Mammalian Genome 4, S154–S163 (1993).

Mammalian Genome

Mouse Chromosome 10

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Received: 2 June 1993

Introduction

The 1993 Mouse Chromosome (Chr) 10 report includes the addition of new genes and other DNA variants, their positions in the linkage and/or cytogenetic maps, deletions, recombinant inbred (RI) strain distribution patterns (SDPs), data pertaining to imprinting, and information about human–mouse linkage homology. New this year is a table showing the apparent gene order and recombination frequencies as determined in multilocus crosses.

Table 1 lists known Chr 10 loci alphabetically by gene symbols. Additional columns are used to denote (a) loci added to the list since the last report, (b) loci designated as reference loci, (c) the approximate map position in centimorgans from the centromere (if known), (d) localization to specific chromosomal bands, (e) classification of the loci (DNA, biochemical, visible, etc.), (f) the method(s) used in mapping, (g) the gene symbol of the human homolog (if known), (h) the location of the human homolog, and (i) selected references pertaining to the mapping of the mouse gene. Formerly used locus symbols are also listed alphabetically within the table.

Chr 10 maps

Figure 1 shows the updated versions of the "consensus map", the "proviral/RI map" and the "SSLP (simple sequence repeat length polymorphism) map". Only a few significant changes have been made to the consensus map. These are indicated in the legend of Fig. 1. Since there are few common loci between the proviral/RI and consensus maps, it is not yet possible to accurately place most RI markers on the consensus map.

Table 2 shows the apparent gene order and recombination frequencies as estimated in seven different multilocus crosses. In all seven, either *Myb* or *Mpmv-12* and either *Ifg* or *Mdm-1* have been scored. *Myb* and *Mpmv-12* are known to be closely linked (Frankel et al. 1990) as are *Mdm-1 and Ifg* (Taylor et al. 1992). The MIT intercross involving *Mus castaneus* has not been typed for these markers but has been typed for markers known to be quite close to these markers. Thus, *D10Mit4* is known to be close to *Mpmv-12* (and hence, *Myb*), and *D10Mit14* is known to be close to *Mdm-1* (Dietrich et al. 1992a; Taylor et al. 1992). These seven crosses include three interspecific crosses involving *Mus spretus* and four intersubspecific crosses, two involving *Mus castaneus* and one each involving *Mus musculus* and *Mus molossinus,* and the pooled results of two small backcrosses involving conventional strains C57BL/6J and A/J. The (*Myb/Mpmv-12*)–(*Mdm-1/Ifg*) two-point distance may be slightly underestimated in three of the crosses owing to undetected double crossovers between widely spaced markers. Six of the cumulative distance estimates are quite consistent with a mean of 56.1 (range: 48–64 cM). The Pasteur *Mus spretus* backcross (Cross B) gave a substantially shorter map distance (40.7 cM). This is one of the smaller of the seven crosses in gametes analyzed (N = 29–69). Thus, there is good evidence that the genetic distance between *Myb* and *Mdm-1/Ifg* is approximately 56 cM. There are few common markers outside this interval, so there is greater uncertainty about map distances in the centrometric and telomeric regions.

Several adjustments have been made in the RI/proviral map to accommodate new information. The orientation of *Hsd, Gad-1ps, D10Nds2,* and *Xmv-31* has been reversed on the basis of RI strain typing of *Mdm-1* and other data (Taylor et al. 1992; B.A. Taylor, unpublished data), although the revised order is not firmly established. Likewise, the position of *pg* relative to *D10Mit14* has been reversed. This is based on

*Chair of Committee for Mouse Chromosome 10

Table 1. Locus list for mouse Chr 10.

New	Symbol	Name	A	M	CL	T	Method	H. symbol	H. location	References
	Acp-2	See Apk								
	Act-2	actin related gene-2		8		D	L			52
	Adn	adipsin				D, B	S			104
	Ahi-1	Abelson helper integration site		14		D	S, L			52, 88
	Amh	anti-Mullerian hormone		41.5		D, B	L	AMH	19p13.3	54
	Apk	acid phosphatase-kidney (ex Acp-2)		32		B	L			121, 122
	Ass-ps2	arginosuccinate synthetase pseudogene-2				D	S			79
	at	atrichosis		66-72		V	L			49
	av	Ames waltzer		42		V	L			80, 95
	Bcr	breakpoint cluster region homolog		34.5		D	L	BCR	22q11	52
	Bpb	See S100b								
	Braf	Braf transforming gene		20.5		D, B	L			52
	Bsg	basigin		39		D, B	L			101
	Cat	dominant cataract		72		V	L			46, 63, 76
	Cd18	See Itgb2								
	Cdc2a	cell division cycle 2 homolog, Chr 10		33.5		D, B	S, L	CDC2	10q21.1	52
	Cis	See Cs								
	Cnx43	See Gja-1								
	Col6a-1	procollagen type VI, alpha 1		35.5		D, B	S, L, P	COL6A1	21q22.3	52, 65, 89, 90
	Col6a-2	procollagen type VI, alpha 2		35.5		D, B	S, L, P	COL6A2	21q22.3	52, 65
*	*Col10a-1*	procollagen type X, alpha 1		20.5		D, B	L	COL10A1	6q21-22	3
	Cs	citrate synthase (ex Cis, Cts)				B	S	CS	12p11-qter	27
	Cts	See Cs								
	D0Nds22	See D10Nds3								
*	*D10Bir1*	DNA segment, Chr 10, Birkenmeier-1		(58)		D	R			9
*	*D10Bir2*	DNA segment, Chr 10, Birkenmeier-2		(2)		D	R			9
*	*D10Bir3*	DNA segment, Chr 10, Birkenmeier-3		(3)		D	R			9
*	*D10Byu1*	DNA segment, Chr 10, Brigham Young University-1		(1.5)		D	R			123
	D10Cos1	DNA segment, Chr 10, Costantini-1		29		D, B	L			52
	D10H12S53E	DNA segment, Chr 10, human D12S53E, ex D12S53Eh (Pmel17; ?= silver)		69		D	S, L	D12S53E	12pter-q21	56
	D10Led1	DNA segment, Chr 10, Leder-1, ex D10Led3		56-58		D	L			7, 48
	D10Led3	See D10Led1								
*	*D10Ler1*	DNA segment, Chr 10, Le Roy-1		3		D	L			60
*	*D10Ler2*	DNA segment, Chr 10, Le Roy-2		78		D	L			60
*	*D10Mc2*	DNA segment, Chr 10, McClelland-2		(55)		D	R			116
	D10Mit1	DNA segment, Chr 10, MIT-1		(5)		D	L			30
	D10Mit2	DNA segment, Chr 10, MIT-2		(10)		D	L, R			30
	D10Mit3	DNA segment, Chr 10, MIT-3		(15)		D	L			30
	D10Mit4	DNA segment, Chr 10, MIT-4		(14)		D	L			30
	D10Mit5	DNA segment, Chr 10, MIT-5		(22)		D	L			30
	D10Mit7	DNA segment, Chr 10, MIT-7		(43)		D	L			30
	D10Mit8	DNA segment, Chr 10, MIT-8		(45)		D	L			30
	D10Mit9	DNA segment, Chr 10, MIT-9		(51)		D	L			30
	D10Mit10	DNA segment, Chr 10, MIT-10		(53)		D	L, R			30
	D10Mit11	DNA segment, Chr 10, MIT-11		(53)		D	L, R			30
	D10Mit12	DNA segment, Chr 10, MIT-12		(54)		D	L			30
	D10Mit13	DNA segment, Chr 10, MIT-13		(64)		D	L			30
	D10Mit14	DNA segment, Chr 10, MIT-14		(72)		D	L, R			30
	D10Mit15	See D10Mit20								
*	*D10Mit16*	DNA segment, Chr 10, MIT-16		(11)		D	L			31
*	*D10Mit17*	DNA segment, Chr 10, MIT-17		(11)		D	L			31
*	*D10Mit19*	DNA segment, Chr 10, MIT-19		(23)		D	L			31
*	*D10Mit20*	DNA segment, Chr 10, MIT-20 (= D10Mit15, Sqr3)		(26)		D	L			31
*	*D10Mit21*	DNA segment, Chr 10, MIT-21		(43)		D	L			31
*	*D10Mit22*	DNA segment, Chr 10, MIT-22		(43)		D	L			31
*	*D10Mit23*	DNA segment, Chr 10, MIT-23		(43)		D	L			31
*	*D10Mit24*	DNA segment, Chr 10, MIT-24		(72)		D	L			31
*	*D10Mit25*	DNA segment, Chr 10, MIT-25		(77)		D	L			31
*	*D10Mit28*	DNA segment, Chr 10, MIT-28		(3)		D	L			31
*	*D10Mit29*	DNA segment, Chr 10, MIT-29		(23)		D	L			31
*	*D10Mit30*	DNA segment, Chr 10, MIT-30		(23)		D	L			31
*	*D10Mit31*	DNA segment, Chr 10, MIT-31		(33)		D	L			31
*	*D10Mit32*	DNA segment, Chr 10, MIT-32		(36)		D	L			31
*	*D10Mit33*	DNA segment, Chr 10, MIT-33		(64)		D	L			31
*	*D10Mit34*	See D10Mit33								
*	*D10Mit35*	DNA segment, Chr 10, MIT-35		(77)		D	L			31
*	*D10Mit36*	DNA segment, Chr 10, MIT-36				D	L			31
*	*D10Mit38*	DNA segment, Chr 10, MIT-38		(22)		D	L			31
*	*D10Mit40*	DNA segment, Chr 10, MIT-40		(22)		D	L			31
*	*D10Mit41*	DNA segment, Chr 10, MIT-41		(53)		D	L			31
*	*D10Mit42*	DNA segment, Chr 10, MIT-42		(44)		D	L			31
*	*D10Mit43*	DNA segment, Chr 10, MIT-43		(53)		D	L			31

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Table 1. *Continued.*

New	Symbol	Name	A	M	CL	T	Method	H. symbol	H. location	References
*	*D10Mit44*	DNA segment, Chr 10, MIT-44		(17)		D	L			31
*	*D10Mit45*	DNA segment, Chr 10, MIT-45		(17)		D	L			31
*	*D10Mit46*	DNA segment, Chr 10, MIT-46		(67)		D	L			31
*	*D10Mit47*	DNA segment, Chr 10, MIT-47		(67)		D	L			31
*	*D10Mit48*	DNA segment, Chr 10, MIT-48		(24)		D	L			31
	D10Nds1	DNA segment, Chr 10, Nuffield Department of Surgery-1		(3)		D	L, R			26, 30
	D10Nds2	DNA segment, Chr 10, Nuffield Department of Surgery-2		(59)		D	L, R			26, 30
	D10Nds3	DNA segment, Chr 10, Nuffield Department of Surgery-3 (ex D0Nds22)		(22)		D	L			26, 30
	D10Pas1	DNA segment, Chr 10, Pasteur Institute-1		37.5		D	L			15
	D10Pas2	DNA segment, Chr 10, Pasteur Institute-2		32.5		D	L			15
*	*D10Pas3*	DNA segment, Chr 10, Pasteur Institute-3		32.5		D	L			97
	D12S53Eh	See D10H12S53E								
	dl	downless		29.5		V, D	L, S			28, 41 87, 98, 107, 122
	Dmdl	dystrophin-like		0.5		D, B	L	DMDL	6q24	15
	dy	dystrophia muscularis		9		V	L			18, 91, 107, 120
	eb	eye blebs		66-72		V	L			49
	Egr-2	early growth response-2			B5	D, B	I	EGR2	10q21.1	24, 51
	Emv-25	endogenous ecotropic MuLV-25		9		D	L			111
	Estr	estrogen receptor		9.5		D, B	L	ESR	6q24-27	52
	Fisp12	fibroblast-inducible secreted protein			A3-B1	D, B	I			93
	Fyn	Fyn proto-oncogene		21.5		D, B	L	FYN	6q21	52
	Gad-1ps	glutamic acid decarboxylase-1 pseudogene		(57)		D	R			14
	Gja-1	gap junction membrane channel protein alpha-1 (ex Cxn43)		26.5		D, B	S	GJA1	6q14-q24.1	45, 47
	gl	grey-lethal		20-47		V	L			58
	Gli	human glioma associated oncogene	1	67		D, B	S, L, R	GLI	12q13	52, 55
*	*Gnaz*	guanine nucleotide binding protein, alpha z subunit		34.5		D, B	L	GNAZ	22q11	117
*	*Gna11*	guanine nucleotide binding protein, alpha subunit-11		37.5		D, B	L	GNA11	19p13	117
*	*Gna15*	guanine nucleotide binding protein, alpha subunit-15		37.5		D, B	L	GNA15	19p13	117
	gr	grizzled		44		V	L			6, 43, 64, 92
	Hal	histidine ammonia lyase			C3-D1	D, B	I	HAL	12q22-24.1	113
*	*Hc10*	heterochromatin, Chr 10		0	A1	D	I, L			23
	hes	hesitant		42 or 72		V				106
*	*hg*	high growth		47		V, B	L			71
	his	histidinemia (mutation at Hal locus?)		48-66		V, B	L			53
	Hk-1	hexokinase-1		30.5		B	S, L	HK1	10q22	57, 86
	Hsd	histidase synthetic rate (variant at Hal locus?)		56		B	R, L			4
*	*Iapls3-21*	intra-cisternal A particle LTR sequence 3-21				D	R			62
	Ifg	interferon gamma		64		D, B	S, L, R	IFNG	12q24.3	52, 55, 77, 81, 100, 108, 112
	Ifgr	interferon gamma receptor		13		D, B	S, L	IFNGR1	6q23-24	55, 68
	Igf-1	insulin-like growth factor-1		46		D, B	S, L	IGF1	12q23	52, 109
	Itgb2	integrin beta-2, ex Cd18, Lfa-1, Mac-1		36.5		D, B	S, P	ITGB2	21q22.3	65, 66, 90, 115
	jc	Jackson circler		29.5		V	L			42, 103
	ji	jittery		34-47		V	L			29
	kd	kidney disease		28		V	L			63
	Lfa-1	See Itgb2								
*	*Lmnb 2*	lamin B2			10C	D, B	I	LMNB2	19p13.3	8, 125
*	*Ly-41*	(Pca-1) lymphocyte alloantigen-41; membrane glycoprotein (alkaline phosphodiesterase I); plasma cell antigen-1		(18)		D, B	R	M6S1	6q22-23	16
	Mac-1	See Itgb2								
*	*Macs*	myristolated alanine-rich protein kinase C substrate		20.5		D, B	L	MACS	6q21	10
	Mdm-1	transformed mouse 3T3 cell double minute-1		64	C	D, B	S, I, L, R	MDM1	12	15, 19, 112
	Mdm-2	transformed mouse 3T3 cell double minute-2			C	D, B	S, I	MDM2	12q13-14	19
*	*Mdm-3*	transformed mouse 3T3 cell double minute-3				D, B	S, P			19, 32
	Mgf	mast cell growth factor (see Sl)								
	mh	mocha		44		V	L			41, 59
	Minta	murine leukemia virus integration site A		39.5		D	L			108
	Mip	major intrinsic protein of eye-lens-fiber cell membranes			D1	D, B	I	MIP	12cen-q14.3	44
	Mpmv-5	modified polytropic murine leukemia virus-5		(0.5)		D	R, L			40
	Mpmv-12	modified polytropic murine leukemia virus-12		(23)		D	R, L			40
	Mpmv-40	modified polytropic murine leukemia virus-40		(25)		D	L			36
	Ms6-3	minisatellite sequence 6-3		(67)		D	R			50

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Table 1. *Continued.*

New	Symbol	Name	A	M	CL	T	Method	H. symbol	H. location	References
	Ms15-8	minisatellite sequence 15-8		(62)		D	R			50
–	*Myb*	myeloblastosis oncogene	1	14		D, B	S, R, L	MYB	6q22-23	15, 52, 55, 78, 97, 100, 108, 111
*	*Myf5*	myogenic factor-5		65.5		D, B	L	MYF5	12	17, 60
*	*Myf6*	myogenic factor-6; herculin		65.5		D, B	P	MYF6	12	72
	Nyfb	nuclear transcription factor-Y alpha			C3-D1	D, B	I			61
	Pah	phenylalanine hydroxylase	1	45	C2-D1	D, B	I, L	PAH	12q22-24.2	12, 54, 70, 100, 108
*	*Pcmt1*	L-isoaspartyl/D-aspartyl protein methyltransferase		6		D	L	PCMT1	6q22.3-24	67
	Pep-2	peptidase-2, ex Trip-1		53	D	B	S, L	PEPB	12q21	35
*	*Pgk-1rs6h*	phosphoglycerate kinase related sequence-6		(18)		D	R			2
	Pfkl	phosphofructokinase, liver form		36.5		D, B	S, L, P	PFKL	21q22.3	65, 89, 90
	Pfp	pore-forming protein		33.5		D, B	S, L	PRF1	10q22	55, 114
	pg	pygmy		66		D, V	L			33, 54, 124
	Pmv-8	polytropic MuLV provirus-8		(33)		D	L			39
	Prim1	DNA primase, small subunit			D	D, B	I			1
	Pyp	pyrophosphatase				B	S	PP	10q11.1-24	57
	Rnu3b-rs4	U3B small nuclear RNA related sequence-4			A4-B2	D	I			69
	Ros-1	Ros-1 proto-oncogene	1	25		D, B	L	ROS1	6q21-22	52
*	*Rrm2-ps4*	ribonucleotide reductase M2 pseudogene-4		32		D	L			67
	S100b	S100 protein, beta polypeptide (neural), ex Bpb	1	35.5		D, B	S, L, P	S100B	21q22	52, 65, 89, 90, 100
	si	silver		71.5		V	L			33, 95
	Sl (Mgf)	steel (mast cell growth factor)	1	57	D1	D, B, V	L, C	MGF	12q14.3-24.3	6, 7, 54, 80, 86, 94, 96, 100, 109, 111, 118, 121, 122
	Sqr3	See D10Mit20								
	Tknsl	translocation in NS-1 plasmacytoma				D	S			85
	Tpi-rs5	triosephosphate isomerase related sequence-5		13.5		D	L			102
	Tpi-rs6	triosephosphate isomerase related sequence-6		23		D	L			102
	Tpi-rs7	triosephosphate isomerase related sequence-7		24.5		D	L			102
	Tra-1	tumor rejection antigen gp96		49.5		D, B	S, L	TRA1	12q24.2-24.3	55, 105
	Trip-1	See Pep-2								
	v	waltzer		28		V	L			6, 11, 28, 41, 64, 86, 107, 122
	Xmv-31	xenotropic MuLV provirus-31		(61)		D	R, L			38
*	*Xmv-39*	xenotropic MuLV provirus-39		(14)		D	R			38
	Xmv-51	xenotropic MuLV provirus-51		(61)		D	R, L			37
	Xmv-54	xenotropic MuLV provirus-54		(22)		D	R, L			37
	Zfa	zinc finger protein, autosomal		26.5	B	D, B	I, L			15, 54, 73, 84

An asterisk in the "New" column denotes a new locus added to last year's list. In the "A" column, "1" denotes a primary reference locus. The "M" column—map position—gives the estimated distance from the centromere. The numbers shown in parentheses denote map positions inferred primarily from RI strain data or the MIT intercross. The parentheses are intended to indicate that these loci are not necessarily well-integrated in the consensus map. The "CL" column—cytogenetic localization—gives localization to specific chromosomal bands by in situ hybridization or analysis of chromosomal rearrangements. In the "T" column, D = DNA (any locus defined by a DNA sequence or clone); P = PCR primers; B = biochemical/protein/immunological; and V = visible/other phenotype. In the "Method" column, I = in situ hybridization; S = somatic cell genetics; R = RI strains; L = linkage analysis by backcross or intercross; C = cytogenetic analysis (translocations, visible deletions, etc.); D = deletion analysis (molecular); H = radiation hybrid analysis; and P = physical mapping (PFGE, YACS, etc.). Information on human genes was taken from the human genomic database, GDB. Evidence for Chr 10 linkage of *Pgk-1rs6* is identity of SDP with *Ly-41* in 12 BXH RI strains.

the apparent close linkage between *D10Mit14* and *Mdm-1* (0/16 recombinants in the BXD RI strains) and the very close linkage between *Mdm-1* and *Ifg*. Since *pg* is distal to *Ifg*, it is likely to be distal to *Mdm-1* as well.

Figure 2 shows the updated Chr 10 cytogenetic map. Several new deletions involving the steel locus have been added (see below).

Microsatellite variants

The major addition to the Chr 10 map consists of 28 additional SSLPs (Dietrich et al. 1992a). These 28 markers were mapped by use of 46 (C57BL/6J-*ob* × CAST/Ei)F_2 mice. Recombination frequencies are not provided for individual linkages, so the map shown here (Fig. 1) is based primarily on the map shown by the authors. The new markers do not extend the SSLP map beyond the previous range of ~75 cM. If these markers are randomly distributed over the linkage map, then it is unlikely that total map distance is much greater than 75 centimorgans (cM), at least as determined in this particular cross (n = 46). A subset of the *D10Mit* markers have been mapped with respect to other markers in the 'Copeland-Jenkins' interspecific backcross. Although preliminary results were presented at the Buffalo meeting (Weaver et al. 1992), the merger of these two maps awaits publication of the data.

A centromeric marker

Also reported at the Buffalo meeting was an estimated distance between the subcentromeric heterochromatin found in most laboratory strains and the *Myb* locus (Ceci et al. 1992). The centromeric heterochromatin marker, *Hc10*, was scored in (C57BL/6Ros × *Mus*

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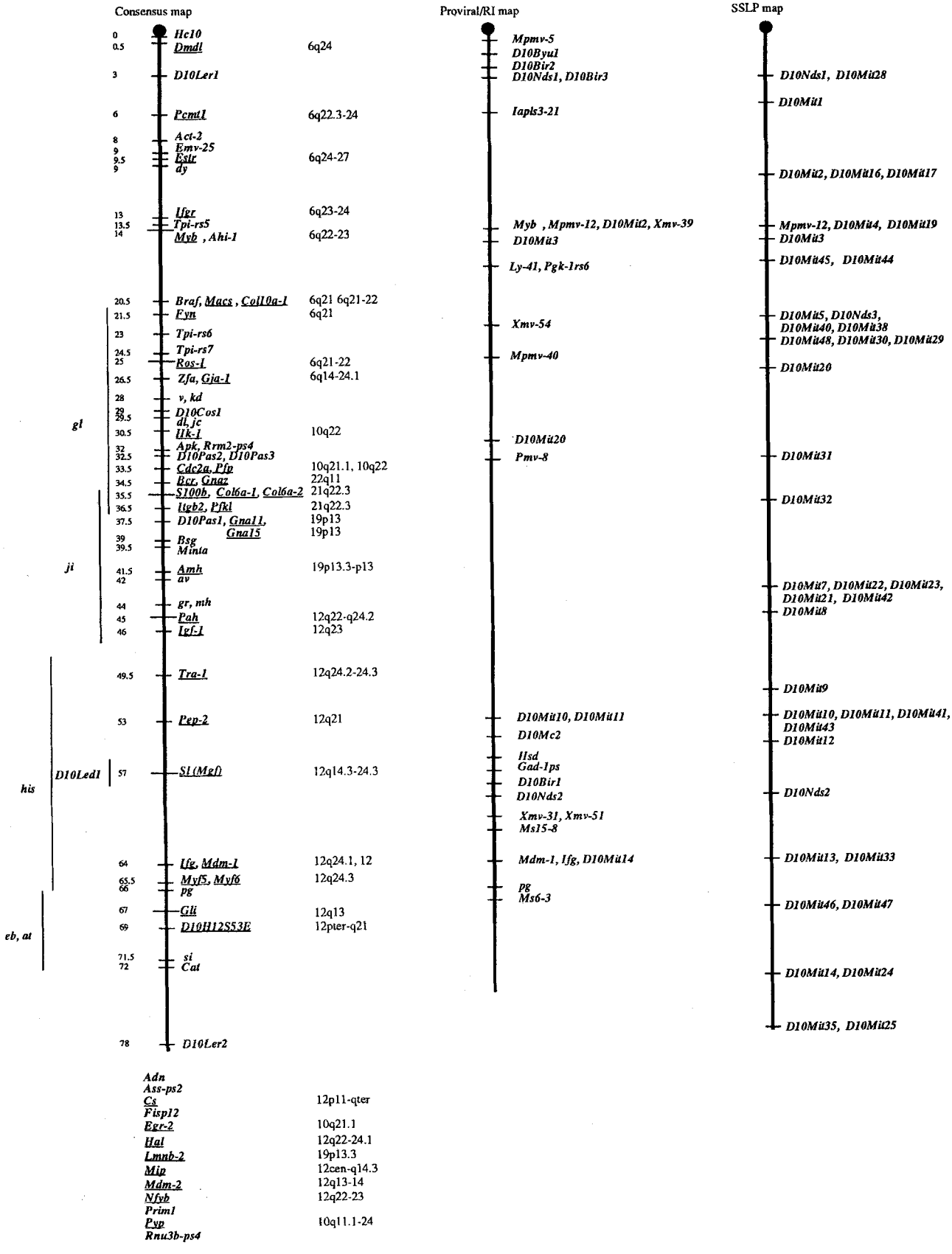

Table 2. Gene order and recombination frequencies determined by multipoint crosses.

Crosses: gene order and recombination frequencies ± standard error	Total map length (cM)	No. of progeny	References
A. (C57BL/6J x *M. spretus*)F1 x C57BL/6J *Act-2*-1.7 ± 1.0-*Estr*-4.8 ± 1.6-(*Tpi-rs5*, *Ahi-1*, *Myb*)-6.1 ± 1.8-*Braf*-3.3 ± 1.5-*Fyn*-1.3 ± 0.9-*Tpi-rs6*-1.5 ± 0.9-*Tpi-rs7*-0.8 ± 0.8-*Ros*-1.0 ± 1.0-*Gja-1*-2.4 ± 1.4-*D10Cos1*-6.2 ± 2.0-*Cdc2a*-0.5 ± 0.5-(*Bcr*, *Gnaz*)-2.5 ± 1.2-(*Col6a-1*, *Col6a-2*, *S100b*)-1.7 ± 1.0-(*Gna15*, *Gna11*)-6.5 ± 1.9-(*Pah*, *Igf-1*)-15.8 ± 2.7-*Sl*-7.6 ± 1.9-*Ifg*-0.5 ± 0.5-*pg*-2.1 ± 1.1-*Gli*-0.5 ± 0.5-*D10H12S53E*	68.4	104-199	25, 52, 56, 102, 117
B. [C57BL/6 x SPE (*M. spretus*)]F1 x C57BL/6 and [BALB/c x SPE (*M. spretus*)]F1 x BALB/c *Dmdl*-14.8 ± 4.5-*Myb*-3.3 ± 3.3-*D10Ler1*-7.7 ± 5.2-*Zfa*-6.7 ± 4.6-*D10Cos1*-2.3 ± 2.3-*D10Pas3*-1.8 ± 1.8-*D10Pas1*-1.7 ±1.7-*Bsg*-4.4 ± 2.5-*Pah*-11.0 ± 3.9-*Mdm-1*-1.5 ± 1.5-*Myf5*-12.5 ± 6.8-*D10Ler2*	67.7	26-69	15, 60, 73, 97, and J.-L. Guenet, p.c.
C. C3H/HeJ-*gld* x *M. spretus*)F1 x C3H/HeJ-*gld* *Myb*-7.0 ± 2.4-(*Col10a-1*, *Braf*, *Macs*)-0.9 ± 0.9-*Fyn*-25.4 ± 4.1-*Minta*-6.1 ± 2.2-*Pah*-18.3 ± 3.6-*Ifg*	57.7	114	3, 10, 108, M. Seldin, p.c.
D. [(AKR/J or C58/J or NFS/N) x *M. m. musculus* (Skive)] x *M. m. musculus* (Skive) *Ifgr*-1.1 ± 1.1-*Myb*-23.3± 4.4-*Pfp*-11.1 ± 3.3-*Tra-1*-14.4 ± 3.7-*Ifg*-5.6 ± 2.4-*Gli*	55.5	90	55
E. (BXD-32 or SWR/J) x (CAST/Ei x MEV)F1 *Emv-25*-6.3 ± 2.5-*Myb*-26.7 ± 4.7-*Igf-1*-11.3 ± 3.8-*Sl*-18.5 ± 4.3-(*Ifg*, *Mdm-1*)	62.8	71-95	109, 111, 112
F. (129/Sv-*Sl*/+ x MOL-MIT)F1 x 129/SvJ-+/+ *Myb*-34.9 ± 4.6-*S100b*-8.5 ± 2.7-*Pah*-8.5 ± 2.7-*Sl*-12.3 ± 3.2-*Ifg*	64.2	106	100
G. (C57BL/6J x *M. spretus*)F1 x C57BL/6J *Pcmt1*-8.2 ± 3.5-*Myb*-23.0 ± 5.4-*Rrm2-4ps*-13.1 ± 4.3-*Pah*	44.3	61	67
H. A/J x (A/J x C57BL/6J)F1 and (A/J x C57BL/6J)F1 x C57BL/6J *D10Nds1*-10.0 ± 4.7-*D10Mit2*-27.5 ± 7.1-*D10Mit10*-22.5 ± 6.6-*D10Mit14*	60.0	40	75

spretus) × *Mus spretus* interspecific backcross progeny by in situ hybridization with a major satellite DNA probe. The estimated distance, 12.4 cM, provides a minimal distance between *Myb* and the centromeric telomere. This result is at variance with the prior placement of *Dmdl* marker at a position 23 cM proximal to *Myb*. Recently, the *Dmdl–Myb* distance has been reduced to 13.5 cM (J.-L. Guénet, personal communication). The latter value is more consistent with the *Hc10–Myb* distance.

New gene loci

Nine newly identified genes (each defined by a DNA probe) have been added to Chr 10. Three guanine nucleotide-binding protein subunit genes have been mapped (Wilkie et al. 1992). Two of these (guanine nucleotide-binding protein alpha subunit-11 and -15) failed to recombine in a *M. spretus* backcross and are reported to be closely linked physically as well. A third gene, (guanine nucleotide-binding protein, alpha z subunit) maps just 1 cM proximal to the other two. The genes encoding myristolated, alanine-rich protein kinase C substrate (*Macs*) and procollagen type X alpha 1 subunit (*Col10a-1*) fail to recombine with one another or the previously mapped *Braf* gene (Apte et al. 1992; Blackshear et al. 1992). The myogenic differentiation factor-5 gene (*Myf5*) was reported to map distal to *Mdm-1* (Le Roy et al. 1992; J.-L. Guénet, pers. comm.). The lamin B2 gene (*Lmnb-2*) was assigned to the Chr 10C band by in situ hybridization (Zewe et al. 1991). The gene encoding L-isoaspartyl/D-aspartyl protein methyltransferase (*Pcmt1*) was mapped 8.2 ± 3.5 cM proximal to *Myb* (MacLaren et

Fig. 1. Comprehensive maps of Chr 10. The consensus map on the left represents a map compiled with multilocus and two-point cross data. All genes that have been mapped in human are underlined, and the location in the human map is given to the right of the chromosome. Reference loci are indicated by a wider bar. Loci that have been mapped in two-point crosses only are shown as bars to the left of the chromosome. Loci that have been assigned to Chr 10 on the basis of somatic cell hybrids are listed at the bottom of the chromosome. The following changes have been made to the consensus map: a) the distance between *Dmdl* and *Myb* was reduced to 13.5 cM, thus moving all loci except *Dmdl* up 9 cM, b) a subcentromeric heterochromatin marker (*Hc10*) was placed at position 0.0, c) the following new loci have been added (proximal to distal): *D10Ler1*, *Pcmt1*, *Macs*, *Col10a-1*, *Rrm2-ps4*, *Gnaz*, *Gna11*, *Gna15*, *Myf5*, and *D10Ler2*; d) *Pfkl* was moved to a more proximal position based on revised mapping data and homology considerations; e) the locus symbol *Cd18* has been replaced by *Itgb2*; f) *Mdm-1* was moved alongside *Ifg*.

The RI/proviral map represents data from RI strains as well as from a (DBA/1J × 129/J)F_1 × 129/J (DX1X1) cross (Frankel et al. 1991), reciprocal backcrosses between NZB/BINJ and SM/J (Frankel et al. 1992) and the typing of RI strains for microsatellite sequences. The following changes to the proviral/RI map should be noted: a) the following loci have been added based on RI strain mapping data: *D10Byu1*, *D10Bir3*, *D10Bir2*, *Iapls3-21*, *Xmv-39*, *Ly-41*, *Pgk-rs6*, *D10Mc2*, *D10Bir1*, *Ifg*, and *Mdm-1*; b) the order of *Ms15-8*, *Xmv-31*, *Xmv-51*, *D10Nds2*, *Gad-1ps*, and *Hsd* has been reversed; c) *D10Mit14* and *Ms6-3* have been moved to a more proximal position on the basis of the apparent close linkage of *D10Mit14* to *Mdm-1*; d) *Mdm-1* and *D10Mit14* are shown proximal to *pg* based on the close linkage of *Mdm-1* to *Ifg*. e) the locus symbol of *D10Mit15* has been replaced by *D10Mit20*; f) *Mpmv-5* is moved closer to *Myb* and *Mpmv-12* on the basis of new backcross data; g) *D10Nds1* is placed close to, but distal to, *Mpmv-5* based on AXB and BXA RI data.

The SSLP map on the right is a representation of the map presented by Dietrich and colleagues (1992a, b).

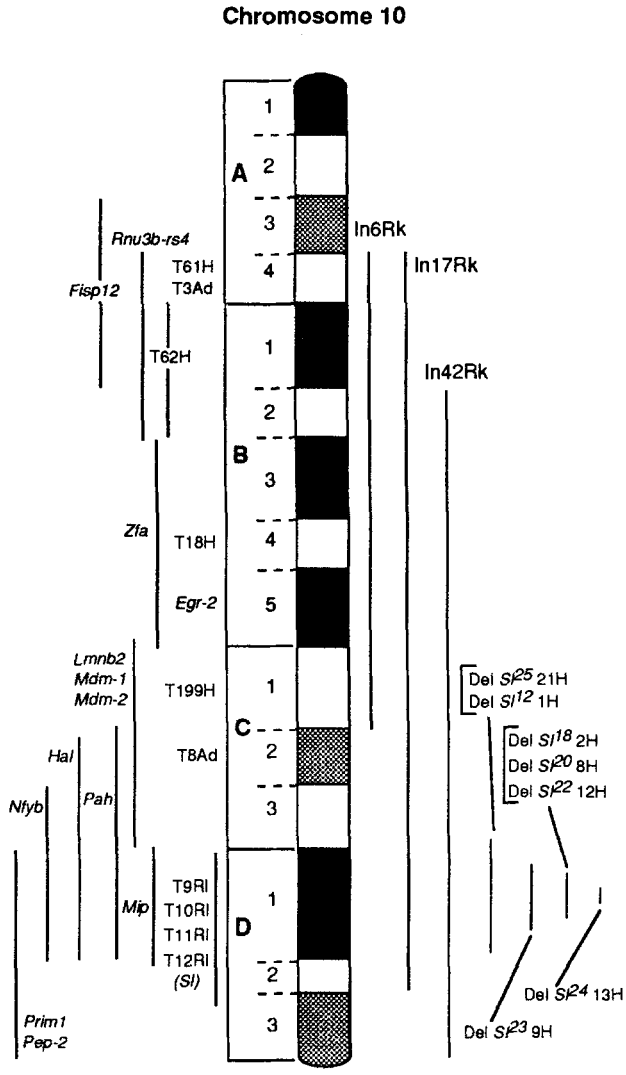

Fig. 2. Cytogenetic map of Chr 10 showing the banding pattern of Nesbitt and Francke (1973) with the positions of inversions, translocations, deletions, and loci mapped by in situ hybridization. New deletions at the *Sl* locus have been added. *Lmnb-2* has been added to band 10C of the cytogenetic map. Note that the cytogenetic positions of *Mdm-1* and *Sl* are inconsistent with their genetic positions relative to one another.

al. 1992). The membrane glycoprotein, alkaline phosphodiester I gene (official name: lymphocyte antigen-41, *Ly-41;* Morse 1992), which has been known for many years as plasma cell antigen-1 (*Pca-1*), was mapped near the *Myb* gene (Buckley and Goding 1992). Finally, the transformed mouse 3T3 cell double minute-3 gene (*Mdm-3*), which is amplified and overexpressed in a spontaneously transformed 3T3 cell line, was found to be physically linked to *Mdm-2* (Fakharzadeh et al. 1991).

DNA variants

Nine DNA sequence variants have been mapped to Chr 10. The xenotropic murine leukemia virus genome, *Xmv-39,* shows linkage to *Ly-41* in RI strains (Buckley and Goding 1992; Frankel et al. 1989). Likewise, a previously described phosphoglycerate kinase-related sequence (proposed designation, *Pgk-1rs6;* Adra et al. 1988) shows an SDP identical to *Ly-41* in 12 BXH RI strains, suggesting that this sequence is also on Chr 10. Six arbitrary oligonucleotide-primed PCR variants (*D10Mc2, D10Byu1, D10Bir1, D10Bir2, D10Bir3,* and *D10Pas3*) were mapped to Chr 10 (Birkenmeier et al. 1992; Serikawa et al. 1992; Welsh et al. 1991; Woodward et al. 1992). Two anonymous genomic clones, *D10Ler1* and *D10Ler2,* were mapped in an interspecific backcross (Le Roy et al. 1992). A pseudogene, ribonucleotide reductase M2 pseudogene-4 (*Rrm2-ps4*), was mapped 23.0 ± 5.4 cM distal to *Myb* and 13.1 ± 4.3 cM proximal to *Pah* (MacLaren et al. 1992). An intra-cisternal A particle long terminal repeat sequence RFLV (*Iapls3-21*) was detected with an oligonucleotide probe and mapped near *D10Byu1* in the BXD RI strains (Lueders et al. 1993).

Visible mutants and other variants

A mutation conferring rapid postweaning growth and large mature body size [designated high growth (*hg*)] has been mapped in the vicinity of the insulin-like growth factor I gene (*Igf-1*). *Igf-1* is considered a candidate gene for the site of the *hg* mutation (Medrano et al. 1992). No other visible mutations or other loci defined by functional variants were mapped to Chr 10.

Human homologies

Loci that have been added to the map which have also been mapped in human are (with the human localization): *Col10a-1* (6q21-q22), *Gnaz* (22q11), *Gnal1* (19p13), *Gnal5* (19p13), *Lmnb-2* (19p13.3), *Ly-41* (6q22-q23), *Macs* (6q21), *Myf5* (12), *Myf6* (12) and *Pcmt1* (6q22.3-q24). Previously mapped Chr 10 loci whose human homologs have now been mapped are: *Pfp* (10q22) and *Mdm-2* (12q13-q14). The gap junction membrane channel protein-1 (*Gja-1*), previously assigned to Chr 10, has been placed in the mouse linkage map and further localized in the human map (6q14-q24.1). This information is summarized in Table 3. No new regions of homology have been identified. In most cases these assignments do not disrupt previously identified homologous segments. However, the placement of *Gnal1* and *Gnal5* 1.7 cM distal to *S100b* and *Col6a-1/Col6a-2* identifies a region of homology that includes the previously mapped anti-Mullerian hormone (*Amh*). These loci appear to straddle the *Pfp* locus, which is now assigned to HSA 10q22. However, the placement of *Pfp* is inexact as the nearest anchored markers in the *Pfp*-mapping cross are *Myb* and *Ifg*. Rather than postulating that an inversion has intermingled HSA10- and HSA19-homologous regions of Chr 10, we have somewhat arbitrarily moved *Pfp* 4 cM toward the centromere until more definitive mapping data are available. This makes *Pfp* contiguous with *Hk-1* and *Cdc2a,* whose human homologs map to HSA10q. The lamin B2 subunit gene (*Lmnb-2*) was

Table 3. Newly identified homologies involving mouse Chr 10.

Symbol	Name	Chr position	Human position	Human symbol	References
Col10a-1	procollagen type X, alpha 1	close to *Macs* and *Braf*	6q21-q22	COL10A1	3
Gja-1	gap junction membrane channel protein-1 (connexin-43)	1 cM distal to *Ros-1*	6q14-q24.1	GJA1	45
Gna11	guanine nucleotide binding protein, alpha subunit-11	0 cM from *Gna15*	19p13	GNA11	117
Gna15	guanine nucleotide binding protein, alpha subunit-15	1.7 cM distal to S100b	19p13	GNA15	117
Gnaz	guanine nucleotide binding protein, alpha z subunit	0.5±0.5 cM distal to *Bcr*	22q11	GNAZ	117
Lmnb-2	lamin B2 subunit	10C	19p13.3	LMNB2	8
Ly-41	lymphocyte alloantigen-41; membrane glycoprotein (alkaline phosphodiesterase I); plasma cell antigen-1	near *Myb*	6q22-23	M6S1	16
Pcmt1	guanine nucleotide binding protein, alpha subunit-11	8.2 ± 3.5 cM proximal to *Myb*	6q22.3-24	PCMT1	67
Pfp	perforin	*Myb* 23 ± 4.5 *Pfp* 11.1 ± 3.3 *Tra-1*	10q22	PRF1	34
Macs	MARCKs (myristoylated, alanine-rich C-kinase substrate)	7 cM distal to *Myb*	6q21	MACS	10
Mdm-2	murine double minutes-2	close to *Mdm-1*, *in situ*, co-amplified	12q13-14	MDM2	83
Myf5	myogenic factor-5	1.5 ± 1.5 cM distal to *Mdm-1*	12	MYF5	60 and J.-L. Guenet (p.c.)
Myf6	myogenic factor-6	physically linked to *Myf5*	12	MYF6	13, 72

assigned to band 10C, while its human homolog was placed at HSA 19p13.3, adding a fourth gene to the Chr 10/HSA19p conserved synteny group. The 10C cytogenetic assignment is consistent with a predicted genetic position near the other members of this synteny group. Four additional genes syntenic with HSA6 have been mapped to the proximal end of Chr 10, bringing the total number to ten. The *Gnaz* gene showed a single recombinant with *Bcr*, indicating the existence of a short region of homology to HSA22q11 located between regions homologous to HSA10q and HSA21q.

Recombinant inbred strains

Table 4 shows the strain distribution patterns for loci typed in various RI strains.

New chromosomal rearrangements

Seven deletions encompassing the steel locus have been identified and analyzed by Cattanach and coworkers (1993). All seven *Sl* mutations show the grey coat with white spotting on the head and belly that characterizes the *Sl* mutation, but of the six tested, none produced the anemic black-eyed white homozygotes on intercrossing. Instead, pre- and postnatal homozygous lethalities were observed, indicating that damage at loci other than *Sl* had occurred. All seven mutations carried deletions at the *Sl* locus, ranging in size from 2.5% to 10% of the chromosome. A new nomenclature has been adopted to describe these deletions. The mutation previously referred to as Df(*Sl*)12H (Cattanach et al. 1988) is now given the complete designation Del(10)Sl^{12}1H, with the abbreviated designation Sl^{12H}. Likewise, Df(*Sl*)18H (Cattanach and Rasberry 1988) is now Del(10)Sl^{18}2H, with the abbreviated designation Sl^{18H}. Five other *Sl* deletions are designated Del(10)Sl^{20}8H, Del(10)Sl^{22}12H, Del(10)Sl^{23}9H, Del(10)Sl^{24}13H, and Del(10)Sl^{25}21H, with abbreviated symbols Sl^{20H}, Sl^{22H}, Sl^{23H}, Sl^{24H}, and Sl^{25H}, respectively. Crosses between Sl^{22H}, SL^{23H}, and Sl^{24H} revealed that Sl^{24H}, which gives an early post-implantation homozygous lethality, complements Sl^{22H} and Sl^{23H}, which give pre-implantation homozygous lethalities, such that anemic black-eyed white compounds are produced and survive to birth. Complementation was not found in Sl^{22H}/Sl^{23H} compounds. Sl^{24H} would therefore appear to represent a deletion in a different region of the chromosome from that of Sl^{22H} and Sl^{23H}. All of the new deletions had breakpoints in 10D1. The authors note that the heterozygous viability of large deletions including the *Sl* locus indicates that the genes in this region are either unimportant in development or else their dosage is not critical. The fact that other genes have not been mapped in the vicinity of *Sl* is consistent with this view.

Imprinting

Experiments have been conducted to test for the effects of imprinting on Chr 10 (Beechey and Cattanach 1992). Mice doubly heterozygous for Rb(1.10)10Bnr and Rb(10.11)8Bnr were intercrossed, and downless (*dl*) was used as a marker for detecting uniparental

Table 4. RI SDPs.

BXD (C57BL/6J x DBA/2J)

Locus	01	02	05	06	08	09	11	12	13	14	15	16	18	19	20	21	22	23	24	25	27	28	29	30	31	32	References
Mpmv-5	D	D	D	B	D	B	B	B	B	B	B	B	D	D	B	B	B	D	B	D	B	D	B	D	B	D	40
*D10Byu1**	D	D	D	B	D	B	B	D	B	B	B	B	D	D	B	B	B	D	B	D	B	D	B	D	B	D	123
*D10Bir2**	D	D	D	B	D	B	B	D	B	B	B	B	D	D	B	B	B	B	B	D	B	D	B	D	B	D	9
*Iapls3-21**	D	D	D	B	D	D	D	D	B	B	B	B	D	D	B	B	B	D	B	D	B	D	B	D	B	D	62
D10Mit3		D	D	B	B	B	B	B	B	D	D	B	B	B	B	D	B	D	D	D	B	D	B				30
D10Mit120		D	D	B	D	B	B	B		D	B	D	D	B	B	D	B	D	D	D	B	B	D	B			30
D10Mit10		D	D	D	D	B	D	B	B	D	B	D	D	B	B	D	B	D	D	D	D	D	D	B			30
D10Mit11		D	D	D	D	B	D	B	B	D	B	D	D	B	B	D	B	D	D	D	D	D	D	B			30
*D10Mc2**	B	D	D	D	B	B	D	B	B	D	B	D	D	B	B	D	B	D	D	D	D						116
*D10Bir1**	B	D	D	D	B	B	D	B	B	B	D	D	D	B	B	D	B	D	D	D	D	D	B	B	B	D	9
Xmv-31	B	D	B	D	B	B	B	B	B	B	D	D	D	B	B	D	B	D	D	D	D	D	B	B	B	D	38
Ms15-8	B	D	B	D	B	B	B	B	B	B	B	D	D	B	B	D	B		D	D	D	D	B	B	B	D	50
*Mdm-1**	B	D	B	D							B	D	D	D	D	D	B	D	D	D	D	D	B	B	D	B	112
D10Mit14		D	B	D	B	B	B	B	B	B	B	D	D	D	D	D	B	D	D	D	D	D	B				30
Ms6-3	B	D	B	D	B	B	D	B	B	B	B	D	D	D	D	D	B		D	D	B	D	B	B	D	D	50

AKXD (AKR/J x DBA/2J)

Locus	01	02	03	06	07	08	09	10	11	12	13	14	15	16	17	18	20	21	22	23	24	25	26	27	28	References
D10Nds1	D	A	A	A	A	A	A	D	D	A	D	A	D	D		D	A	A	A	D	A	A	D	D	D	26
*D10Bir3**	D	A	A	A	A	A	A	D	D	A	D	A	D	D	D	D	A	A	A	D	A	A	D	D	D	9
Mpmv-12	A	A	A	A	A	A	A	D	D	A	D	A		D		D	D	D	A	D	D	A	A	D	D	40
Gad-1ps	D	D	D	A	A	D	D	A	D	A	D	A	A	A	A	A	A	D	A	D	D	A	A	A	D	14
D10Nds2	A	D	D	A	A	D	D	A	D	A	D	A	A	A		A	A	D	A	D	D	A	A	A	D	26
Xmv-31	A	D	A	A	A	D	D	A	A	A	D	A	A	A	A	A	A	D	A	D	D	A	A	D	D	38
*Mdm-1**	A	D	A	D	A	D	D	A	A	A	A	D	A	A	A	A	D	D	A	A	D	A	A	A	D	112

AKXL (AKR/J x C57L/J)

Locus	05	06	07	08	09	12	13	14	16	17	19	01	04	15	18	20	07	18	References
*Xmv-39**	L	A	A	L	L	L	L	L	L	A	A	A	L	A	A	A	A	A	38
*Myb**	L	A	A	L	L	L	L	L	L	A	A	A	L	A	A	A	A	A	16
*Ly-41**	A	A	A	A	L	L	L	L	L	A	L	A	L	A	A	A	A	A	16
Gad-1ps	L	A	A	L	A	L	A	A	A	L	A	A	L	L	L	L	A	L	14
*Mdm-1**	A	A	L	L	A	L	A	L	A	L	A	L	L	L	A	L	A	L	112

SWXL (SWR/J x C57L/J)

Locus	04	07	12	14	15	16	17	Reference
Hsd	S	S	L	S	L	S	S	4

BXH (C57BL/6J x C3H/HeJ)

Locus	02	03	04	06	07	08	09	10	12	13	14	19	Reference
Mpmv-5	H	B	H	B	H	H	H	B	H	B	H	H	40
*Pgk-rs6**	H	B	H	B	H	H	B	B	B	H	H	H	2
*Ly-41**	H	B	H	B	H	H	B	B	B	H	H	H	16
Hsd	B	H	B	H	H	B	H	H	B	H	B	H	4
Gad-1ps	B	H	B	H	H	H	H	H	B	H	B	H	14, 112
*Mdm-1**	B	B	B	B	H	H	H	H	B	H	B	H	112

CXB (BALB/cBy x C57BL/6By)

Locus:	D	E	G	H	I	J	K	Reference
Mpmv-5	C	B	B	B	B	B	C	40
*Myb**	C	B	B	B	B	B	C	16
Mpmv-12	C	B	B	B	B	B	C	40
*Ly-41**	C	B	B	B	B	B	C	16
Hsd	B	C	B	C	B	C	C	4
Xmv-31	B	C	B	B	B	C	C	38
*Mdm-1**	B	C	B	C	B	B	B	112
Gli	B	C	B	B	C	B	B	55

Continued on next page

Table 4. *Continued.*

AXB (A/J x C57BL/6J)

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	17	18	19	20	21	23	24	25	Reference
Mpmv-5	B	A	B	B	A	B	B	A	A	A	B	A	B	B	A	A	B	A	B	A	B	B	A	40
*D10Ndx1**	B	A	B	B	A	B	B	A	A	A	B	A	B	B	A	A	B	B	B	A		B	B	75
*D10Mit2**	A	A	A	B	A	A	B	A	A	A	B		B	B	A	A	B	B	B	B		B	A	75
*Myb**	A	A	A	B	A	A	B	A	A	A	B	B	B	B			B		B	B	B	B	A	A	40
Mpmv-12	A	A	A	B	A	A	B	A	A	A	B	B	B	B	A	A	B	B	B	B	B	B	A	A	40
*D10Mit10**	B	A	B	B	A	B	A	B	A	A	B	B	B	B	B	B	B	B	B	B		A	B	75
*D10Mit14**	B	B	A	B	A	B	A	A	A	A	A	B	B	B	A	B	A	B	B	B		B	B	75

BXA (C57BL/6J x A/J)

Locus	1	2	4	6	7	8	9	10	11	12	13	14	16	17	18	19	20	21	22	23	24	25	26	Reference
Mpmv-5	A	A	A	B	B	B	B	A	B	B	A	B	A	B	A	B	A	A	B	B	B	A		40
*D10Ndx1**	A	A	A		B	B	B		B	B	A	B	A	B	A		A	A	B	A	B	A		75
*D10Mit2**	B	A	A		B	B	B		B	B	A	B	A	B	A		B	A	B	A	B	B		75
Myb	B	A	A	B	B	B	B	A	B	B	A	B		B	A	A	B	A	B	A	B			40
Mpmv-12	B	A	A	B	B	B	B	A	B	B	A	B	A	B	A	A	B	A	B	A	B	B		40
*D10Mit10**	B	A	B		B	B	B		B	B	A	B	B	B	A		A	A	A	B	B	A		75
*D10Mit14**	B	B	B		B	A	B		B	B	A	B	B	A	B		B	B	A	B	A	A		75

NXSM (NZB/BINJ x SM/J)

Locus	A	C	D	E	F	I	L	N	P	Q	T1	T2	U	V	W	X	Z	Locus
Mpmv-12	S	S	S	N	N	S	S	N	N	S	N	N	N	N	S	S	N	37
Xmv-54	S	S	S	N	N	S	S	N	N	N	N	N	N	N	S	N	N	37
Xmv-31	S	N	S	N	N	N	N	N	S	S	N	N	S	N	S	S	S	37
Xmv-51	S	N	S	N	N	N	N	N	S	S	N	N	S	N	S	S	S	37
pg	N	S	S	N	N	N	N	N	S	S	N	N	S	N	S	S	S	37

NX8 (NZB/Icr x C58/J)

Locus	3	4	5	6	9	13	15	16	17	18	19	20	Reference
*Ifg**	N	E	N	E	E	E	N	N	N	N	E	E	112
*Mdm-1**	N	E	N	E	E	E	N	N	N	N	E	E	112

SWXJ (SWR/Bm x SJL/J)

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	Reference
*Ifg**	S	J	S	S	J	J	J	S	S	S	J	J	S	S	112
*Mdm-1**	S	J	S	S	J	J	J	S	S	S	J	J	S	S	112

CXJ (BALB/cKe x SJL/J)

Locus	1	3	4	6	8	9	10	13	15	Reference
*Ifg**	C	J	J	J	C	C	J	C	C	112
*Mdm-1**	C	J	J	J	C	C	J	C	C	112

NX129 (NZB/BINJ x 129/J)

Locus	1	2	5	7	10	12	17	19	Reference
*Ifg**	9	9	N	9	9	9	N	N	112
*Mdm-1**	9	9	N	9	9	9	N	N	112

SDPs of Chr 10 loci in RI strains of mice. The RI strain sets, (e.g., BXD), were derived from crosses between the two progenitor inbred strains (e.g., C57BL/6J × DBA/2J) shown at the top of each table. Numbers or letters in the second row of each table identify individual RI strains, and letters in the body of each table denote the inheritance of marker alleles from the respective parents. Newly defined SDPs are denoted by asterisks. Letters in bold are used to highlight alleles inherited from one of the two progenitor strains of each RI set.

disomy. Both paternal and maternal disomic mice were recovered and were phenotypically normal although they were substantially smaller than their littermates. The authors conclude that the difference in body weight might be explained by homozygosity for *dl*. Thus, there are evidently no genes on Chr 10 for which uniparental inheritance is incompatible with survival. Previous analysis of the D(10.18)18H translocation had shown that there were no vital genes distal to the Chr 10 breakpoint (band B4).

Reference loci

Although the six reference loci (*Myb, Ros-1, S100b, Pah, Sl,* and *Gli*) recommended last year by the committee have the shortcoming that their polymorphism among common inbred strains is largely unknown, we do not feel that there is sufficient grounds for adopting a new set of reference loci at this time.

Acknowledgments. We thank Dr. Eric Lander for providing data prior to publication and Drs. Larry Mobraaten and Joseph Nadeau for their comments on the manuscript. The writing of this report was facilitated by access to GBASE, a mouse genetic database maintained at The Jackson Laboratory by L.J. Maltais, A.L. Hillyard, D.P. Doolittle, M.T. Davisson, J.N. Guidi, and T.H. Roderick. B.A. Taylor received support from National Institutes of Health research grant CA33093. W.N. Frankel is a Special Fellow of The Leukemia Society of America, Inc.