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Function and regulation of the bacillus subtilis addAB genes in homologous recombination

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Document Version

Publisher's PDF, also known as Version of record

Publication date:

1996

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Haijema, B. J. (1996). *Function and regulation of the bacillus subtilis addAB genes in homologous recombination*. s.n.

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Summary and general discussion

Homologous recombination is a biological process essential to all organisms, prokaryotes and eukaryotes, because it is involved in the generation of genetic diversity, the maintenance of genomic integrity and the proper segregation of chromosomes. The first part of chapter 1 gives a brief overview of our knowledge of the molecular mechanisms of homologous recombination derived from studies in the prokaryote *Escherichia coli*. This process has only been studied to some degree in the species *Bacillus subtilis*, as described in the second part of chapter 1. To date, in this Gram-positive, spore forming soil bacterium, 13 genes, including *addA* and *addB*, which are involved in the complex process of homologous recombination, have been identified. The products of these genes are involved in many cellular processes such as natural transformation, DNA repair, bacteriophage-mediated transduction and DNA repair.

The work, described in chapter 2 to 6, is mainly focused on the *B. subtilis* *addAB* genes and their gene products. The *B. subtilis* *addA* and *addB* genes encode the two subunits of the ATP-dependent deoxyribonuclease enzyme complex, which is involved homologous recombination and DNA repair. The heterodimeric enzyme is an ATP-dependent helicase and exonuclease.

Chapter 2 shows that the *B. subtilis* AddAB enzyme is the functional equivalent of the *E. coli* RecBCD enzyme, although no extended amino acid sequence similarity exists between the proteins. The introduction of the *addAB* genes into an *E. coli* *recBCD*⁻ strain nearly completely restored the viability, the ability to repair U.V. damaged DNA and recombination in conjugation. However, the *B. subtilis* AddAB enzyme did not show Chi-activity in phage lambda recombination. The individual *B. subtilis* Add proteins neither complemented *recB* nor *recC* mutations.

Chapter 3 and 4 communicate the characterization of AddAB enzymes, mutated in the ATP binding site of subunit A and B, respectively. Chapter 3 shows that the lysine to glycine substitution in the ATP binding site of AddA led to significantly reduced transformation with chromosomal DNA, cell viability, the capacity to repair DNA damage inflicted by U.V irradiation or mitomycin C treatment, and bacteriophage PBS-1 mediated transduction. These effects could be related to significantly reduced rates of ATP-dependent exonuclease- and helicase activities,

suggesting that at least one of the mutations had a marginal effect on these processes. The characterization of the wild type AddAB enzyme demonstrated that the lysine of subunit A is essential for the helicase- and exonuclease activity. The hydrolysis of ATP and not for the exonuclease activity is the corresponding lysine of subunit B.

Chapter 5 describes the characterization of the *B. subtilis* AddA. In this chapter it is shown that the *addA* gene product has helicase activity but not for the helicase- and exonuclease activity, an AddAB enzyme complex, AddA, could almost fully complement the *addB* gene product with respect to homologous recombination. The results obtained with those obtained in chapter 4 show that the *addB* exonuclease- activity, is essential for the function of AddA. AddA shows a high degree of functional similarity to the *E. coli* RecBCD enzyme. The *B. subtilis* AddA has a similar function in exonuclease activity.

Chapter 6 deals with the characterization of the *addB* genes. The *addB* genes are located in an overlapping promoter region. An overlap between the two open reading frames and a type promoter with a low, but functional, promoter competence development, a competence defect was observed. A direct interaction between the *addB* gene and the promoter region of *addA* was demonstrated in *in vitro* assays. These findings indicate a functional interaction between the establishment of the competence and the *addB* gene product in homologous recombination.

The transcription of the *addAB* genes is regulated. Chapter 7 demonstrates that the *addAB* genes are transcribed to its promoter upstream region. Chapter 8, in which it was demonstrated that the *addAB* promoter region, forcing the recombination, analyses demonstrated that C

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suggesting that at least one of these activities is involved in homologous recombination. A similar mutation in the ATP-binding site of subunit B had only marginal effects on these processes. Chapter 4 describes the purification and characterization of the wild type AddAB enzyme and the two mutant enzymes. It was demonstrated that the lysine of the ATP binding site of subunit AddA is essential for the helicase- and exonuclease activities of the enzyme, because it is required for the hydrolysis of ATP and not for the binding of ATP. No function could be attributed to the corresponding lysine of subunit B.

Chapter 5 describes the examination of the C-terminal region of subunit AddA. In this chapter it is shown that this region is required for the exonuclease activity but not for the helicase activity of the enzyme. Despite the lack of the exonuclease activity, an AddAB enzyme, containing a C-terminal truncated subunit A, could almost fully complement an *E. coli recBCD* and a *B. subtilis recBCD* mutant with respect to homologous recombination and DNA repair. These results, together with those obtained in chapter 3, suggest that the helicase-, but not the exonuclease- activity, is essential for these processes. The C-terminal region of AddA shows a high degree of homology with the C-terminal region of subunit RecB of the *E. coli RecBCD* enzyme, the functional equivalent of AddAB, suggesting a similar function in exonuclease activity for this region in RecB.

Chapter 6 deals with the transcriptional regulation of *addAB*. The *addA* and *addB* genes are located in an operon structure as was suggested by the limited overlap between the two open reading frames. The genes are transcribed from a σ^a type promoter with a low, constitutive level of expression. However, during competence development, a *comK*-dependent induction of *addAB* transcription was observed. A direct interaction between ComK, the competence transcription factor, and the promoter region of *addAB* was demonstrated by means of gel retardation assays. These findings indicate that a direct regulatory link exists between the establishment of the competent state and the synthesis of AddAB, required for recombination.

The transcription of *recA* is regulated in a similar way as that of *addAB*: chapter 7 demonstrates that ComK also stimulates the expression of *recA* by binding to its promoter upstream region. This binding was studied in more detail in chapter 8, in which it was demonstrated that at least 4 ComK molecules bind to the *recA* promoter region, forcing the region to bend. DNaseI and hydroxyl radical protection analyses demonstrated that ComK covers an extended region of the *recA* promoter

region, spanning almost 100 bp. Chapter 7 shows that the expression of *recA* is also regulated by DinR, the transcriptional repressor of the SOS DNA repair system. It was demonstrated that ComK and DinR can bind simultaneously to the *recA* promoter region, which suggest that the ComK-dependent transcriptional activation of *recA* during competence development is not caused by competition for binding between ComK and DinR.

In conclusion, the present results indicate that AddAB plays an important role in homologous recombination and DNA repair for which the helicase activity, but not the exonuclease activity, seems essential. Possibly, the enzyme plays an important role in the initiation stage of recombination: the unwinding of dsDNA molecules to generate ssDNA tails, which are essential substrates for further processing by the recombination machinery. However, the exact role of AddAB, in, for instance, the transformation process with chromosomal DNA, still remains to be established. This process can be examined by studying the fate of internalized DNA in various AddAB mutants.

Samenvatting en algemeen

Homologe recombinaat eukaryoten. Het is betrokke handhaven van de integriteit chromosomen. Het eerste mechanisme van homologe *Escherichia coli*. Het tweede bekend is over dit proces in vormende grondbacterie. T gevonden die betrokken zijn zijn betrokken bij verscheidene schade, transformatie, trans

Het werk, zoals dat be gericht op de *B. subtilis* specificeren de twee subeen complex. Het complex is be DNA schade.

Hoofdstuk 2 laat zien *E. coli* RecBCD complex is gebracht in een *E. coli* *recB* om DNA schade te herstellen. De AddAB eiwit bacteriofaag lambda recom staat een *E. coli* *recBCD* s

Hoofdstuk 3 en 4 be ofwel gemuteerd zijn in de A 3 laat zien dat de substitutie bindings plaats van subeen transformatie efficiëntie me herstellen en transductie me sterk verlaagde helicase en van deze activiteiten van k mutatie in de ATP bindings