

cDNA sequence and chromosomal localization of the mouse parvalbumin gene, *Pva*

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Summary

In the homozygous condition, the mutation *adr* (*arrested development of righting response*) of the mouse causes a myotonia and a drastic reduction of the Ca²⁺-binding protein parvalbumin (PV) in fast muscles. Using a rat PV probe, a mouse cDNA clone was isolated from a λ gt11 wild-type fast-muscle library and its nucleotide sequence was determined. The protein coding and the 3' non-translated regions of the mouse gene show extensive homology with the rat PV gene. The result of Southern blot hybridization is consistent with a single copy gene for parvalbumin. Restriction fragment length polymorphisms (RFLPs) between *Mus musculus domesticus* (e.g. C57BL/6) and *Mus spretus* (SPE) were detected with the enzymes *Eco* RI, *Pst* I, and *Sst* I. The restriction fragment patterns of DNA samples from 65 individual offspring of (C57BL/6 \times SPE)F1 \times C57BL/6 backcrosses were tested with the PV probe and matched, for linkage detection, to pre-existing patterns established with various RFLP probes on the same samples. A co-distribution of PV-RFLPs with *Pvt-1* and *Mlvi-2*, which had been localized on chromosome 15, was detected. Thus, the structural gene for PV, designated *Pva*, maps to chromosome 15 of the mouse whereas the *adr* mutation shows no linkage with markers on this chromosome. Gene locus homology between chromosome 15 of the mouse and chromosome 22 of man (which carries the human PV gene) is discussed.

1. Introduction

Parvalbumin (PV), a high-affinity Ca²⁺-binding protein, is synthesized in high amounts in fast contracting/relaxing muscles of small mammals (Heizmann *et al.* 1982). It is also expressed in certain non-muscle tissues such as brain. The expression of PV in muscle is neurally and developmentally regulated (Leberer & Pette, 1986; Müntener *et al.* 1987; Berchtold, 1988). Northern blot analysis in rat and mouse revealed two PV mRNA species of 1100 and 700 nt of which the smaller species is more abundant (Epstein *et al.* 1986; Kluxen *et al.* 1988).

The PV content of muscle is reduced in certain hereditary neuromuscular diseases of the mouse e.g. '*dystrophia muscularis*', DY^{2j} (Klug *et al.* 1985) and '*arrested development of righting response*', ADR* (Stuhlfauth *et al.* 1984; Jockusch *et al.* 1988a). The ADR syndrome has been characterized as a myotonia (Reininghaus *et al.* 1988) caused by a hyperexcitability

of muscle fibres (Mehrke *et al.* 1988). This condition can be phenotypically cured by tocainide (Reininghaus *et al.* 1988), a drug that stabilizes the membrane potential. In tocainide treated animals the PV protein and mRNA levels are partially restored (Jockusch *et al.* 1988a; Kluxen *et al.* 1988). This indicates that the myotonic phenotype interferes with the regulation of PV synthesis.

The genomes of mouse and man are far more extensively characterized than those of other vertebrates. A number of mutations are known in mouse that may serve as models for hereditary diseases of man. In addition, regions of homology between human and mouse chromosomes have been identified (Peters, 1988; Kaplan *et al.* 1987). Therefore, based on the knowledge of the rat PV gene (Berchtold *et al.* 1987), we have begun to characterize the PV gene of the mouse.

Here we present the isolation of a parvalbumin cDNA clone from a mouse fast-muscle library, its nucleotide sequence and the deduced amino-acid sequence. By the identification and use of RFLPs for PV we were able to map this gene in the mouse

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Lower case mutant symbols designate alleles, upper case symbols designate phenotypes.

genome. A preliminary report of part of this work has been given (Zühlke *et al.* 1988).

2. Material and methods

(i) Animals

In addition to standard laboratory mouse strains, wild-type (+/*adr*?) and homozygous mutant (*adr/adr*) individuals of the A2G inbred strain (Watkins & Watts, 1984) were used for DNA and RNA isolation. Genomic DNA was also prepared of the *Mus spretus* strains SPE (Guénet, 1986) and SEG (kindly provided by Dr O. v. Deimling, Freiburg).

(ii) Isolation of mRNA

Fast muscles were obtained from adult A2G wild-type mice. The tissue was frozen in liquid nitrogen immediately after dissection and stored at -70°C . For the preparation of total RNA, the tissue was homogenized in 4 M guanidinium thiocyanate buffer according to Chirgwin *et al.* (1979). The RNA was pelleted by centrifugation through a 3 ml, 5.7 M-CsCl cushion. Poly(dT) paper (Medac, Hamburg) affinity chromatography was used to obtain messenger RNA (Werner *et al.* 1984). A total of 1–5 μg of poly(A)⁺ RNA was used for cDNA synthesis.

(iii) cDNA synthesis and cloning

First strand synthesis starting from the 3' end of the poly(A)⁺ RNA was primed by oligo(dT) and elongated by MMLV reverse transcriptase (Maniatis *et al.* 1982). The DNA/RNA hybrids were treated with RNase H, providing 3'OH primers for DNA polymerase I (second-strand synthesis according to Gubler & Hoffmann, 1983). Double-stranded cDNAs were protected from *Eco* RI restriction by methylation (Huynh *et al.* 1985). *Eco* RI linkers were added to the cDNA and cleaved with *Eco* RI to generate cohesive termini. An appropriate cDNA fraction was size selected by low-melting-temperature agarose gel electrophoresis (Maniatis *et al.* 1982). The purified cDNAs were ligated in *Eco* RI digested phage vector $\lambda\text{gt}11$ (Young & Davis, 1983*b*) and packaged *in vitro* according to Maniatis *et al.* 1982.

(iv) Screening of the $\lambda\text{gt}11$ library

Overnight (o.n.) cultures (100 μl) of *E. coli* Y1088 (Young & Davis, 1983*a*) were infected with 10^3 p.f.u. of recombinant $\lambda\text{gt}11$, diluted with 3 ml of top-agar, plated on LB-plates and incubated o.n. at 37°C (Maniatis *et al.* 1982). Plaques were transferred onto nitrocellulose filters and processed according to Davis *et al.* 1980. Hybridization was performed with a rat parvalbumin cDNA probe (Berchtold & Means, 1985). The isolated fragment of the coding region was

labelled with [$\alpha^{32}\text{P}$]dCTP by random deoxyoligonucleotide-priming (Feinberg & Vogelstein, 1983). Positive clones were purified by single plaque passages. Phage DNA was isolated (Maniatis *et al.* 1982) and subcloned for sequencing.

(v) DNA sequencing

M13mp18 and M13mp19 were used as cloning vectors for DNA sequencing by the dideoxy chain termination method (Sanger *et al.* 1977). Single-stranded DNA was isolated from plaques suspended in 1 ml LB-medium and incubated with 10 μl of an o.n. culture of *E. coli* JM103 for 6 h at 37°C . Bacteria were pelleted in a microfuge, 250 μl 20% PEG was added to the supernatant, mixed and incubated for 15 min at room temperature. After centrifugation (5 min) the phage pellet was resuspended in 100 μl TES-buffer. The suspended virus particles were extracted twice with phenol and phenol- CHCl_3 , the aqueous phase was ethanol precipitated and the viral DNA was dissolved in 20 μl TE-Buffer. The 17-mer universal primer (Boehringer, Mannheim), the 15-mer $\lambda\text{gt}11$ primer and the $\lambda\text{gt}11$ reverse primer (Clontec, Palo Alto) were used to prime the sequencing reactions. Deletions of the cDNA were produced by exonuclease III. Double stranded DNA was isolated and cut with *Bam* HI and *Sph* I. Exonuclease III was added and the reaction was stopped after different time intervals. After treatment with S1 nuclease the deleted fragments were blunt ended by the Klenow fragment of *E. coli* polymerase I and ligated to the vector by T4 DNA ligase. Competent JM103 cells were transformed with the ligation product and plated onto agar medium. Recombinant clones were analysed by digestion with *Eco* RI and *Hin* dIII. Single-stranded DNA of selected clones covering entirely both strands of the cDNA was prepared as described above and used for sequencing.

(vi) Preparation of mouse genomic DNA, Southern blot and hybridization

High-molecular-weight DNA was prepared from organs (lung, liver, heart, brain) of adult mice. The organs were frozen in liquid nitrogen, crushed and resuspended in 5 ml of 1% sarcosyl, 0.1 mM-EDTA. The mixture was incubated with proteinase K and RNase A. DNA was extracted with phenol and phenol- CHCl_3 and purified by dialysis (Weydert *et al.* 1983) and 8 μg DNA were digested with 20 units of restriction enzyme, run on 0.8% agarose/TBE gels and stained with ethidium bromide. The DNA was denatured, neutralized and transferred to nitrocellulose or nylon filters according to Southern (1975).

Radioactive probes were prepared by random priming of 100 ng of electrophoretically purified mouse cDNA fragment. Hybridization was carried out at 42°C in 50% formamide o.n. Blots were

ATG	TCG	ATG	ACA	GAC	GTG	CTC	AGC	GCT	GAG	GAC	ATC	AAG	AAG	GCG	ATA	GGA	GCC	TTT	GCT	+ 60
Met	Ser	Met	Thr	Asp	Val	Leu	Ser	Ala	Glu	Asp	Ile	Lys	Lys	Ala	Ile	Gly	Ala	Phe	Ala	
GCT	GCA	GAC	TCC	TTC	GAC	CAC	AAA	AAG	TTC	TTC	CAG	ATG	GTG	GGC	CTG	AAG	AAA	AAG	AAC	+ 120
Ala	Ala	Asp	Ser	Phe	Asp	His	Lys	Lys	Phe	Phe	Gln	Met	Val	Gly	Leu	Lys	Lys	Lys	Asn	
CCG	GAT	GAG	GTG	AAG	AAG	GTG	TTC	CAT	ATT	CTG	GAC	AAA	GAC	AAA	AGT	GGC	TTC	ATT	GAG	+ 180
Pro	Asp	Glu	Val	Lys	Lys	Val	Phe	His	Ile	Leu	Asp	Lys	Asp	Lys	Ser	Gly	Phe	Ile	Glu	
GAG	GAT	GAG	CTG	GGG	TCC	ATT	CTG	AAG	GGC	TTC	TCC	TCA	GAT	GCC	AGA	GAC	TTG	TCT	GCT	+ 240
Glu	Asp	Glu	Leu	Gly	Ser	Ile	Leu	Lys	Gly	Phe	Ser	Ser	Asp	Ala	Arg	Asp	Leu	Ser	Ala	
AAA	GAA	ACA	AAG	ACG	CTT	CTG	GCC	GCT	GGA	GAC	AAG	GAT	GGG	GAC	GGC	AAG	ATT	GGG	GTT	+ 300
Lys	Glu	Thr	Lys	Thr	Leu	Leu	Ala	Ala	Gly	Asp	Lys	Asp	Gly	Asp	Gly	Lys	Ile	Gly	Val	
GAA	GAA	TTC	TCC	ACT	CTG	GTG	GCT	GAA	ACG	TAA	GTGGCGCTGACTGCTTGGGTCCCCCACCTCTCCATCCCCA								+ 373	
Glu	Glu	Phe	Ser	Thr	Leu	Val	Ala	Glu	Thr	***										
ACGCCCCATCTCAGCCCTTCTCGCGGCCCTCTGAGTTTCTGTTCAAGTTTGTGGTTATTTTTACTCCCCCATCTCTATGGCCCTCGGA																				+ 466
TGACGCCATTCTTCTGGAAATGCTGGAGAAACAATAAAGGCTGTACCAATCGGACACC																				+ 524

Fig. 1. (a) cDNA and deduced amino-acid sequence of a mouse parvalbumin cDNA clone in 5' → 3' orientation.

Numbering refers to the A (+1) in the start codon. A putative polyadenylation signal is underlined.

washed with 2 × SSC, 0.1 % SDS and 0.2 × SSC, 0.1 % SDS at 65 °C (Maniatis *et al.* 1982).

Kodak XAR film or Amersham Hyperfilm-MP were used for autoradiography with two Cronex lightning intensifying screens (Dupont) for 2–8 days at –70 °C.

3. Results and discussion

(i) Isolation and sequencing of a mouse parvalbumin cDNA clone

A cDNA library was constructed in λgt11 using as template poly(A)⁺ RNA from fast muscles, tibialis anterior and vastus, of the A2G wild-type mouse (genotype +/adr?). Putative PV clones were identified by several rounds of screening with a 240 bp *Pst* I/*Eco* RI fragment of a rat parvalbumin cDNA (Berchtold & Means, 1985). One clone containing an insert of 0.5 kb, termed *mpv*, was chosen for further characterization.

The identity of clone *mpv* as a PV cDNA was demonstrated by hybridization to electrophoretically separated mRNAs from wild-type and myotonic mouse muscle. Similar hybridization patterns were detected for PV mRNAs (700 and 1000 nt) using the mouse (data not shown) or the rat probe (Kluxen *et al.* 1988).

The parvalbumin cDNA fragment was subcloned and sequenced in both orientations. A stretch of 524 bp containing the coding sequence and a part of the 3' non-coding region was determined (Fig. 1a). Although the 5' non-coding region is lacking, the comparison with the rat cDNA sequence (Epstein *et al.* 1986) suggests the ATG (+1) as the initiation codon. Strong homologies of nucleotide (96%) and amino-acid (94.5%) sequences were found between mouse and

rat. The 3' non-coding region of the mRNA sequences is also conserved and putative polyadenylation signals for the short mRNAs are located at identical positions (+498 to +504). In rat, one poly(A)⁺ site was found 10 nt downstream of the sequence AATAAA. The mouse cDNA clone lacks the poly(A) tail of the mRNA although it contains a stretch of 20 nt beyond a putative polyadenylation signal. It is possible that this clone represents a shortened fragment derived from the longer, less abundant mRNA species.

Comparing the amino-acid sequences of three mammalian species homologies of 85% to 95% were found (Fig. 1b). Out of 110 amino acid residues, 8 are exchanged between mouse and rat, 18 between mouse and rabbit (Enfield *et al.* 1975) and 16 between rat and rabbit. Five residues are identical in rat and rabbit, but differ in mouse PV. This finding suggests a relationship between rodents and lagomorphs. Between carp (Coffee & Bradshaw, 1973) and mammals about 60% of the amino acids are identical. None of the amino-acid residues involved in calcium binding of carp III parvalbumin (Kretsinger & Nockolds, 1973) are exchanged, indicating the strong evolutionary conservation of these Ca²⁺-binding domains.

(ii) Identification of RFLPs and mapping of the mouse parvalbumin gene Pva

Genomic DNA of *Mus spretus*, *Mus musculus domesticus* A2G (+/adr? and *adr/adr*) and from five additional laboratory strains was isolated and digested with *Eco* RI, *Hin* dIII, *Bam* HI, *Kpn* I, *Pst* I, *Pvu* II, *Sst* I and *Taq* I. After gel electrophoresis the DNA was blotted and hybridized with the mouse cDNA probe. No differences in the hybridization patterns between the laboratory mouse strains could be detected (data not shown). The results of Southern-

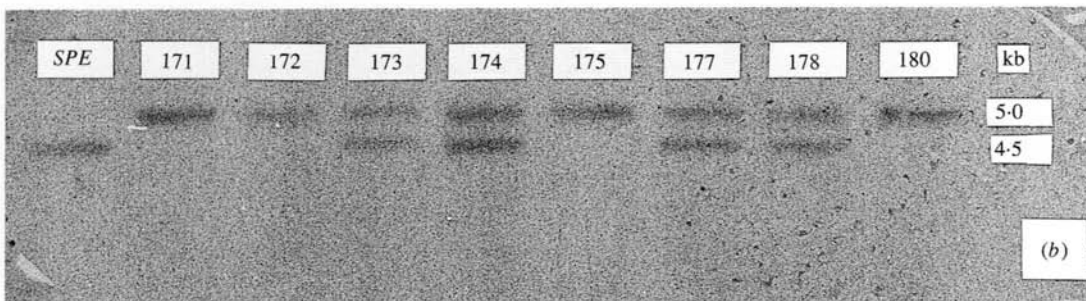
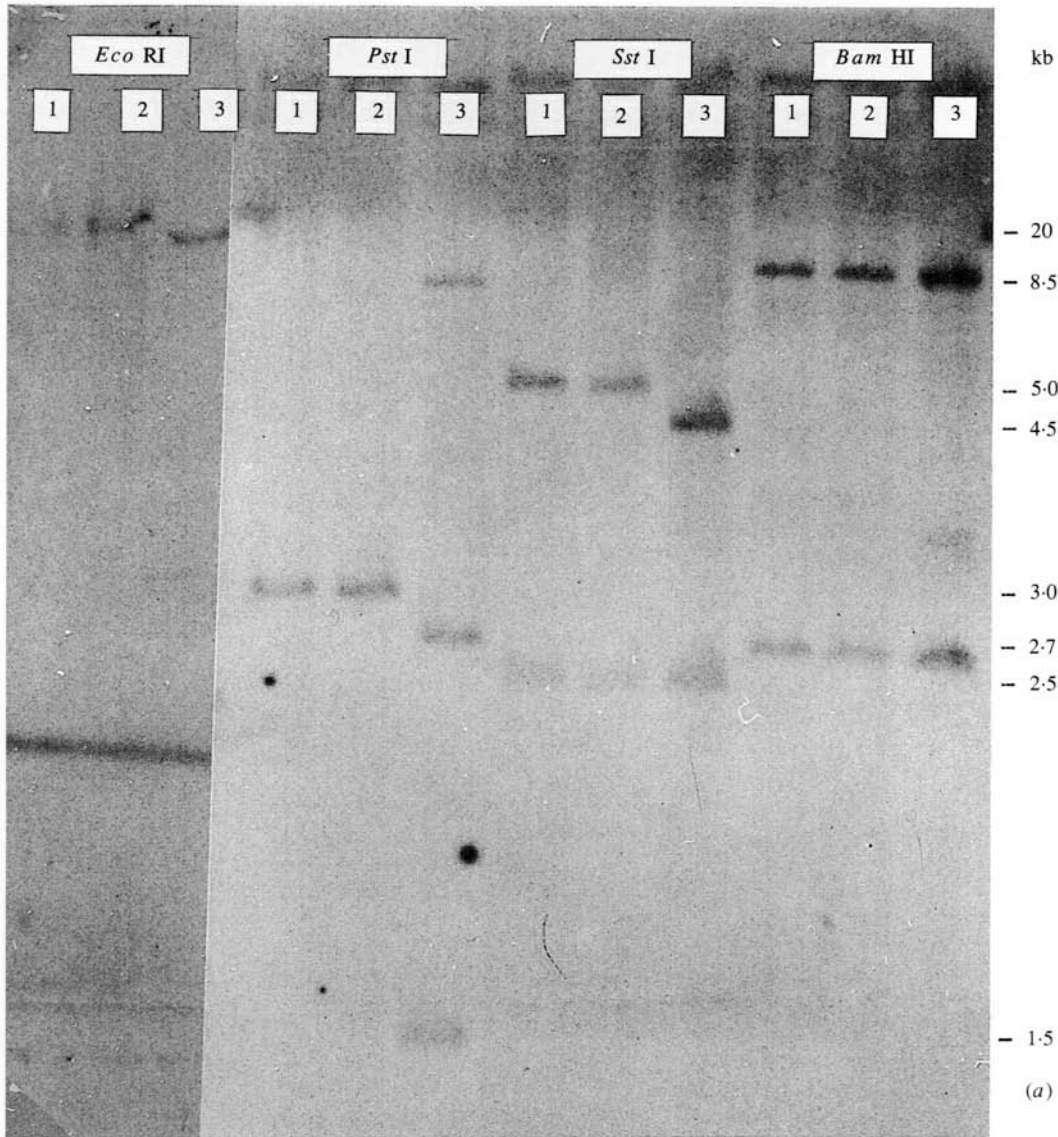


Fig. 2. Restriction fragments of the parvalbumin gene *Pva* in mouse strains and intercrosses. (a) Southern blot hybridization of genomic DNA from *Mus musculus domesticus* wild-type (A2G, lanes 2), the myotonic mutant (ADR, lanes 1) and *Mus spretus* (SPE, lanes 3). Genomic DNA, 10 μ g respectively, extracted from lungs, were digested with the restriction enzymes *Eco* RI, *Bam* HI, *Sst*₁ I or *Pst* I and analysed by Southern blotting. A fragment

of the mouse PV gene was labelled and used as a probe. (b) RFLPs for *Sst* I in eight individuals of interspecific backcrosses. The DNA from (C57BL/6 \times SPE)F1 \times C57BL/6 and from *Mus spretus* SPE was digested with *Sst* I, blotted and hybridized with the mouse cDNA probe. Animals homozygous and heterozygous for the *Pva* fragment are characterized by, respectively, 1 and 2 hybridizing fragments.

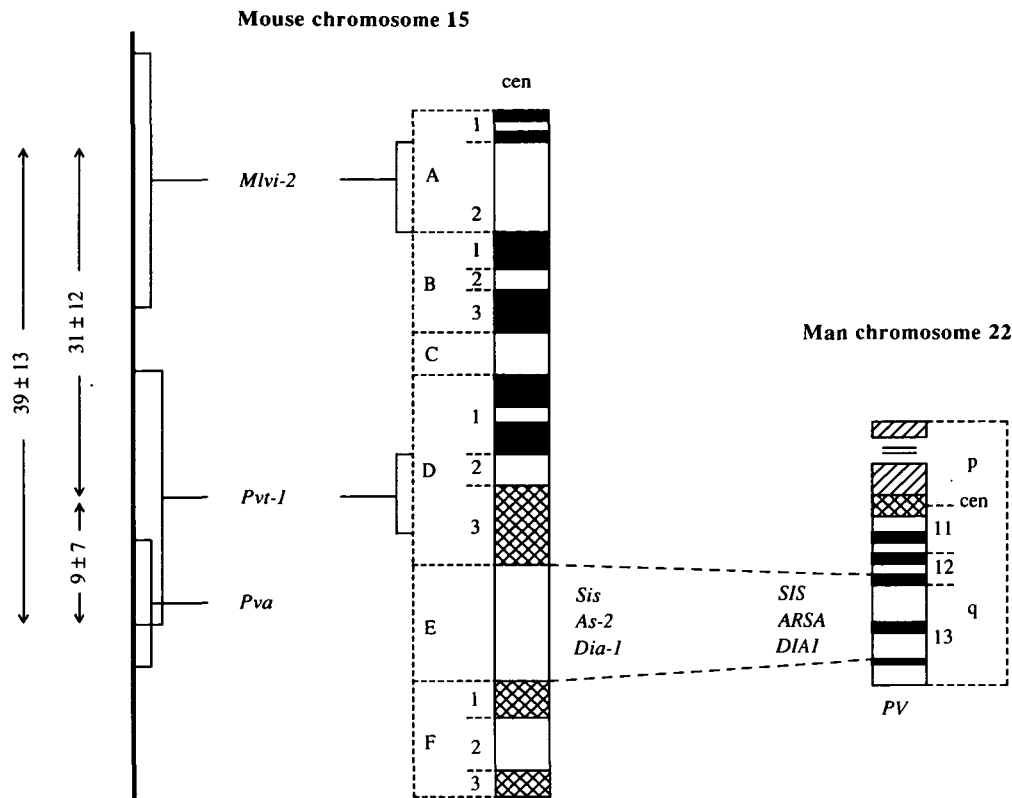


Fig. 3. Schematic representation of linkage and G-banding patterns of mouse chromosome 15 and the G-banding pattern of human chromosome 22. Linkage distances to the marker genes *Pvt-1* (plasmacytoma variant translocation, Banerjee *et al.* 1985) and *Mlvi-2*

(Moloney virus integration site 2, Kozak *et al.* 1985) are given in cM with $P \leq 0.05$. Chromosomal segments presumed homologous between mouse and man are indicated by dashed lines. The lengths of the mouse and the human chromosomes are not to scale.

proto-oncogene is the most proximal gene in this syntenic group (Kaplan *et al.* 1987). The extent of this man-mouse synteny is further supported by the localization of the gene for cytochrome P450IID and a hemoglobin pseudogene on chromosome 15 of the mouse (Peters, 1988) and chromosome 22 of man (Kaplan & Carritt, 1987).

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