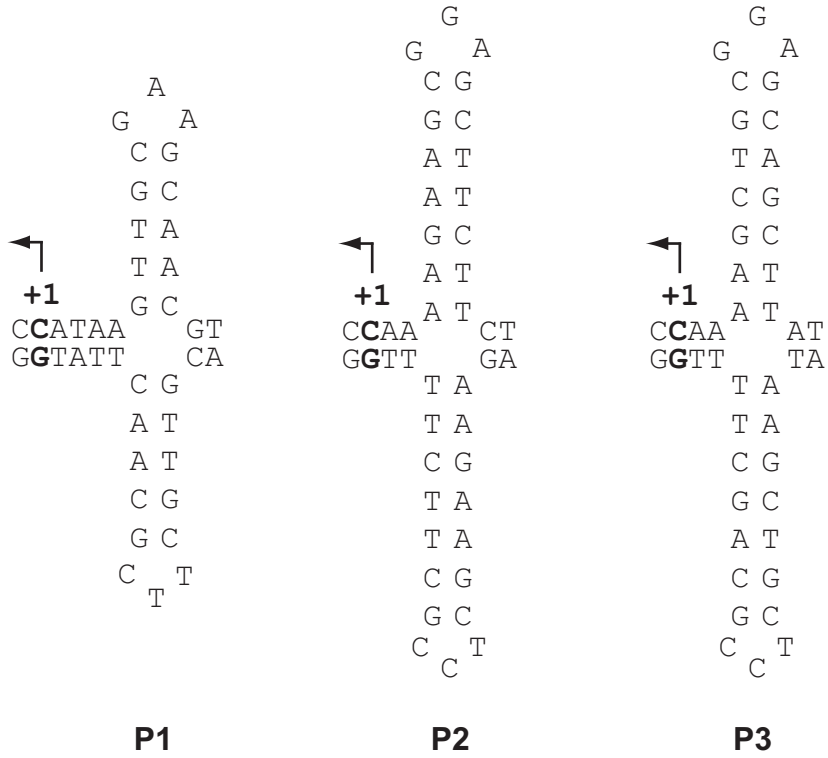


Figure 6. N4 virion hairpin promoters. The three promoters of N4 controlling the expression of the early genes as cruciform structures.

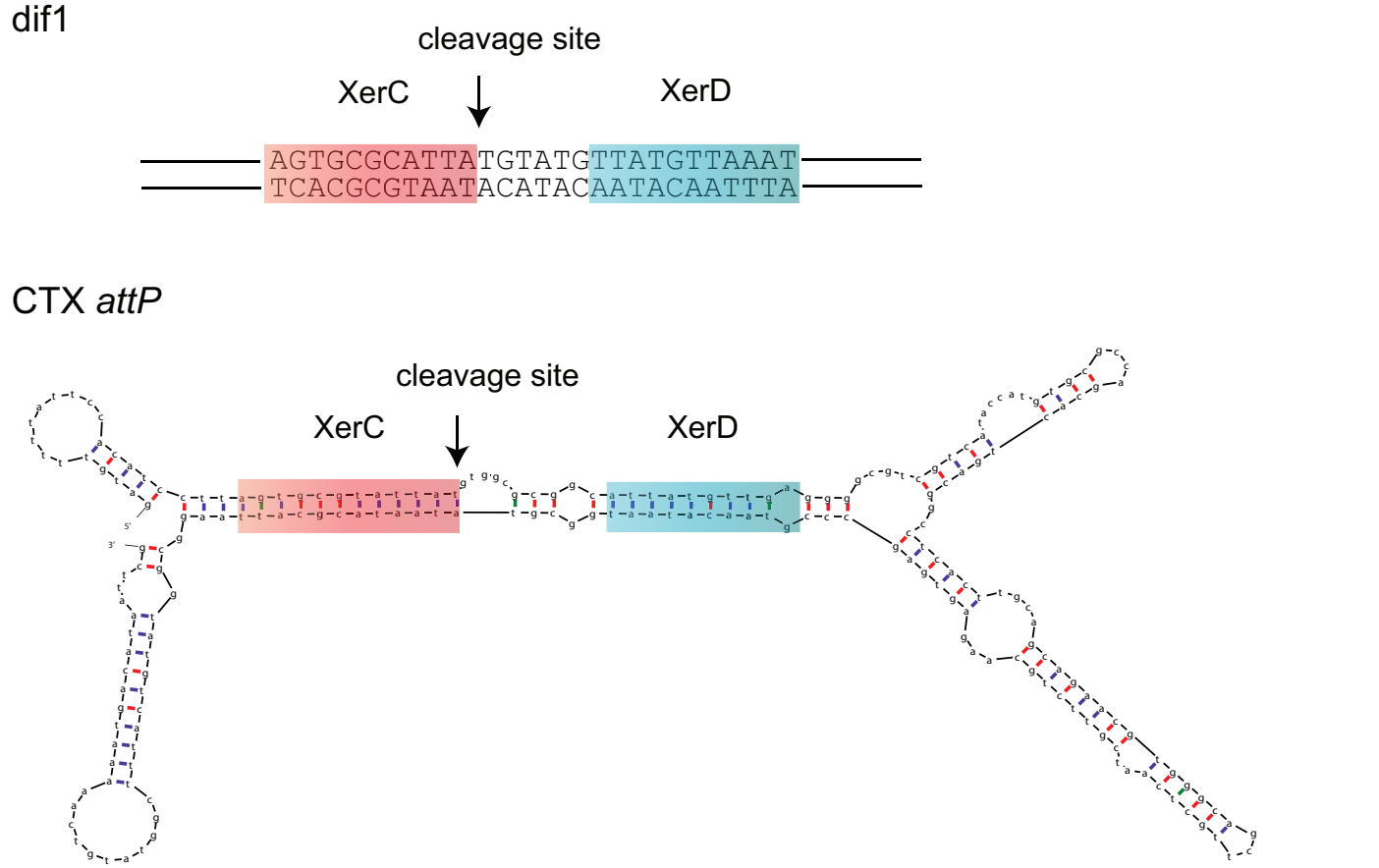


Figure 7. The *V. cholerae* chromosome I dif site and the CTX phage hairpin. The CTX *attP* region folds into a forked hairpin mimicking the *V. cholerae dif*1. This enables the CTX phage to use the host XerC/D recombinase to catalyze its integration into the chromosome.

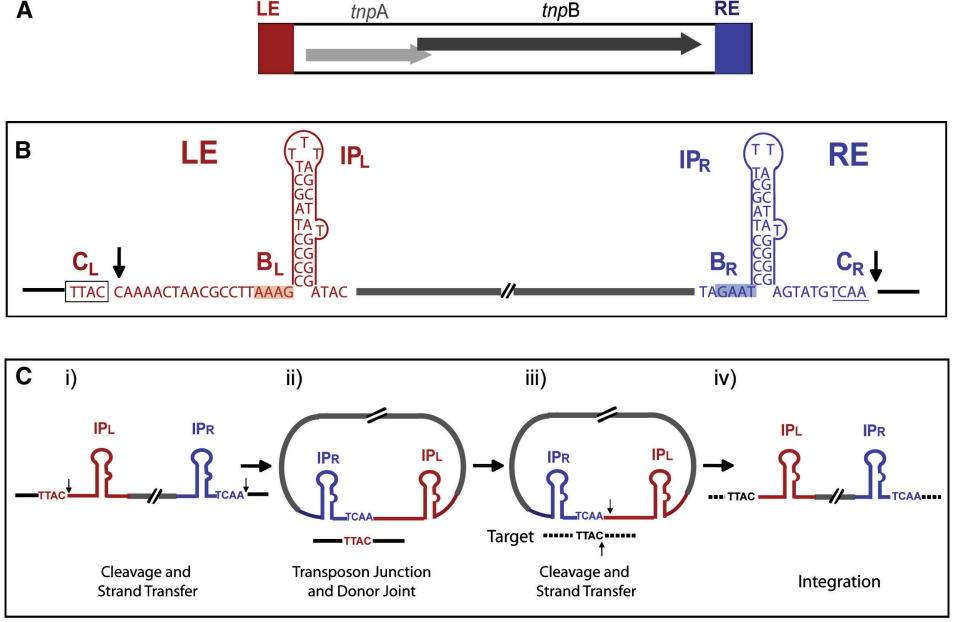


Figure 8. Organization of IS608 and Overall Transposition Pathway (adapted from Guynet, 2009 (52)). (A) Organization. *tnpA* and *tnpB* open reading frames (light and dark arrows, respectively). Left end (LE) and right end (RE) (red and blue boxes, respectively).(B) Sequence of LE and RE. Sequence and secondary structures, IP_L and IP_R, at the LE and RE IS*608* are shown. Left and right tetranucleotide cleavage sites are boxed in black (C_L) and underlined in blue (C_R). C_R forms part of IS*608*, whereas C_L does not. B_L and B_R are shown on a red and blue background, respectively. Position of cleavage and of formation of the 5′ phosphotyrosine TnpA-DNA intermediate (vertical arrows).(C) Transposition pathway. (i) Schematized IS*608* with IP_L and IP_R, left (TTAC; C_L) and right (TCAA; C_R) cleavage sites. (ii) Formation of a single-strand transposon circle intermediate with abutted left and right ends. The transposon junction (TCAA) and donor joint (TTAC) are shown. (iii) Pairing with the target (TTAC) and cleavage (vertical arrows). (iv) Inserted transposon with new left and right flanks (dotted black lines).

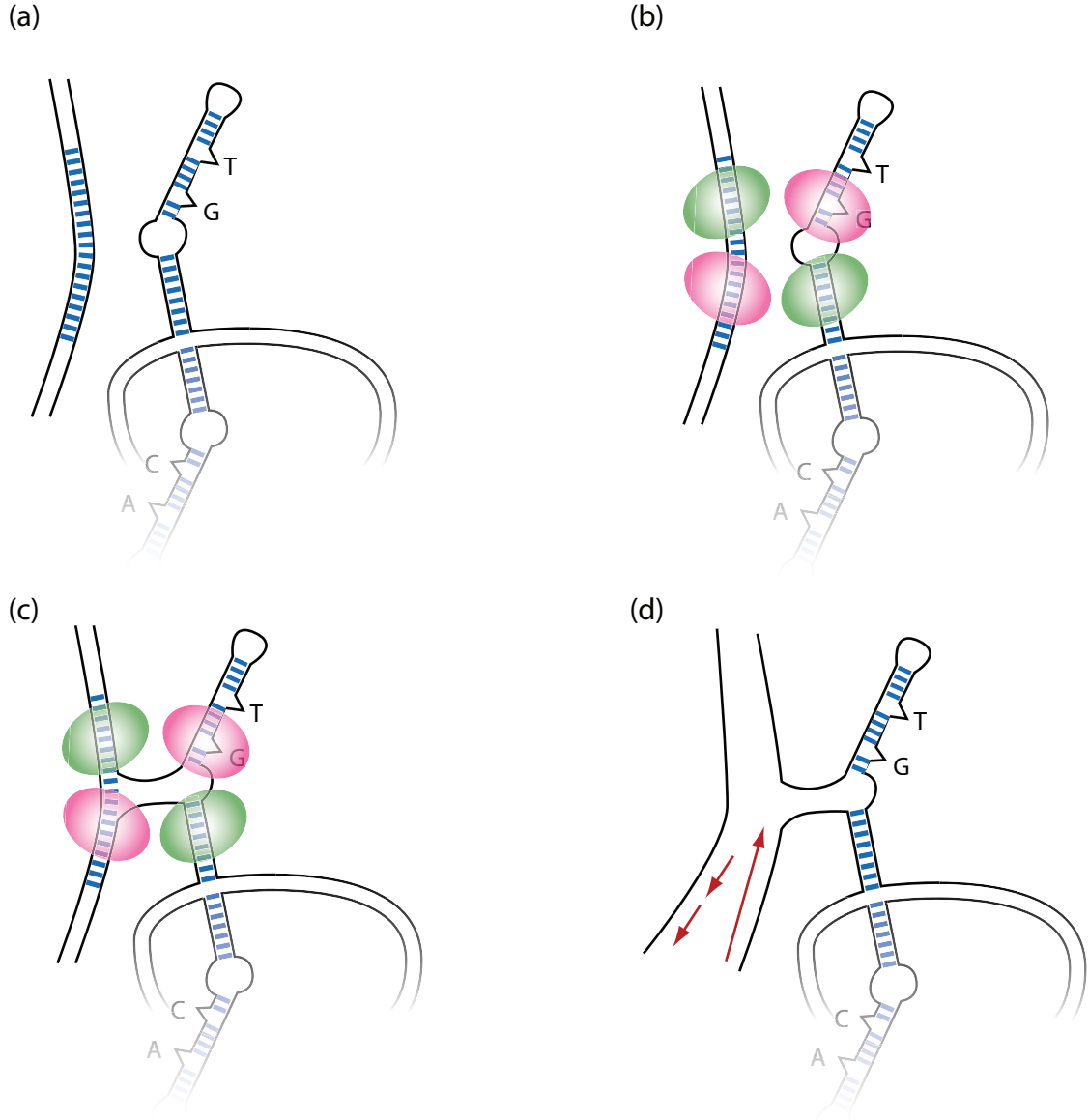
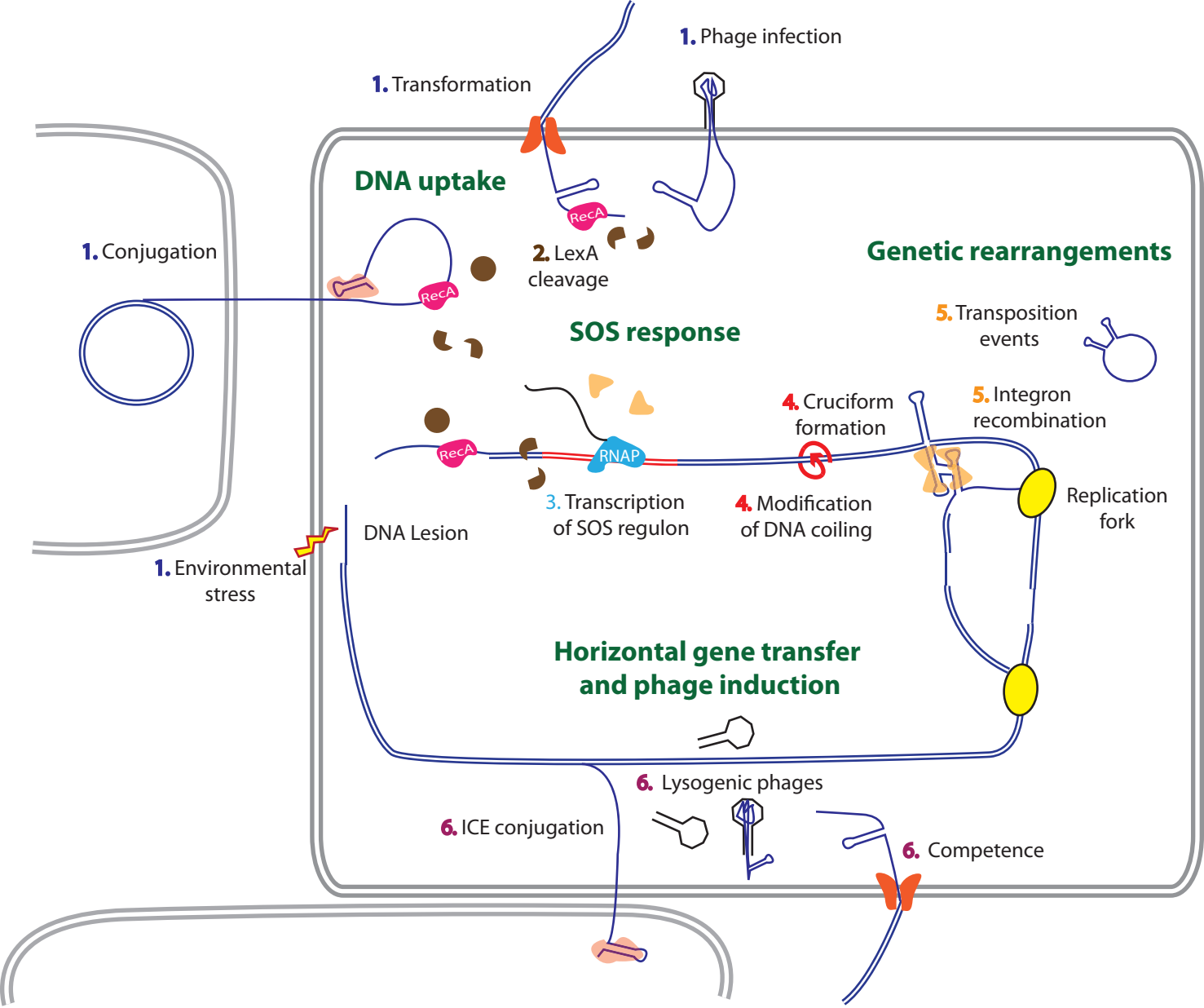


Figure 9. Recombination between an attC site hairpin of an integron cassette and a double-stranded attI site. The first recombination steps (a-c) between the folded attC site and the dsDNA attI site are identical to classical recombination steps catalyzed by other tyrosine recombinases. (b) Four integrase monomers bind to the core sites (the proper strand of the attC site being recognized through a specific binding with the extrahelical G). Binding to structural determinants makes the pink monomers inactive, leaving to the green monomers the possibility to realize the first strand exchange (c). The pseudo-holliday junction formed cannot be resolved by a second strand exchange as occurs with classical tyrosine recombinases. The current model is that replication is involved to solve the junction in a process that remains to be understood (d).



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