

Keith

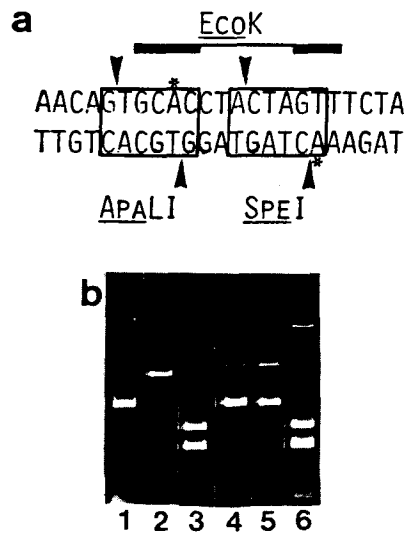
The sensitivity of DNA cleavage by *SpeI* and *ApaLI* to methylation by *M.EcoK*

Bernd Hofer

Gesellschaft für Biotechnologische Forschung mbH, Mascheroder Weg 1, D-3300 Braunschweig, FRG
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During work on site-directed mutagenesis of the human interleukin-2 gene an *EcoK* site (1) was created which overlapped recognition sequences for *SpeI* (1) and *ApaLI* (1) (Fig. 1a). Isolation of the DNA from m_K^+ strain DH1 (2) and m_K^- strain HB101 (3) and subsequent incubation with the two restriction endonucleases revealed that *EcoK* methylation completely or almost completely protected both DNA strands from cleavage by *SpeI*, but did not prevent cleavage of either strand by *ApaLI* (Fig. 1b). Thus, methylation of only one of the 5'-terminal A's of the *SpeI* site is sufficient to protect it against *SpeI*, whereas methylation of one of the two A's of the *ApaLI* sequence does not interfere with its cleavage by *ApaLI*.

Figure 1. a: Overlap of the *EcoK* site with the *ApaLI* and *SpeI* sites as created by site-directed mutagenesis. The *EcoK* heptanucleotide, separated by a 6 nt spacer, is overlined by bars. The A's modified by *M.EcoK* are marked with asterisks. The restriction sites are boxed; potential cleavage positions are indicated by arrows. b: Analysis of cleavage of the sequence shown in fig. 1a by *SpeI* and *ApaLI*. Lanes 1-3: unmethylated DNA, lanes 4-6: methylated DNA. Lanes 1 and 4: intact vector, lanes 2 and 5: vector incubated with *SpeI*, lanes 3 and 6: vector incubated with *ApaLI*.



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Nucleotide sequence of

Ye-Shih Ho, Adriann J.

Laboratory of Molecular Medicine, Duke University
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Glutathione p cells to protect mer isolated cDNA clon rat liver cDNA lit Alto, CA) with a s nucleotide residues hybridized clones bacteriophages. T showed that, simila the active site is e the underline). Th 86% homologous to

G TCATACCCAC GTGGATATTC ATA
GCC CCAGGGAGAT ACCCTGAGAC A
CCCTG AAAAAGCCAA CATCACAGGT

ATTITTTG AGTCCATAT CTTCTACA
Ala Gly Gly Glu Pro Val Ser
GCC GGC GGG GAG CCC GTG ACC

Asp Tyr Thr Glu Met Asn Asp
CAC TAC ACC GAA ATG AAT GAT

Glu Asn Gly Lys Asn Glu Glu
GAG AAT GGC AAG AAT GAA CAG

Cys Glu Val Asn Gly Glu Lys
TCC GAG GTG AAT GGT GAG AAG

Thr Asp Pro Lys Tyr Ile Ile
ACC GAC CCC AAG TAC ATC ATT

Pro Val Arg Arg Tyr Ser Arg
CCA GTG CCC AGA TAC ACC AG

GCCATTCCTG GATCTGGCC TTGG

A AATCCCTCA GATGGCCCT GG

Figure 1. Nucleotide s

Acknowledgement and RJR-Nabisco,

References:

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