Volume 11 Number 1 1983 Nucleic Acids Research

The effect of site specific methylation on restriction endonuclease cleavage (update)

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Introduction

I present here an update of the compilation published in 1981 in this journal on the effects of site specific methylation on restriction endonuclase cleavage (45). The amount of information available has increased by nearly 50% since that time.

Table 1 is organized by length of restriction endonuclease recognition sequence and then alphabetically by sequence. Isoschizomers are listed alphabetically by name. Only the effects of methylation at the N6 position of adenine and C5 of cytosine are considered. References to the purification of restriction enzymes and the determination of their recognition sequences can be found in R.J. Roberts review (43).

Notes

a) Crude extracts of M.Msp I methylate both cytosines in the Msp I recognition sequence to produce 5'mCmC G G 3' (29) However
3' G GmCmC 5'
an M.Msp I clone methylates only 5'mC C G G 3' (71).

b) Bst NI cuts dcm+ (CmCXGG) and M.Apy I (mCCXGG) methylated DNA (43). Bst NI also cuts DNA hemimethylated at both cytosines in one strand 5' mCmC X G G 3' (25)

c) Bst 1503 I is an isoschizomer of Bam HI. M.Bst 1503 I is reported to methylate at adenine and protect against both Bst 1503 I and Bam HI (36).

d) Endonucleases which do not totally cleave dam+ or dcm+ E.coli DNA are assumed to be inhibited by methylation at GmATC (14)(64) or CmCXGG (6)(42) respectively.

e) Brooks and Roberts have found that Sma I and Nci I cut (mCmCGG) methylated DNA. Possibly the second methylation site negates the effect of the CmCGG methylation (8).

f) R.Walder reports that mCCGG protects against Hpa II(71) However other authors observe cleavage of this sequence (39)(48)(63).

g) There is one report that Xma I cuts CCmCGGG (70).

0305-1048/83/1101-r169$2.00/0

table 1.

# denotes a known modification methylase specificity
* denotes a probable modification methylase specificity
J= A or C, K= G or T, N= A,C,G or T, R= A or G, Y= Cor T, Y= C or T, X= A or T, Z= G or C

Restriction Enzyme(65)	Restriction Sequence	Methylated Sequences cut	Methylated Sequences not cut	Effect of Methylation Unknown	References
Alu I	AGCT	?	AGmCT	mAGCT	25
Hap II	CCGG	?	CmCGG#	mCCGG	15,69
Hpa II	CCGG	mCCGG	CmCGG#	-----	15,39,69
Msp I	CCGG	CmCGG	mCCGG#(a)	-----	15,29,64,69,71
BstE III	GATC	?	GmATC(d)	GATmC	46,52
Dpn I	GATC	GmATC	GATC	(only cuts methylated DNA)	33
Dpn II	GATC	?	GmATC*	GATmC	33,52,68
FnuA II	GATC	?	GmATC(a)	GATmC	46,52
FnuC I	GATC	?	GmATC(d)	GATmC	52
FnuE I	GATC	GmATC	?	GATmC*	37,52
Mbo I	GATC	?	GmATC(d)	GATmC	13,23,42,52,62
Mno III	GATC	?	GmATC(d)	GATmC	46,52
Mos I	GATC	?	GmATC(d)	GATmC	52
Mph I	GATC	?	GmATC(d)	GATmC	52
Pfa I	GATC	GmATC	?	GATmC*	52,65
Sau 3A	GATC	GmATC	GATmC*	-----	13,15,44,51,52,62
Hha I	GCGC	-----	GmCGC# GCGmC	-----	15,38,40,61
BsuR I	GGCC	?	GGmCC#	GGCmC	26
Hae III	GGCC	GGCmC	GGmCC#	-----	38,39
Taq I	TCGA	TmCGA	TCGmA#	-----	25,44,64
Tth I	TCGA	TmCGA	TCGmA#	-----	56
Hin fI	GANTC	GANTmC	?	GmANTC*	25,48
Fnu4 HI	GCNGC	?	GmCNGG	GCNGmC	63
Sau 96	GGNCC	?	GGNCmC	GGNmCC	42,48
Aac I	CCXGG	CmCXGG	?	mCCXGG*	8
Apy I	CCXGG	CmCXGG	mCCXGG*	-----	11,43,51,52
Atu BI	CCXGG	?	CmCXGG(d)	mCCXGG	52,53
Atu II	CCXGG	?	CmCXGG(d)	mCCXGG	52
Bst NI	CCXGG	CmCXGG mCCXGG(b)	?	?	52,43
Eca II	CCXGG	?	CmCXGG(d)	mCCXGG	52
Ecl II	CCXGG	?	CmCXGG(d)	mCCXGG	52
Eco RII	CCXGG	mCCXGG	CmCXGG#	-----	6,7,42,43,52,47
Mph I	CCXGG	?	CmCXGG(d)	mCCXGG	30,52
Taq XI	CCXGG	mCCXGG	?	CmCXGG	16
Nci I	CCZGG	?	CmCZGG(e)	mCCZGG	43
Bby I	GCXGC	?	GmCXGC#	GCXGmC	27,67
Ava II	GGXCC	?	GGXCmC	GGXmCC	3,43
Eco PI	AGACC	?	AGmACC# AGAmCC AGACmC GGTmCT	mAGACC	2,28
Mbo II	GAAGA	?	GAAGmA C methylation	GmAAGA GAmAGA	3,25
Ava I	CYCGRG	?	CYmCGRY	mCYCGRG	5,15,31,43
Aos II	GRCGYC	?	GRmCGYC	GRCGYmC	25,64
Acc I	GTJKAC	?	GTJKmAC	GTJKAmC	44
Hind II	GTYRAC	GTYRAmC	GTYRmAC#	-----	25,54
Hae II	RGCGCY	?	RGmCGCY	RGCGmCY	15
Xho II	RGATCY	RGmATCY	RGATmCY*	-----	8

Hind III	AAGCTT	?	mAAGCTT# AAGmCTT	AmAGCTT	25,54
Bgl II	AGATCT	AGmATCT	AGATmCT	mAGATCT	4,8,13,49
Cla I	ATCGAT	?	ATCGmAT#	ATmCGAT mATCGAT	44
Pvu II	CAGCTG	?	C methylation	?	12
Sma I	CCCGGG	?	CCmCGGG(e)	CmCCGGG mCCCGGG	8,15,22,50
Xma I	CCCGGG	?	CCmCGGG CmCCGGG	mCCCGGG	8
Sac II	CCGCGG	?	C methylation	?	15
Pvu I	CGATCG	CGmATCG	CGATmCG	mCGATCG	8
Xor II	CGATCG	CGmATCG	CGATmCG	mCGATCG	8,15
Xma III	CGGCCG	?	CGGmCCG	mCGGCCG CGGCmCG	63
Xho I	CTCGAG	?	CTmCGAG CTCGmAG	mCTCGAG	15,44,64,8
Pst I	CTGCAG	?	C methylation	?	12,25
Sal PI	CTGCAG	?	C methylation	?	10
Eco RI	GAATTC	?	GAmATTC# GAATTmC	GmAATTC	14,24,17
Bam HI	GGATCC	GGATCmC GGmATCC	GGATmCC#	-----	8,13,27,39
Apa I	GGGCCC	?	GGGmCCC	GGGCmCC GGGCCmC	63
Sal I	GTCGAC	?	GTCGmAC GTmCGAC	GTCGAmC	8,15,44,64
Hpa I	GTTAAC	GTTAAmC	GTTAmAC#	GTTmAAC	8,25,72
Xba I	TCTAGA	?	TmCTAGA	TCTmAGA TCTAGmA	18
Atu CI	TGATCA	?	TGmATCA(d)	TGATmCA TGATCmA	28,52,58
Bcl I	TGATCA	TGATmCA	TGmATCA(d)	TGATCmA	4,8,28,52
Cpe I	TGATCA	?	TGmATCA(d)	TGATmCA TGATCmA	19,28,52
Bal I	TGGCCA	?	TGGmCCA	TGGCmCA TGGCCmA	63

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