

BRIEF MAPPING REPORTS

The Mouse *Fubp* Gene Maps near the Distal End of Chromosome 3

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Functional gene description: The far upstream element binding protein (FUSE binding protein; FUBP) was identified as binding to single-stranded DNA of the far upstream element in the *c-myc* promoter (3). This protein is implicated in the transcriptional regulation of *c-myc*. The 70-kDa FUBP polypeptide contains several domains including a central region containing single-strand nucleic acid binding motifs and a C-terminal domain that can activate transcription when fused to the Gal-4 DNA binding domain.

Name of clone or DNA source: Mouse *Fubp* was the genomic DNA clone used.

Description of clone or DNA: A 260-bp PCR fragment generated from nucleotides 353–613 of the human *KSRP* cDNA (GenBank Accession No. U94832; 5) was used as a probe to screen a mouse genomic library in the Lambda DASH II vector (Stratagene). One of the positive clones contained a 2.5-kb insert, and sequence analysis revealed high homology to the human *FUBP* gene (GenBank Accession No. U05040). Therefore, this is a genomic DNA clone for the mouse *Fubp* gene. The sequence was deposited with GenBank (Accession No. AF094697).

Method used to validate gene identity: When two different mouse *Fubp*-specific PCR primer pairs were used in mapping experiments, consistent results were obtained.

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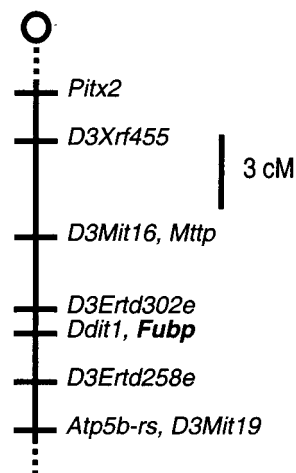
Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under Accession No. AF094697.

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Flanking markers: No flanking markers were used.

Methods of mapping: The mouse *Fubp* gene was initially localized to a specific chromosome by PCR analysis of DNA from a panel of mouse × Chinese hamster and mouse × rat somatic hybrid cell lines (4). The mouse-specific PCR primers used are 5'-GAG CAA AAA TCA AGT GGA AAG C-3' and 5'-TTC AAC TCT CCC CTC ATT GG-3'. The *Fubp* locus was also mapped genetically by studying DNA of the Jackson BSS 2 backcross panel (6). PCR amplification with primers 5'-ATG ATT TGA AAT CAA AGG GTG G-3' and 5'-CCC AAT TTT TGC TGC AAT CT-3' and single-strand conformation analysis of the amplicons allowed detection of strain-specific variation between the parental strains. The

(A) Jackson BSS Chromosome 3



(B) Jackson BSS Chromosome 3

		R	SE
<i>Mtp</i>	■ □ ■ □ □ □ ■	3.19	1.81
<i>D3Erd302e</i>	■ □ □ □ ■ □ □	1.06	1.06
<i>Ddit1, Fubp</i>	■ □ □ □ ■ □ □	2.13	1.49
<i>D3Erd258e</i>	■ □ □ □ ■ □ □	2.13	1.49
<i>D3Mit19</i>	■ □ □ □ ■ □ □		
	48 38 2 1 1 2 2		

FIG. 1. Chromosome localization of the mouse *Fubp* gene. (A) BSS linkage map of the mouse chromosome 3 around the *Fubp* locus. The centromere is toward the top. A 3-cM scale is shown on the right. (B) Haplotypes of the *Fubp* locus and the flanking markers of the 94 Jackson Laboratory BSS backcross animals studied. The black boxes represent the C57BL6/Ei allele, and the white boxes represent the SPRET/Ei allele. The number of animals with each haplotype is shown at the bottom of the column of boxes. The percentage recombination (*R*) between adjacent loci is given to the right of the figure, with the standard error (SE) for each *R*.

mouse *Fubp* strain distribution patterns were sent to The Jackson Laboratory backcross mapping service for comparison to the BSS panel database at <http://www.jax.org/resources/documents/cmdata>.

Results: The mouse *Fubp* gene was assigned to chromosome 3 by using a somatic cell hybrid panel. Its map location was further defined by typing the Jackson BSS 2 backcross panel, and *Fubp* was found to cosegregate with *Ddit1* in all 94 animals analyzed (Fig. 1B). Thus, the *Fubp* gene was placed on the linkage map of mouse chromosome 3 at 70.5 cM from the centromere, in the distal end of mouse chromosome 3 (Fig. 1A).

Additional comments: Searching the Mouse Genome Informatics Database (<http://www.informatics.jax.org/locus.html>) for mouse mutants near the *Fubp* locus revealed *Va*, *varitint-waddler*. *Va* is a semidominant mutation. Heterozygous *Va* mice are deaf and show circling behavior, head-tossing, and hyperactivity. Their coats are variegated with patches of normal-colored, diluted, and white fur. Viability of heterozygotes is nearly normal, while mortality is very high in homozygotes, and very few of the survivors are fertile (1, 2). *Fubp*'s map position and its function as a nucleic acid binding protein and genetic regulator make it a potential candidate gene for this mutant.

Homologies: Conserved synteny with human chromosomes would suggest a possible location of the human FUBP gene on 4q, as suggested by flanking loci NFKB1 (at 4q24) and ADH1 and ADH3 (at 4q21–q23). The human homologue of *Ddit1*, DDIT1 for DNA-damage induced transcript-1 encoding a protein also known as GADD45, however, has been assigned to 1p31.2–p31.1(GDB). Therefore, it is most likely that FUBP will be found in that location.

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Genetic Mapping of Mouse Heat Shock Protein Genes *Hsc4a* to Chromosome 11 and *Hsc74* to Chromosome 18 and Two *Hsc74* Pseudogenes to Chromosomes X and 8

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Functional gene description: The heat inducible Hsp70 gene is the prototype that defines a family of highly homologous Hsp70-related genes. In mice, DNA cloning studies have identified seven Hsp70 members. The mouse gene *Hsc74* is the homologue of the nuclear encoded human Hsp70 gene, whose product is targeted to the mitochondria to aid in protein folding (1). However, some evidence suggests that HSC74 is not solely mitochondrial and has additional functions. The HSC74 protein is also referred to as mortalin, peptide binding protein (PBP74), C3H strain-specific antigen (CSA), and glucose regulated protein 75 kDa (Grp75).

A human cDNA clone (Hsp70RY) originally isolated from a B lymphocyte library was identified as an Hsp70 gene family member based on amino acid homology (2). Subsequent isolation of heat inducible and endoplasmic reticulum Hsp110 gene family members indicated that Hsp70RY was a member of that family, which is itself a subfamily of the larger Hsp70 family. The precise function of Hsp70RY is unknown but probably involves modulating protein–protein interactions, as do all HSP70-related proteins.

Name of DNA clone: Mapping of mouse *Hsc74* was carried out with a 1.5-kb *EcoRI* fragment isolated from an *Hsc74* pseudogene (plasmid pHsc74R1.5). It spanned the 3' coding amino acids 507 to 679 and noncoding terminus (Accession No. D17651). Mapping of the mouse Hsp70RY gene was carried out with a 1.2-kb *BglII* genomic fragment that had been subcloned into pLit28 (plasmid pR14/3). Complete DNA sequence analysis of the insert indicates that it contains a single 184-bp exon, corresponding to amino acids 460–520 in the human Hsp70RY cDNA sequence (2), and is flanked on both ends by intronic sequences.

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