
Application of DNA fragment length polymorphism analysis for identification of small rodents

Eglė Juškevičiūtė,
Algimantas Paulauskas

Vytautas Magnus University,
Department of Biology,
Vileikos 8,
LT-3500 Kaunas, Lithuania
E-mail: a.paulauskas@gmf.vdu.lt
egle_juskeviciute@fc.vdu.lt

The DNA fragment length polymorphism (RFLP) analysis is used for determining genetic variations in different species of mouse-like rodents. These methods give a possibility to investigate variations of DNA sequences in a population or species. Genomic DNA isolated from the liver of *Clethrionomys glareolus*, *Microtus agrestis*, *Microtus arvalis*, *Microtus rossiaemeridionalis* and *Microtus oeconomus* was investigated on the basis of restriction fragment length polymorphism (RFLP) analysis. The enzymes *ScaI* and *XbaI* gave restriction patterns that differed among all 5 species analyzed. Using *XbaI* for DNA cleavage, the polymorphism of fragments was more distinct.

Key words: DNA RFLP, identification of species, voles, *Clethrionomys glareolus*, *Microtus agrestis*, *M. arvalis*, *M. rossiaemeridionalis*, *M. oeconomus*

INTRODUCTION

The analysis of DNA is an important tool in studying of evolutionary ecology, population genetics, systematics (Avice, 1994). DNA has several advantages over alternatives such as proteins for molecular systematics: the genotype rather than phenotype is analyzed; the methods are common to any type of DNA (Delidow et al., 1997).

One of the methods for DNA research is restriction fragment length polymorphism (RFLP) analysis. This method gives a possibility to investigate variations of DNA sequences in a population or species (Dowling et al., 1996). For population level comparison RFLP analysis of plant chloroplast DNA and animal mitochondrial DNA (Dowling et al., 1996; Watanabe et al., 1985, 1989) is often used. For species or higher-level analysis, specific sequences of genomic DNA could be chosen (Leiro et al., 2000).

In some cases it is difficult to determine the species according to morphological data alone. Individuals of closely related rodent species have a similar morphology (Lietuvos..., 1988; Mažeikytė et al., 1999), they can produce interspecies hybrids (Kaneke et al., 1998), but have different genotypes. In this case DNA RFLP analysis may help. Specific restriction fragments could be species markers.

MATERIALS AND METHODS

Genomic DNA was isolated from fresh liver of 4 individuals of *Clethrionomys glareolus*, 5 – *Microtus*

arvalis, and 2 – *M. rossiaemeridionalis*, as well as from frozen liver (it was kept at –20 °C for 6 months) of 3 individuals of *C. glareolus*, 2 – *M. oeconomus* and 4 – *M. agrestis*. About 800 mg of tissue was chopped and digested overnight at 37 °C in 10 ml of lysis buffer (20 ml of 0.05 M Tris–HCl, pH 8.0, 0.585 g of NaCl and 0.75 g of EDTA) to which 1 ml of proteinase K (0.1 mg/ml) and 50 µl of 10% SDS were added. In 10 samples the proteins were precipitated by adding NaCl to lysate (1.5 ml of 4 M NaCl added to 5 ml of lysate) followed by centrifugation at 3000 g for 15 min (Miller et al., 1998). DNA from 20 samples was phenol-extracted with phenol-chloroform-isoamyl alcohol (8 g of phenol dissolved in 24 ml of chloroform, 1 ml of isoamyl alcohol is added) followed by centrifugation at 3000 g for 15 min and precipitated with 1.5 ml of 3 M sodium acetate and 10 ml (2 volumes) of ethanol for 4 h and centrifuged at 3000 g for 10 min (Darbre, 1988).

The extracted DNA was digested at 37 °C for 12 h with an appropriate amount of the restriction enzymes (1 unit of enzyme digests 1 µg of DNA in one hour in 50 µl of solution). In this research, *ScaI* and *XbaI* restriction enzymes were used. For 50 µl of restriction reaction solution up to 20 µg of DNA was taken, 5 µl (1/10 volume) of 10 × restriction buffer was added. Restriction enzymes and 1 µl of BSA were added (Darbre, 1988).

The DNA fragments produced by digestion with restriction endonucleases were sorted according to

their size by electrophoresis in 1% agarose and 5% polyacrylamide gels.

For 1% agarose gel 1 g of agarose was dissolved in 100 ml of 10 × TBE buffer (109.3 g of Tris, 9.3 g of Na EDTA 2H₂O and 55.4 g of boric acid were dissolved in water to make 200 ml of solution). The agarose solution was boiled for 2 min (Dowling et al., 1996).

For 5% polyacrylamide gel to 20 ml of 20% AKA solution 8 ml of 10 × TBE buffer and 0.08 ml of TEMED H₂O was added to make 75 ml of solution. 0.08 g of PCA was added (Harwood, 1997).

About 10 µg of the substance was mixed with 1 µl of bromophenol blue and casted on gel. Electrophoresis was run for 4 h at 120 V in agarose gel and for 2 h 30 min at 200 V in polyacrylamide gel. After electrophoresis the gel was stained with 0.1 µg/ml ethidium bromide for 30 min at room temperature (Harwood, 1997). For estimating the size of fragments the molecular weight marker pBR 322/*Alu*I was used.

RESULTS AND DISCUSSION

There were no significant differences in DNA isolated from fresh and from frozen tissue. Restriction fragments of *Clethrionomys glareolus* DNA isolated from both fresh and frozen liver were identical. The results showed that the method of DNA extraction was more important. Better results were achieved using phenol-extraction rather than salt-extraction. Using the former method, purer DNA with less protein admixtures was obtained, which is important for RFLP analysis.

DNA digested by *Sca*I enzymes was fractionated by electrophoresis in 5% polyacrylamide gel. DNA treated with *Xba*I was electrophoresed in both 1% agarose (Fig. 1) and 5% polyacrylamide gels (Fig. 2). In both cases the molecular weight marker pBR 322/*Alu*I was used.

After treating *C. glareolus* DNA with *Sca*I, two restriction fragments, 990 ir 670 bp, occurred. One fragment of 940 bp in *M. arvalis*, one fragment of 1000 bp in both *M. oeconomus* and *M. rossiaemerdionalis* were observed. *Sca*I didn't cleave DNA of *M. agrestis*.

In both agarose and polyacrylamide gels, DNA/*Xba*I fragments of one species were identical, but the resolution was better and more fractions were observed in polyacrylamide gel (Table). In both gels, fractions of 1000 and 510 bp in *C. glareolus* were observed. Two additional smaller fragments of 210 and 120 bp occurred in polyacrylamide gel. In both gels two identical fragments of 980 and 620 bp in *M. agrestis*, one fragment of 640 bp in *M. oeconomus*, a fragment of 960 bp in *M. rossiaemerdionalis* and a fragment of 890 bp in *M. arvalis* were observed. Additional frac-

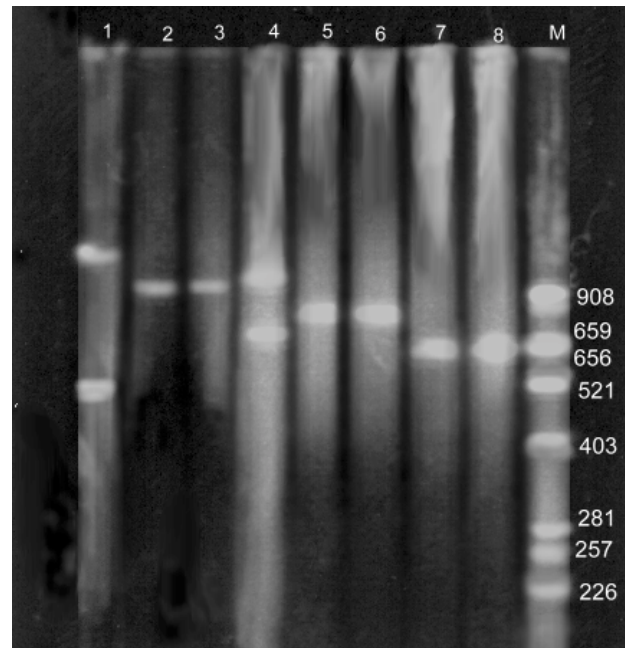


Fig. 1. DNA/*Xba*I restriction patterns in 1% agarose gel among 5 vole species: 1 – *C. glareolus*; 2, 3 – *M. rossiaemerdionalis*; 4 – *M. agrestis*; 5, 6 – *M. arvalis*; 7, 8 – *M. oeconomus*; M – molecular weight marker pBR 322/*Alu*I

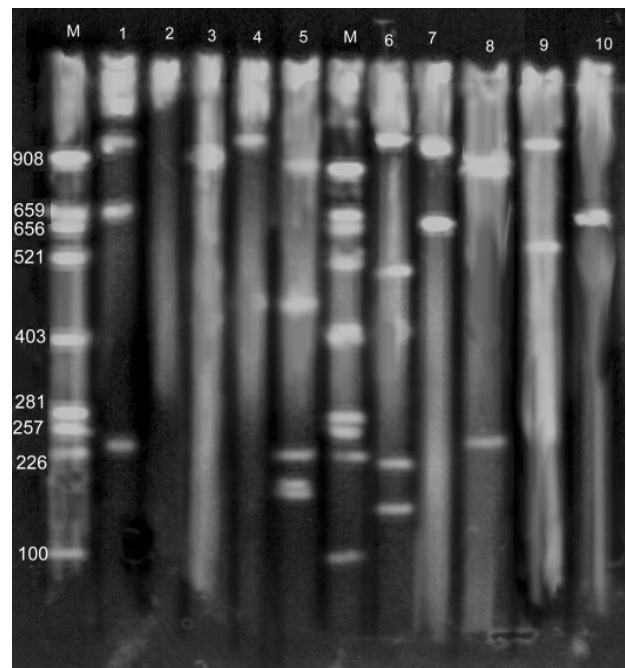


Fig. 2. DNA/*Sca*I (1–5) and DNA/*Xba*I (6–10) restriction patterns in 5% polyacrylamide gel of 5 vole species analyzed: 1, 6 – *C. glareolus*; 2, 7 – *M. agrestis*; 3, 8 – *M. arvalis*; 4, 9 – *M. rossiaemerdionalis*; 5, 10 – *M. oeconomus*; M – molecular weight marker pBR 322/*Alu*I

tions of 540 bp in *M. rossiaemerdionalis* and of 220 bp in *M. arvalis* were noted in polyacrylamide gel.

The enzymes *Sca*I and *Xba*I gave restriction patterns that differed among all five vole species ana-

Table. Comparison of vole DNA/*Xba*I restriction fragments

Species	1% agarose gel		5% polyacrylamide gel	
	Number of fragments	Length of fragments, bp	Number of fragments	Length of fragments, bp
<i>Clethrionomys glareolus</i>	2	1000 510	4	1000 510 210 120
<i>Microtus agrestis</i>	2	980 620	2	980 620
<i>Microtus arvalis</i>	1	890	2	890 220
<i>Microtus rossiaemeridionalis</i>	1	960	2	960 540
<i>Microtus oeconomus</i>	1	640	1	640

lyzed, but using *Xba*I for DNA cleavage the polymorphism of fragments was more distinct. *Xba*I could be used for identification of the vole species.

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Eglė Juškevičiūtė, Algimantas Paulauskas

DNR RESTRIKINIŲ FRAGMENTŲ ILGIO POLIMORFIZMO PANAUDOJIMAS PELINIŲ GRAUŽIKŲ RŪŠIAI NUSTATYTI

S a n t r a u k a

Atlikta Lietuvoje paplitusių Microtinae šeimos pelėnų *Clethrionomys glareolus*, *Microtus agrestis*, *M. arvalis*, *M. rossiaemeridionalis*, *M. oeconomus* DNR restrikcinių fragmentų analizė. Skaidant pelėnų DNR restriktaze *Xba*I gautami polimorfiški specifiniai skirtingoms rūšims priklausančių pelėnų DNR restrikciniai fragmentai. Naudojant šį fermentą atskirų rūšių skirtumai išryškėja geriau nei naudojant restriktažę *Sca*I. Restriktažę *Xba*I galima panaudoti nustatant pelėnų rūšį.

Raktažodžiai: DNR fragmento ilgio polimorfizmas, rūšies identifikavimas, pelėnai, *Clethrionomys glareolus*, *Microtus agrestis*, *M. arvalis*, *M. rossiaemeridionalis*, *M. oeconomus*