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Cleavage Maps of Weakly Oncogenic Human Adenovirus Type 7 DNA by Restriction Endonuclease Bam HI and Sal I

Kouichi Yoshida, Kenji Sekikawa and Kei Fujinaga¹

Department of Molecular Biology, Cancer Research Institute Sapporo Medical College, Sapporo 060, Japan

SUMMARY

Weakly oncogenic human adenovirus type 7 DNA (Grider strain) was cleaved into ten and three specific fragments by the restriction endonuclease *Bam* HI and *Sal* I, respectively. These specific fragments were mapped on the adenovirus type 7 genome by analyzing partial digestion products and by the DNA-DNA hybridization.

INTRODUCTION

Restriction endonuclease (EndoR) have been used to obtain specific fragments of the human adenovirus (Ad) genome and study the transcription and translation of adenovirus DNA, and cell transformation by these fragments (1).

We previously reported that EndoR *Hind* III and *Eco* RI cleaved Ad 7 DNA into 10 and 2 specific fragments, respectively (10), and the *Hind* III-I•J fragments was used to transform rat embryo cells (9). These *Hind* III fragments of Ad 7 DNA have been also used to construct transcriptional maps of "early" mRNA in lytically infected cells and viral specific RNA in transformed cells on the genome of Ad 7 (manuscript in preparation).

In this study, the fragments of Ad 7 DNA cleaved by Bam HI and Sal I were mapped on the genome of Ad 7 by the analyzing partial digestion products and by the DNA-DNA hybridization.

METHODS AND MATERIALS

Virus and viral DNAs

The Grider strain of Ad 7 was grown in KB cells and virions were purified as described previously (3). Viral DNA was extracted from purified

^{1:} Author to whom reprint requests should be addressed.

virion by the method of Green and Pina (3, 4). To prepare \$\$^2P\$-labeled Ad 7 DNA, KB cells were infected in phosphate-free Eagle's minimum essential medium containing 100 \$\$\mu\$Ci/ml [\$^2P]\$ orthophosphate and 5% dialyzed calf serum, as described previously (10). The specific activity of Ad 7 [\$^2P]\$-DNA was $1-2\times10^6$ cpm/\$\$\$\mug.

Restriction endonuclease digestion and gel electrophoresis

Eco RI and Bam HI were purchased from Boehringer Mannheim. Sal I was obtained from New England Biolabs. Hind III was purified from Haemophilus influenzae Rd strain by the method of Lai and Nathans (6). Reaction buffers for each of the enzymes were as follows: Bam HI [6 mM Tris-HCl (pH 7.4), 6 mM MgCl₂, 6 mM β-mercaptoethanol]; Sal I [6 mM Tris-HCl (pH 7.9), 6 mM MgCl₂, 6 mM β-mercaptoethanol]; Hind III [10 mM Tris-HCl (pH 7.6), 7 mM MgCl₂, 7 mM KCl, 7 mM β-mercaptoethanol]; Eco RI [0.1 M Tris-HCl (pH 7.6), 10 mM MgCl₂, 50 mM NaCl]. One unit of these enzyme was defined as the minimum amount which could digest 1.0 μg of Ad 7 DNA at 37°C for 1 h. EndoR digestion and agarose gel electrophoresis were carried out as described previously (9, 10).

Hybridization and labeled probes

Hybridization was performed as follows: Sal I fragments of Ad 7 DNA were transferred to a nitrocellulose membrane filter after electrophoresis by the Southern's blotting technique (11) as described by Fujinaga et al (2). The Ad 7 Hind III fragment A and J were prepared as decribed previously (9) and labeled in vitro by nick translation (5) as described by Mackey et al (7). ³²P-labeled probes were annealed to Ad 7 Sal I fragments on a filter in 1 ml of 0.2 M Tris-HCl (pH 7.9), 0.6 M NaCl, 0.02 M EDTA, 0.5% SDS, and 50% (v/v) Formamide at 37°C for 40 h as described by Fujinaga et al (2). The filter was washed, air-dried, and autoradiographed.

RESULTS AND DISCUSSION

Ad 7 DNA was cleaved by Bam HI and fractionated by electrophoresis in 1.4% agarose. Figure 1 B shows a photograph of an ethidium bromidestained slab gel containing nine distinct Ad 7 Bam HI fragment bands. Molecular sizes were estimated from electrophoretic modility of each fragment using Ad 7 DNA fragments produced by Eco RI and Hind III, and Ad 12 DNA fragments produced by Eco RI as size markers (8, 10). Percentages of each fragment to the whole genome of Ad 7 were calculated from their molecular weights as follows: A (27.4%), B (22.6%), C (12.7%), D (9.3%), E (7.2%), F (3.4%), G (2.7%), H (2.0%), and I (1.4%). The plot of the relative [\$^2P\$] radioactivity versus percentages of each fragment to the whole genome

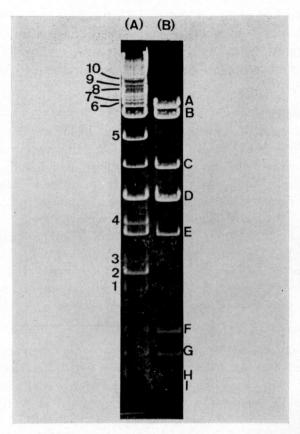


Fig. 1. Partial digestion of Ad7 DNA by EndoR Bam HI.

Ad 7 [32P] DNA (13 μ g) was partially cleaved with 6 units of Bam HI for 10 min at 37°C. The digestion products were electrophoresed in a 1.4% agarose slab gel (0.5×16×22 cm) at 50 V for 20 h. Five μ g of Ad 7 DNA was digested with 5 units of Bam HI for 1 h at 37°C and the digestion products were coelectrophoresed. Bands were labeled as A, B, C. D, E, F, G, H, and I for complete digestion fragments and as 1 to 10 for the partial digestion products.

Slot A.: Partiol digestion. Slot B: Complete digestion.

showed that fragment D was present in two-time molar amounts as the other fragments (data not shown).

The order of Ad 7 Bam HI fragments along the viral genome was determined by the analysis of partial digestion products. Ten partial digestion products (numbered in Fig. 1.) were recovered from the gel and purified by phenol extraction. The DNA was redigested with an excess amount of Bam HI and the digestion products were resolved by electrophoresis, followed by autoradiography (data not shown).

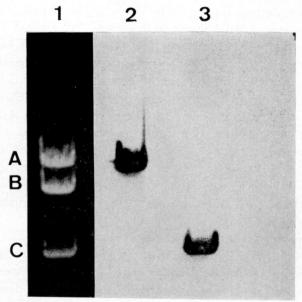


Fig. 2. Hybridization of ³²P-labeled Ad7 Hind III fragment A and J with Ad7 Sal I fragments.

Nick-translated Ad 7 Hind III fragment A (map position: 29.2–51.4) and J (4.3–8.1) were annealed to Ad 7 Sal I fragments on the nitrocellulose filter. Slot 1 represents 1.0 μg of Ad 7 Sal I fragments on 1.0% agarose gel and stained with ethidium bromide. The same amount of DNA was present in Slot 2 and 3. Slot 2 represents Ad 7 Sal I fragment hybridized with [32 P] Hind III fragment A (5×10 4 cpm). Slot 3 represents Ad 7 Sal I fragments hybridized with [32 P] Hind III fragment J (5×10 4 cpm).

Table 1. Cleavage of Partial Digestion Products with Bam HI

Partial digestion products	Complete cleavage products
1	G I
2	H F
3	F G
4	H F G
5	DE
6	I A
7	HFGIA
8	DCDE
9	I A B
10	врср
	HFGIABDCDE

Ten bands containing partial digestion products were cut from the gel shown in figure 1. The DNA was extracted from these gels as described previously (9) and redigested with *Bam* HI. The digestion products were resolved by electrophoresis and autoradiographed.

Table 1 summarizes the result of the analysis of partial digestion products. For instance, partial digestion fragment "1" yielded G and I; "2" yielded H and F; "3" yield F and G; "4" yielded H, F and G. From their overlappings in each partial digestion product, the order of the Bam HI fragments along the viral genome can be determined as H F G I A B D C D E.

 $Sal \, I$ digestion of Ad 7 DNA yields three fragments (Slot 1 in Fig. 2), and their molecular weights are 11.4×10^6 , 7.59×10^6 , and 4.00×10^6 corresponding to 49.6, 33.0, and 17.4% of the whole genome. The order of Ad 7 $Sal \, I$ fragments along the viral genome was determined by filter hybridization (Slot 2 and 3 in Fig. 2). Ad 7 $Hind \, III$ fragments A (map position: 29.2–51.4) and J (4.3–8.1) were labeled $in \, vitro$ by nick-translation and hybridized with three $Sal \, I$ fragments immobilized on nitrocellulose membrane filter.

Sal I fragments A and C hybridized only with Hind III fragments A and J, respectively. Thus, the order of the Sal I fragments must be CAB.

Cleavage maps of Ad 7 DNA by Bam HI and Sal I were constructed from above results, as shown in figure 3. Ad 7 Bam HI fragment H was located at the left hand end of the genome, because its DNA sequence was homologous with the Ad 7 Hind III fragment I (0.0-4.3). Similary, Ad 7 Sal I fragment C was located at the left hand end of the genome, because its DNA sequence was homologous with the Ad 7 Hind III fragment J (4.3-8.1) (Figure 2). The Sal I cleavage map of Ad 7 Grider strain thus determined agrees with that of Ad 7 Gomen strain reported by Tibbetts (12), but the Bam HI cleavage map does not. Some differences were observed between cleavage maps of above two strains of Ad 7 by Hind III and Eco RI (10).

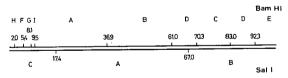


Fig. 3. Restriction endonuclease Bam HI and Sal I cleavage maps of Ad7 DNA.

Bam HI and Sal I cleavage sites on Ad 7 DNA were shown on the horizontal line. Sites of cleavage are indicated by vertical lines and numerial coordinates, and letters give the nomenclature of each cleavage pattern.

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