# RESTRICTION ENDONUCLEASE ANALYSIS OF THE DNA OF $RICKETTSIA\ PROWAZEKII\ VACCINE\ STRAIN\ E$ AND ITS REVERTANT<sup>1</sup>

N. M. BALAEVA, E. B. RYDKINA, M. I. ARTEMIEV, V. F. IGNATOVICH

The N. F. Gamaleya Research Institute of Epidemiology and Microbiology, U.S.S.R. Academy of Medical Sciences, 123098 Moscow, U.S.S.R.

Received June 15, 1988

Summary. — The DNA of Rickettsia prowazekii vaccine strain E was analysed by restriction analysis with 17 endonucleases in comparison with its virulent revertant — Evir and the virulent reference strain Breinl. The DNA of cloned and uncloned strains showed identical restriction endonuclease patterns. In spite of stable differences in virulence, strains E and Evir displayed a totally identical DNA cleavage pattern indicating the absence of marked structural differences between their genomes. On the other hand 9 endonucleases showed differences in the restrictograms of the DNA strain Breinl as compared with strains E and Evir.

Key words: variability; Rickettsia prowazekii; weakly pathogenic strain E; virulent revertant strain Evir; restriction endonuclease analysis of DNA

## Introduction

Low virulent strain E of *Rickettsia prowazekii* used for vaccination is a batch empirically selected in the course of chick embryos (CE) passages of the virulent strain (Clavero and Perez-Gallardo, 1944; Perez-Gallardo, 1963). The attenuation of stran E is known to be unstable and dependent on the cultivation conditions. Low pathogenicity of strain E is preserved in the course of passages in CE. The passage of strain E in weakly susceptible albino mice (intranasal inoculation) and guinea pigs (intraperitoneal inoculation), leads to an irreversible increase of its virulence (Balaeva, 1969; Balaeva and Nikolskaya, 1973a,b; Kazár et al., 1973). This rise in virulence occurred in human amnion cells (Ignatovich, 1975; Balaeva et al., 1976), as well as upon successive passages in clothes lice and then in CE (Balaeva et al., 1976). The mechanism of attenuation and reversion of the virulence of Rickettsia strain E is unclear. It should be noted that strain E rickettsiae are similar to the virulent strain with respect to the toxic and haemolytic activities, the presence of a capsule and cell penetration characteristics

Reported at the World Conference on Rickettsiology in Palermo, Italy, June 21-28, 1987

(Pshenichnov et al., 1976; Perez-Gallardo and Fox, 1948; Silverman and Wisseman, 1978; Winkler and Miller, 1980). The differences between them are in the inability of strain E to multiply in the cytoplasm of phagocytic cells (Gambrill and Wisseman, 1973; Turco and Winkler, 1982; Winkler and Daugherty, 1983). Differences were described in electrophoretic mobility of some proteins and in the DNA cleavage pattern by endonucleases (Oaks et al., 1981; Regnery et al., 1983, 1985).

The purpose of the present paper was to compare the genome of isogenic strains: the weakly pathogenic strain E and its virulent revertant strain Evir, produced by passaging in the lungs of albino mice. The total DNA has been investigated by restriction endonucleases with simultaneous analysis of the

DNA of reference virulent strain Breinl of Rickettsia prowazekii.

## Materials and Methods

Rickettsiae. Three strains of Rickettsia prowazekii have been studied: E, Evir and Breinl. Both standard passage variants of the strains and cloned variants were used. The cloning was carried out by plaque method and by limiting dilutions method in CE. Characteristics of the strains are

Table 1. The Rickettsia prowazekii strains

Strain	Passage history				
	Uncloned culture	Cloned culture			
E	Isolated by Clavero and Perez-Gallardo (1944) Obtained from Prof. Wisseman (U.S.A.) in 1969; underwent 270 passages in CE				
E	282-285 passages in CE	278 passages in CE + 1 passage in tissue culture (cloning by plaque method) + 6 passages in CE			
Evir	Prepared by 13 passages in albino mice lungs from strain E (obtained from the U.S.A. in 1969) by Balaeva (1971)				
	7 passages in CE	13 passages in CE + 3 passages in CE in li- miting dilutions (clo- ning) + 1 passage in CE			
Breinl	Isolated by Wolbach <i>et al.</i> (1922); passaged in guinea pigs (passage history unknown)				
	134 passages in CE	9 passages in CE + 3 passages in CE in limiting dilutions (cloning) + 1 passage in CE			

given in Table 1. Yolk sacs from recently died CE that were found to have the greatest amount of rickettsiae were collected and kept at -60°. They were inactivated with 0.1 % formalin at

6 °C for 24 hr (Regnery et al., 1983).

Purification of rickettsiae from CE tissues. The inactivated rickettsiae were purified by differential centrifugation and verografin density gradient (76 % verografin, Spofa, Č.S.S.R.) using a somewhat modified technique of Weiss et al. (1975). At the first step K36 was used as solvent (Weiss et al., 1967). In the second step, the rickettsial suspension was layered over sucrose verografin solution in K36 (30 % sucrose and 7.6 % verografin) and centrifuged at 22 000 × g for 1 hr. The pellet was resuspended in K36 and recentrifuged. At the third stage, discontinuous verografin gradient (20, 30, 37.5, 39, 45 %) was used. Centrifugation was carried out for 1 hr at 87 000 × g (VAK-25 centrifuge, G.D.R.) bucket-rotor 3312, Beckman tubes or the rotor SW 25.1. The rickettsiae formed two layers at 37.5 and 39 % levels. The upper and lower layers were collected, the verografin was removed by washing in K36 and the centrifugation in verografin gradient was repeated. Then verografin was removed by washing in K36, the latter were resuspended in SSC buffer.

Isolation of rickettsial DNA. Total rickettsial DNA was isolated according to the method of Priefer et al. (1984). Purified rickettsial cells were diluted to the density equal to OD 5 at wavelength 440 nm. Proteinase K (Serva, F.R.G.) was then added to a final concentration of 250 µg/ml and 10 % sarcosyl (N-lauroylsarcosine, Sigma, U.S.A.) to at final concentration of 0.5 %. The mixture was incubated for 1 hr at 50 °C and then for 15 hr at 37 °C. The lysate was deproteinized 2 or 3 times with phenol and then 2 times more with a mixture of chloroform and isoamyl alcohol (24:1). The DNA was precipitated by addition of 0.54 volume of isopropanol in the presence of 0.3 mol/l sodium acetate at room temperature for 15 min. The DNA pellet was rinsed 3 to 5 times with cooled ethanol (70 %) and dissolved in TE buffer, pH 8 at

4 °C for 18 hr.

Restriction endonuclease digestion and electrophoresis. Restriction analysis was carried out as recommended by Maniatis et al. (1982) under standard conditions: 1 unit of enzyme was used to cleavage 1  $\mu$ g DNA at 37 °C for 2 hr with subsequent inactivation of the enzyme for 10 min at 65 °C.

Table 2. Comparison of the restrictograms of Rickettsia prowazekii strain Breinl and of group E strains (E and Evir)

Restrictase	Number of visually discernible DNA bands			Range of fragment distribu-	Size of additional fragments (tnp)	
	Breinl	E	Evir	tion (tnp)	Breinl	E, Evir
BamHI	8	9	9	7 - 50	*	9.5
BglI	9	9	9	10 - 50	20	23
Cfr13I	36	35	35	1 - 15	8	_
EcoRI	40	41	41	2 - 25	_	18
HindIII	39	38	38	1 - 15	9	
MspI	50	50	50	0.5 - 15	9	8
MvaI	46	45	45	1 - 20	18	
PstI	50	51	51	1 - 30	15	20; 16
XhoI	12	13	13	6 - 50		15
BcnI	19	19	19	8 - 50	_	- 1000
BspRI	32	32	32	1 - 30	_	
CfrI	30	30	30	2 - 25	-	_
Cfr91	1	1	1	30		
Eco81I	21	21	21	5 - 25	BING AL LINE	VIIII LINE
PvuII	44	44	44	2 - 30	- 100 - 100	
SalI	3	3	3	10-30	_	-
SmaI	1	1	1	30 - 40	_	_

<sup>\*</sup> no additional fragment

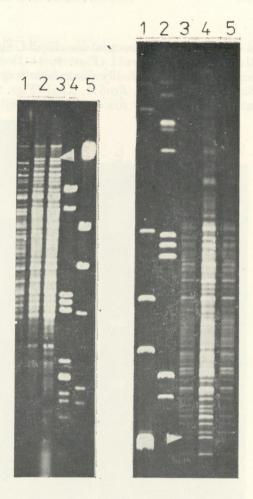


Fig. 1.

Restrictograms of Rickettsia prowazekii

DNA cleaved by PstI endonuclease

In the left — DNA of cloned strains, in the right — DNA of uncloned strains. Tracks 1, 2, and 3 — DNA of strains Breinl, Evir, E, respectively, cleaved by PstI; track 4 — phage  $\lambda$  DNA cleaved by PstI; track 5 — phage  $\lambda$  DNA cleaved by HindIII.

Here and thereafter the arrows indicate the additional DNA fragments. Cleavage and electrophoresis conditions are described in Materials and Methods.

The following restrictases were used: BcnI, BspRI, CfrI, Cfr91, Cfr13I, EcoRI, EcoRI, (SauI), HindIII, MspI, MvaI, PstI, PvuII, SalI, SmaI, XhoI, CfuI (DpnI), Sau3A ("Enzyme" Manufacturers, Vilnius, U.S.S.R.) as well as BamHI, BglI (Serva, F.R.G.).

Electrophoretic separation of DNA fragments was carried out in horizontal 0.6 % agarose gels (agarose type II, Sigma U.S.A.), first at 5 V/cm for 4 to 6 hr and then at 1 or 2 V/cm for 16-18 hr in tris-acetate buffer. Phage  $\lambda$  DNA (native and HindIII-cleaved) was used as a molecular standard.

The gels were stained with ethidium bromide (Sigma U.S.A.) They were photographed with Zenith E camera with orange light filter, film Micrat 300 and a UV radiation source (Desaga, F.R.G.).

#### Results

Each of the seventeen most commonly used restriction endonucleases yielded a characteristic and reproducible cleavage pattern (Figs. 1—10). The data of the analysis of restrictograms are presented in Table 2.

It can be seen that restrictases BspRI, CfrI, CfrI3I, EcoRI, HindIII, MspI, MvaI, PstI, and PvuII (Figs. 1; 4—7) cleaved the rickettsial DNA into a larger number of visually discernible fragments (from 30 to 51). Restrictases BamHI, BcnI, BglI, Eco81I, XhoI (Figs. 2, 3, 8) cleaved the rickettsial DNA into 8 to 21 visually discernible fragments. Cleavage with restrictases Cfr91,

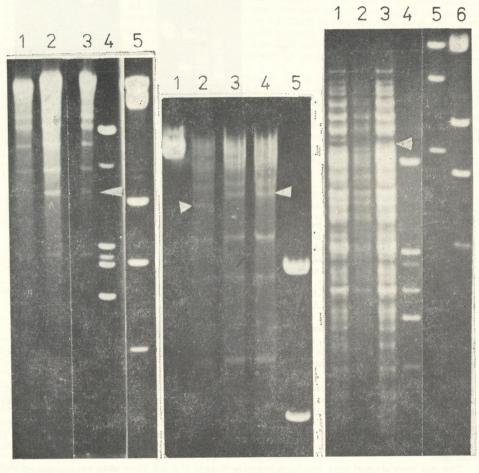


Fig. 2.

Fig. 3.

Fig. 4.

Fig. 2. Restrictograms of Rickettsia prowazekii cleaved by endonuclease BamHI Tracks 1, 2, 3, and 4 — the DNA of strains Breinl, Evir, E, and phage λ, respectively, cleaved by BamHI; track 5 — phage λ DNA cleaved by HindIII.

Fig. 3. Restrictograms of Rickettsia prowazekii DNA cleaved by endonuclease BglI

Track 1 — phage  $\lambda$  DNA (native), tracks 2, 3, 4, 5 — the DNA of strains Breinl, Evir, E, phage  $\lambda$ , respectively, cleaved by BglI.

Fig. 4. Restrictograms of Rickettsia prowazekii cleaved by endonuclease CfrI31

Tracks 1, 2, 3, 4 — DNA of strains Breinl, Evir, E, and phage  $\lambda$ , respectively, cleaved by CfrI31; tracks 5 and 6 — phage  $\lambda$  DNA cleaved by Eco81I and HindIII, respectively.

SalI, and SmaI yielded only a small number of fragments (Fig. 9). These data have been confirmed (Wood et al., 1984).

Restrictograms of the DNA of both cloned strains of Rickettsia prowazekii



Fig. 5. Fig. 6. Fig. 7.

Fig. 5. Restrictograms of Rickettsia prowazekii DNA cleaved by endonuclease EcoRI Track 1 — phage λ DNA (native); tracks 2, 3, 4, 5 — DNA of strains Breinl, Evir, E, phage λ, cleaved by EcoRI, respectively.

Fig. 6. Restrictograms of Rickettsia prowazekii DNA cleaved by endonuclease HindIII Tracks 1, 2, 3, 4 — DNA of strains Breinl, Evir, E, phage λ, respectively, cleaved by HindIII; track 5 — phage λ DNA (native).

Fig. 7. Restrictograms of Rickettsia prowazekii cleaved by endonucleases MvaI and MspI Tracks 1, 2, 3, 4 — DNA of strains Breinl, Evir, E, phage λ, respectively, cleaved by MvaI; tracks 5, 6, 7, 8 — DNA of strains Breinl, Evir, E, phage λ cleaved by MspI, respectively; track 9 — phage λ Dna cleaved by HindIII.

and those continuously passaged under standard conditions were totally identical with all the restrictases used (Fig. 1). It should be noted that the passage history of the cloned strain Breinl and of the uncloned one differed greatly, by more than 100 passages in CE (Table 1). The analysis of the restrictograms has shown identical DNA restriction patterns for strains E and Evir with all the 17 restrictases tested (Figs. 1—9, Table 2).

Strain Breinl appeared to be different from the group E strains (E and Evir) with respect to restriction patterns by 9 restrictases out of 17: PstI

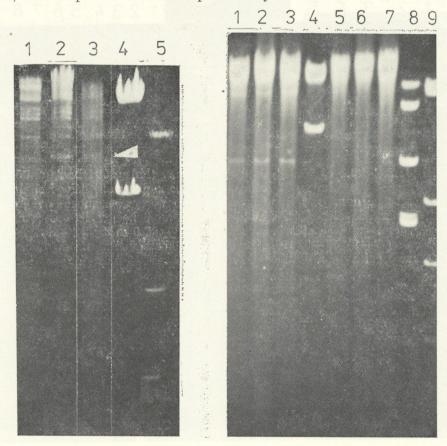


Fig. 8.

Fig. 9,

Fig. 8. Restrictograms of Rickettsia prowazekii cleaved by endonuclease XhoI Tracks 1, 2, 3, 4 — DNA of strains Breinl, Evir, E, phage λ, respectively, cleaved by XhoI; track 5 — phage λ DNA cleaved by HindIII.

Fig. 9. Restrictograms of Rickettsia prowazekii DNA cleaved by endonucleases SalI and SmaI Tracks 1, 2, 3, 4 — DNA of strains Breinl, Evir, E, phage λ, respectively, cleaved by SalI; tracks 5, 6, 7, 8 — DNA of strains Breinl, Evir, E, phage λ, respectively, cleaved by SmaI; track 9 — phage λ DNA cleaved by HindIII.

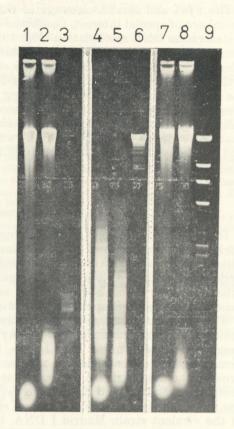


Fig. 10.

Restrictograms of Rickettsia prowazekii cleaved by Sau3A and CfuI

Tracks 1, 2 — DNA of strains Evir and Breinl (native); tracks 3, 4, 5 — DNA of phage λ, strains Evir, Breinl, respectively, cleaved by Sau3A; tracks 6, 7, 8 — DNA of phage λ, strains Evir, Breinl, respectively, cleaved by CfuI; track 9 — phage λ DNA cleaved by

HindIII.

(Fig. 1), BamHI (Fig. 2), BgII (Fig. 3), Cfr13I (Fig. 4), EcoRI (Fig. 5), HindIII (Fig. 6), MspI, MvaI (Fig. 7), XhoI (Fig. 8). In all cases these differences concerned 1 or 2 bands in the restrictogram and were in the range of 8 to 20 thousand nucleotide pairs (tnp, Table 2). Thus, for example, strain Breinl was found after BqII cleavage to have an additional band in the 20 tnp range found neither at E nor at Evir (Fig. 3); this band was in 9 tnp range by HindIII cleavage (Fig. 6). By Cfr13I cleavage it was in the 8 tnp range (Fig. 4), by MspI — in the 9 tnp range (Fig. 7), by MvaI — in the 18 tnp range (Fig. 7), and with PstI — in the 15 tnp range (Fig. 1). Group E strains (E and Evir) also had an additional band (about 9.5 tnp) not found in strain Breinl digest after the cleavage with BamHI (Fig. 2), by BglI the additional band was about 23 tnp (Fig. 3), by EcoRI about 18 tnp (Fig. 5), by MspI — 8 tnp (Fig. 7), by PstI about 20 and 16 tnp, respectively (Fig. 1), and by XhoI - 15 tnp (Fig. 8). The data obtained with BamHI were also confirmed by others: during cleavage of the DNA strain Breinl and strain E DNA with BamHI an additional band of about 9.55 tnp was found in the strain E digests (Wood et al., 1984; Regnery et al., 1985).

The CfuI and Sau3A cleavage of rickettsial DNA from strains Evir and Breinl are of special interest. Combined application of these restrictases helps to determine DNA methylation (Fig. 10) as they recognize the same sequence 5'... GATC ... 3'. but CfuI cleaves this sequence only if it is methylated in adenine 5'... GATC ... 3', (Maniatis et al., 1982; Kessler et al., 1985). The action of restrictase Sau3A is independent of methylation. The character of the cleavage of the DNA of strains Evir and Breinl with Sau3A indicated the presence of a large amount of sequences 5'... GATC ...3' in the rickettsial DNA (Fig. 10, tracks 4 and 5). The absence of cleavage with CfuI showed that the sequence 5'... GATC ...3' was not methylated (Fig. 10, tracks 7 and 8). Hence, Rickettsia prowazekii do not possess a methylase activity with a site-specificity similar to that of dam-methylase of Escherichia coli (Hattman et al., 1978).

## Discussion

It should be noted that the restrictograms of the DNA of cloned strains of *Rickettsia prowazekii* and those continuously passaged under standard conditions are totally identical. Thus, such rickettsial DNA probably does not undergo variations in the course of passages. This result was confirmed by others (Regnery and Spruill, 1984) and is of methodological importance

for the analysis of Rickettsia prowazekii DNA cleavage.

The genomes of isogenic strains E and Evir failed to reveal any differences between their restrictograms with any of the 17 restrictases tested. It has been shown that strains E and Evir, though showing stable differences in virulence, do not have marked genetic structural differences. These findings provide the first evidence for isogenicity of the weakly pathogenic *Rickettsia prowazekii* strain E and its virulent revertant strain Evir. They also confirm the biological data on the isolation of strain Evir (Balayeva, 1971). Cleavage of the virulent strain Madrid I DNA, the parent strain of strain E (Clavero and Perez-Gallardo, 1944; Perez-Gallardo, 1963) would be of value for the study of the variability of the weakly pathogenic *Rickettsia prowazekii* strain E.

The differences between restrictograms of strain Breinl and group E strains (E and Evir) have been observed during cleavage with 9 endonucleases. Up to the present, evidence for the differences between strain E and strain Breinl has been obtained with restrictases SacI and BamHI (Regnery et al., 1983, 1985; Wood et al., 1984). We have detected an additional fragment in the strain E cleavage pattern with BamHI and the same additional fragment (about 9 tnp) in the strain Evir isogenic to strain E. Complete identity of restrictograms of isogenic strains E and Evir which, however, differed in virulence, and their differences from reference strain Breinl seemed

to reflect the strain peculiarities unrelated to virulence.

It should be noted that differences in DNA restriction between strain Breinl and group E strains (E and Evir) only concern 1 or 2 fragments, whereas in general the restriction patterns of all three strains show a marked similarity. This confirms the genetic conservation of the genome of *Rickettsia* 

prowazekii described in previous papers (Regnery and Spruill, 1984; Wood et al., 1984; Regnery et al., 1983, 1985, 1986).

The data obtained indicate that restriction endonuclease analysis has good prospects for further differentiation of *Rickettsia prowazekii* strains.

Acknowledgements. The authors wish to thank N. G. Shafranskaya for the excellent technical assistance.

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