Mammalian Genome 3: S44–S54, 1992

Mammalian Genome

Mouse Chromosome 3

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Received March 30, 1992

Introduction

This report provides an update to the first Chromosome (Chr) 3 report (Meisler and Seldin 1991), which should be consulted for descriptions of mutant genes and conserved linkage groups. We have included an expanded locus list with 17 new loci, strain distribution patterns (SDPs) for Chr 3 loci which have been typed in recombinant inbred (RI) lines, chromosome maps derived from three multilocus backcrosses, and primer sequences for 39 polymorphic markers that can be detected by the polymerase chain reaction (PCR).

Locus table and composite map

The approximate positions of Chr 3 loci are presented in the locus list (Table 1) and are graphically represented on the composite map in Fig. 1. Map positions were calculated by Seldin, using the methods previously described (Meisler and Seldin 1991; Seldin et al. 1991). Entries that have been added or changed since the previous report are marked with an asterisk. It is important to be aware of the uncertainty associated with these map positions, which are composites based on a large number of measurements. The 95% confidence intervals for the primary data are in most cases greater than 2 cM, and those for the composite data greater than 5 cM. As discussed in the previous report, there may be errors in the indicated gene orders for closely linked loci that have not been mapped in the same cross. More precise information about the confidence of relative map positions between different loci can be obtained from the notes and references cited in Table 1.

*Chair of Committee for Mouse Chromosome 3

Anchor loci

Six loci with well-established locations and readily available probes have been selected as anchors for Chr 3 (Table 1). The order and estimated distances between anchor loci are: centromere–5–*Car-2*–14–*Il-2*–28–*Gba*–4–*Tshb*–3–*Amy-1*–18–*Adh-1*. In addition, *D3Mit19* will provide a valuable terminal marker when its apparent location 20 cM distal to Adh-1 (Fig. 2) is confirmed. These anchor loci can be detected either by RFLV or by PCR with the primers described in Table 2. Inclusion of these loci in future crosses is recommended to facilitate integration of new genetic data with the current map.

Multilocus backcrosses

Reliable information about gene order can be obtained from multilocus backcrosses in which many genes are typed in the same individuals (reviewed in ref. 21a). Chr 3 maps that were generated from three large backcrosses are presented in Fig. 2. Two of these are interspecific crosses with *Mus spretus*. Gene order is consistent for loci that were typed in more than one cross, while some variation in distance between pairs of loci is observed in different crosses.

PCR primers for Chr 3 loci

The development of PCR-based assays that detect genetic variation has greatly reduced the time and effort required for genotyping, as well as the amount of genomic DNA required per assay. PCR primers amplify products of different lengths as a result of variation in simple sequence repeat length. Published gene sequences have been used to derive primers that detect variation at known loci. In addition, a large number of

Table 1. Locus list for mouse Chr 3.

New	Locus	Gene name	A	M (cM)	T	Method	H. symbol	H. location	Notes	Reference
	Acrb-2	acetylcholine receptor beta 2 neural		39.6	D	L			3	8
	Acts	skeletal alpha actin		X	D	S,R	*ACTA*	1p21-qter	3,7	23
	Adh-1	alcohol dehydrogenase-1	1	72.1	B,D	L,R	*ADH1*	4q21-q23		11,15,16,38,48
	Adh-1ps	alcohol dehydrogenase-1 pseudogene		56.0	D	R				15
	Adh-1t	alcohol dehydrogenase-temporal		72.1	B	L			8	3,51
	Adh-3	alcohol dehydrogenase-3		72.1	B	R,L	*ADH3*	4q21-q23	7	31,47,48,49,52,73,81
	Adh-3t	alcohol dehydrogenase-3-temporal		72.1	B	L			7	46,49
	Adh-5	alcohol dehydrogenase-5		X	B	S	*ADH5*	4q21-q25		37a
	Ahr-1	aldehyde reductase-1		72.1	B	R,L			7	31
	Ampd-1	AMP deaminase-1 (muscle form)		51.4	D	L	*AMPD1*	1p13	1	55
	Ampd-2	AMP deaminase-2 (nonmuscle form)		54.2	D	L			1	72
	Amy-1	amylase, salivary	1	53.6	B,D	L,R	*AMY1*	1p21	3,5,7	9,11,33,59,80,101
	Amy-2	amylase, pancreatic		53.6	B,D	L,R	*AMY2*	1p21	1,2	9,10,70,80
	Ap2	adipocyte protein aP2		4.6	B	R				42
	Arnt	aryl hydocarbon receptor nuclear translator		X	B	S	*ARNT*	1pter-q12		12
	Atp1a1	Na, K ATPase alpha-1		51.3	D	L	*ATP1A1*	1p13	1,8	54,55,70
	Atpa-1	alternative symbol for Atp1al								
	Bmn	Beta-mannosidase activity (liver, kidney)		72.1	B	R				64
	Cacy	calcyclin		46.9	D	L	*CACY*	1q21-q25	1	28,55,70
	Call1	calpactin I light chain		46.9	D	R				87,97
	Calla	alternative symbol for Mme								
	Capl	calcium binding protein, placental		46.9	D	R	*CAPL*	1q12-q22		28,97
	Car-1	carbonic anhydrase-1		4.6	B	L	*CA1*	8q13-q22	8	32
	Car-2	carbonic anhydrase-2	1	4.6	B,D	L,R	*CA2*	8q13-q22	1,3,8	11,21,32,34a,70,77,80,101
	Car-3	carbonic anhydrase-3		7.0	D	L	*CA3*	8q13-q22	8	6
	Cd1	cluster designation 1		47.9	D	L	*CD1*	1q22-23	1	72
	Cd2	cluster designation 2		50.4	D	L	*CD2*	1p13	1	55,70
	Cd10	alternative symbol for Mme								
	cdm	cadmium resistance		65.6	V	R				95, 96a
	Cnp-2	cyclic nucleotide phosphodiesterase-2		42.8	D	R				7
*	*Cnx40*	connexin		49.5	D	L				41
	coa	cocoa		8.5	V	L			8	77,92
	Csfm	colony stimulating factor, macrophage (alternative for op)		52.4	B,D,V	L	*CSF1*	5q33	2,3	13, 38, 59, 108
*	*D3J1*	DNA segment, Chr 3, Jackson Lab 1		46.3	D	L				75
*	*D3J2*	DNA segment, Chr 3, Jackson Lab 2		69.6	D	L				75
*	*D3J3*	DNA segment, Chr 3, Jackson Lab 3		56.6	D	L				75
	D3Mit19	DNA segment, Chr 3, MIT 19		92.5	D	L			9	Fig. 2
	D3Nds1	DNA segment, Chr 3, Nottingham Dept. Surgery		33.3	D	L			4	Fig. 2
*	*D3Sel1*	DNA segment, Chr 3, Seldin 1		52.1	D	L				105
*	*D3Sel2*	DNA segment, Chr 3, Seldin 2		34.1	D	L				105
	D3Tu33	DNA segment. Chr 3 Tubingen-33		61.9	D	R				99
	D3Tu51	DNA segment, Chr 3 Tubingen-51		46.9	D	L,R			1	99
	de	droopy ear		52.4	V	L			7,8	22,48,59,60
	Egf	epidermal growth factor		66.1	D	L,R	*EGF*	4q25	1	70,73,109
	Emv-27	endogenous ecotropic MuLV-27		53.6	D	L			8	96
	Es-16	esterase-16		12.1	B	L			7	100, 101, 103
	Es-26	esterase-26		37.3	B	L			7	77, 100, 101, 103
	Es-27	esterase-27, serum cholinesterase		27.3	B	L			7	102, 103
	Evi-1	ecotropic viral integration site-1		14.2	D	L,R	*EVI1*	3q24-q28	1,2	20,21,38,70,73
	Fabpi	fatty acid binding protein intestinal		56.6	D	R	*FABP2*	4q28-q31		93
	Fcgr1	high affinity FC gamma receptor		46.9	D	L			1	79
	Fgfb	fibroblast growth factor basic		19.7	D	L		4q25-27	1	M. Seldin, unpublished
	Fgg	gamma fibrinogen		46.3	D	R	*FGG*	4q28		9
	Fim-3	Friend MuLV integration site-3		14.2	D	L	*FIM3*	3q27	3	20,38,90
*	*Fpsl-rs1*	farnesyl pyrophosphate synthetase - like 1		46.6	D	L	*FPSL*	1q24-q31		105
	ft	flaky tail		46.4	V	L				58,59
	Gba	beta glucocerebrosidase	1	46.6	B,D	L	*GBA*	1q21	1	70,78
	Gbp-1	guanine nucleotide-binding protein-1		68.3	D	L,R			7	81
*	*Glut-2*	glucose transporter 2		16.0	D	L	*GLUT2*	3q26	9	Fig. 2
*	*Gnai-2*	guanine nucleotide binding protein, alpha inhibiting activity-2		52.0	D	L	*GNAI2*		9	107a
*	*Gnai-3*	guanine nucleotide binding protein, alpha inhibiting activity-3		52.0	D	L	*GNAI3*		9	107a
	H-23	histocompatibility-23		63.6	B	L,R			7	1b,67
	H-28	histocompatibility-28		83.3	B	L,R			7	1b,67
	H-37	histocompatibility-37		(X)	B	R				1b
	Hao-2	hydroxyacid oxidase-2 (kidney)		44.0	B	L			3,7	38,44,45
	Hist2	histone gene (2)		X	D	S				39
	Hnl	hypothalamic norepinephrine level		63.6	V	L				34
*	*Hsdb3*	3-beta-hydroxy steroid dehydrogenase		49.0	D	L	*HSDB3*	1p11-p13	9	2
*	*Hsp86-ps2*	heat shock protein 86 - pseudogene 2		23.3	D	S,L				68,69
	Idd-3	insulin dependent diabetes 3		X	V	L				96b
	If-1	interferon inducibility locus		88.6	V	L,R			7	26,67
*	*Il-2*	interleukin 2	1	19.0	D	S,L	*IL2*	4q26-q27	1,4	35; Fig. 2
*	*Il-7*	interleukin 7		6.8	B,D					89
	Lef-1	lymphoid enhancer-binding factor 1		X	D	R,S	*LEF1*	4q23-q25		66a

Continued on next page

Table 1. *Continued.*

New	Locus	Gene name	A	M (cM)	T	Method	H. symbol	H. location	Notes	Reference
	Ly-37	alternative symbol for Cd2								
	Ly-38	alternative symbol for Cd1								
	ma	matted		44.4	V	L			5,7	58,59,60,67
*	*Mme*	membrane metallo-endo peptidase (neutral endopeptidase)		34.1		L	*MME*	3q21-27		17
	Mmv-2	MCF endogenous virus-2		X	D	S				43
	Mmv-12	MCF endogenous virus-12		X	D	S				43
	Mov-10	Moloney leukemia virus-10		X	D	S				53,74
	Mpmv-9	modified polytropic murine leukemia virus-9		92.2	D	L,R			6	37
	Mpmv-20	modified polytropic murine leukemia virus-20		11.3	D	R				37
	Mtv-48									
	my	blebs		34.4	V	L			5	14,25,33
	Ngfb	nerve growth factor beta		51.4	D	L			1,2	13,30,55,110
	Nras	Nras oncogene		51.4	D	L	*NRAS*	1p13	1,2	13,84
*	*Oat-rs2*	ornithine aminotransferase related sequence 2		56.4	D					83
	Odc-3	ornithine decarboxylase-3		X	D	R				82
	op	osteopetrosis (alternative for Csfm)								
*	*Otf-3c*	octamer transcription factor - 3c		4.8	D	L				89
*	*Otf-3d*	octamer transcription factor - 3d		66.7	D	L				89
	Oua-1	ouabain resistance-1		X	V	S				57
	Pgk-1ps3	phosphoglycerate kinase-1 pseudogene 3		9.4	D	S,R				1
	Pk-1	pyruvate kinase (may be the same as Pklr)		37.6	B	L	*PKLR*	1q21	3	38,90
	Pklr	pyruvate kinase liver, red blood cells (see Pk-1)		46.6	D	L			1	Unpublished data
	Pmv-26	polytropic murine virus-26		75.8	D	R				36
	Pmv-28	polytropic murine virus-28		46.9	D	R				36
	Pmv-38	polytropic murine virus-38		47.1	D	R				36
	Pmv-39	polytropic murine virus-39		57.8	D	R				36
*	*Rap1a*	member of RAS oncogene family		51.4	D	L	*RAP1A*	1p12-p13		29
	rcm	rostral cerebellar malformation		69.4	V	L			7	62
	Rnu1b-1	U1b1 small nuclear RNA		46.7	D	R	*RNU1*	1p36.1		63
	Rnu1b-3	U1b3 small nuclear RNA		46.9	D	R				9,63
	soc	soft coat		47.4	V	L			5	33, 91
	spa	spastic		41.4	V	L			5	58,59
	suc-1	alternative symbol for Suc-1r								
	Suc-1r	sucrase-isomaltase, regulatory		37.3	B	L				8a
	Suc-1s	sucrase-isomaltase, structural		37.3	D	R	*SI*	3q25-26		8a
	sut	subtle gray		16.2	V	L			7	61
	Tmevd-2	TMEV induced demyelinating disease susceptibility		8.8	V	R				66
	Tshb	thyrotropin stimulating hormone beta subunit	1	51.4	D	L	*TSHB*	1p13	1	30,55,56,70,76
	Va	varitint-waddler		75.6	V	L			5,7	22,31,33,47,48,59,60,67
	Xmmv-22	xenotropic-MCF leukemia virus - 22		46.3	D	R				9
	Xmmv-47	xenotropic-MCF leukemia virus - 47		35.0	D	R				106
	Xmmv-65	xenotropic-MCF leukemia virus - 65		46.3	D	L,R			7	106

The Chr 3 map positions are based at the centromere (25). Since recombination frequencies may vary depending on the specific cross, composite map positions may distort gene order when loci have not been mapped in an individual backcross. In deriving the composite map, RI strain data was used to determine gene position only as a supplement to backcross data. RI data is included in Fig. 3 of this report. For a fuller discussion of the generation of map positions, see text and (84a). Data used to derive map positions, in addition to the references, is described in "Notes." (1) Complete haplotypes in 114 and incomplete haplotypes in 338 interspecific backcross mice (references and M.F. Seldin, unpublished data; Fig. 2); (2) complete haplotypes in 83–198 interspecific backcross mice (specific references); (3) incomplete haplotypes in 38–74 interspecific backcross mice (specific references); (4) complete haplotype data in 92–299 interspecific backcross mice (J. Todd, unpublished data; Fig. 2); (5) included in nine overlapping three- or four-point crosses that derive from analysis of 125–500 meiotic events in each of multiple individual crosses (specific references); (6) haplotype data in 75 interspecific backcross mice (W.N. Frankel, unpublished data); (7) three-point mapping data (see specific references in table for data); (8) two-point mapping data (see specific references in table for data); and (9) location has not been integrated with the rest of the map.

primers that detect (CA)n repeat length variation have been developed from anonymous genomic clones by the Mouse Genome Center at MIT (Dietrich et al. 1992). Primer sequences for Chr 3 loci of both types are presented in Table 2.

RI lines

Like multilocus backcrosses, RI lines provide a cumulative mapping resource. New loci can be mapped by typing the existing RI lines and comparing strain distribution patterns with the corresponding data for previously typed markers. Strain distribution patterns for Chr 3 loci that have been typed on Recombinant Inbred lines are presented in Fig. 3.

Disease-related genes

A gene (or genes) that controls the development of autoimmune insulitis and insulin-dependent diabetes in the nonobese diabetic (NOD) mouse has been mapped to the *Il-2–Tshb* interval in two reciprocal backcrosses of (NOD × C57BL/10)F_1 × NOD and NOD × (NOD × C57BL/10)F_1 (Todd et al. 1991). The NOD allele is not fully recessive and also appears to segregate in crosses of NOD with NON (nonobese

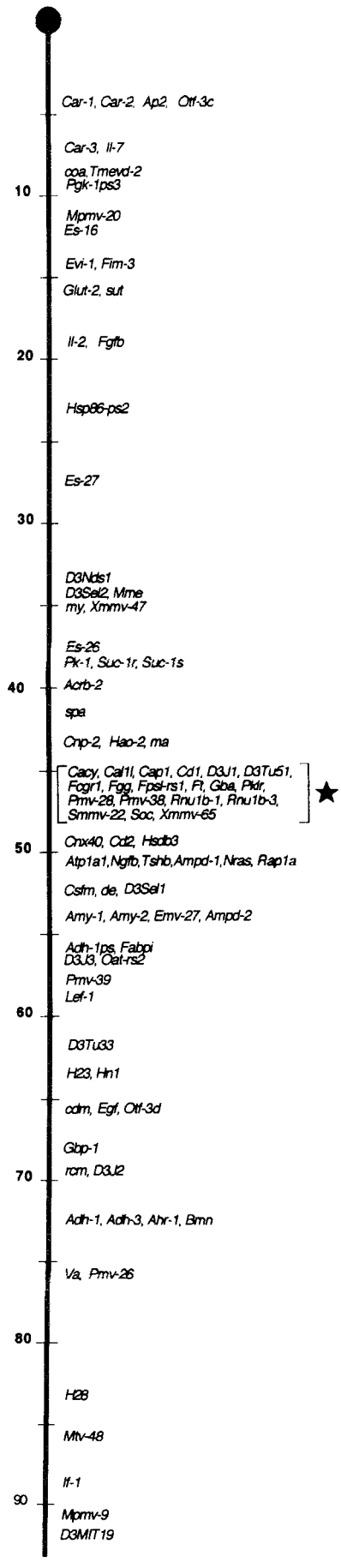

Fig. 1. Composite map of mouse Chr 3. Loci are positioned according to their approximate location, based on the information in Table 1. For genes separated by less than 2 cM, order is not specified on this map. *Loci within the bracket are found within the 2-cM region from 46–48 cM.

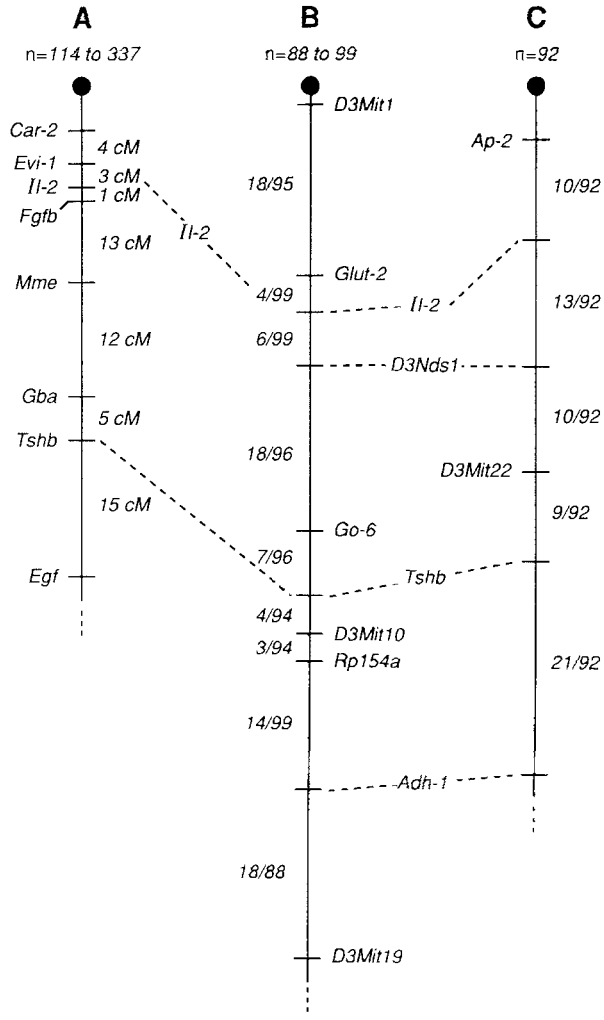

Fig. 2. Analysis of Chr 3 loci in multilocus backcrosses. Cumulative data are presented for three backcrosses. **(A)** Data from an interspecific backcross [(C3H/HeJ-*gld*/*gld* × *M. spretus*) F_1 × C3H/HeJ-*gld*/*gld*] that has been characterized for more than 400 genetic markers in the laboratory of M.F. Seldin. **(B)** Data from the cross [(NOD/Uf × C57BL/6J)F_1 × NOD/Uf] from the laboratory of E.K. Wakeland. In this cross, the RAPD polymorphism Go6 is detected with the primer GTGCCTAACC, and Rp 154 a is detected with the primer TGCTCACTGA. **(C)** Data from the laboratory of J.A. Todd for the European Collaborative Interspecific Backcross [(C57BL/6 × SPR)F_1 × SPR] produced by the United Kingdom's Human Genome Mapping Project, with the support of the Medical Research Council.

nondiabetic) and B6.PL (J. Todd, unpublished data). *Idd-3* appears to be a major gene in the development of autoimmune diabetes in mice, second only to the susceptibility determinants encoded by the MHC on Chr 17.

Conserved linkage groups

In addition to the previously described conserved linkage groups on human Chrs 1, 4, and 8, five loci on

Table 2. PCR primers for amplification of polymorphic loci on Chr 3. Mg^{2+} concentrations and annealing temperatures should be established in individual laboratories, based on the guidelines in the references. *Tshb* (1a); *D3Mit1-22* (27); and *Amy-1* (41a,65a). For other loci see (21b) and (41a).

Sequence	Locus	Primer forward (5'-3')	Primer reverse (5'-3')	PCR product size	Size variation
MMLBPA	*Ap2*	TCCATAGCATTCATGCGTGCA	GTCTGTTGCTTACTATGTGC	146	*NON>CBA>B10/W=B6.PL=NOD=SPE=B6/J>DBA/2J*
MMNGFBA	*Ngfb*	AGGTTCATCCGGATAGACACA	TTCGGTATACAGGATGCTTTG	232	NOD=B10/W=NON=SPE=B6/J=DBA/2J
MUSTSHBA2	*Tshb*	TCTGAAGAGTTGTCCTCATC	TGAATAAAGGACTCCTGAGCT	145	NOD-AKR/J>>NON-B10/J-B6/J-DBA/2J>>SPE
AMYI	*Amy-1*	ATGAACATATGTGTAAGTAAAATG	AAATAAAAAGGCCACTATTTGA	153	CBA=MOLD=YBR=C3H=NOD>BRcdJ>AKR>SPE (B6/J=BLANK)
AMY1	*Amy-1*	GAACATATGTGTAAGTAAAATGTAC	GATTTTAATTCATTAATTAAGGGTTAG	190	CBA=MOLD=YBR=C3H=NOD>BRcdJ>AKR>SPE (B6/J=BLANK)
Cloned	*Gba*	GAAGGAAAGGACTTAGTCTACC	GGCCTTGGCTCTGTTATTCTGT	190	SPE(2)>>NOD=B10.H-2NOD=B6.PL=B6/J=DBA/2J
MMIL01	*Il-2*	GTGCTCCTTGTCAACAGCGCA	CTCCTGTAGGCTCTGTTATTCTGT	129	NOD=B10/W=B6/J=B6.PL=NON=DBA/2=AKR>>SPE
MMIL2A3	*Il-2*	TGTACCTCCTGCTTACAACAC	TACCTACACATGATATTTAAC	224	NOD=B10/W=B6/J=NON=DBA/2J=SP
MMLBPA	*Ap2*	TATAAGATTCCAGAACACATT	GATAAGAGCATGGATTTAACT	133	NOD=B10/W=B6.PL=B6/J=DBA/2J=NON>SPE
CA72	*D3Nds1*	GGATCTGGCACCTCCAGGG	TATGTTGCCTTGGCAAATAGATG	90	NOD=NON>>AKR/J>B10/W=B6.PL=B6/J=DBA/2 (SPE=BLANK)
GT3	*D3Nds2*	ACACATTGGAGATGCACAGCG	TCTGCATGCCAGGGTTGTGAT	128	SPE>>DBA/2J>>NOD=NON=B10/W=B6.PL=B6/J=AKR/J
TJT14	*D3Nds3*	CTGTGAAATTTGCCATCAACT	CATAATATTCATATATAATGC	165	NOD=NON=B10/W=B6.PL=B6/J=AKR/J>>DBA/2J>>SPE
IL2		GTGGGAGTGTGTGCAAAAGAC	AAGTATGGGTCAGAGTTGTGTGGG	170	SPE>B6.PL=B10/W=B6/J>NON>AKR/J>DBA/2J>NOD
SGT8	*D3Nds4*	ATTTTAAATATTCATTCATTTGGG	CTCACAAATACCTTCAGAGGA	110	NON>B6/J=B10/W=B6PL>DBA/2J>NOD
	Ly-38	GTGTAAAATCAACACCAACAGTAT	GGCAGGTTTGATTCTAAGGTAG	166	NOD=B10/W=B6.PL=B6/J=NON=DB2/J=AKR/J=SPE
	Ly-38	GGGGTTTTGTTTGCTGGTTAGT	GGACAGCCAGGACTATACAGA	164	NOD=B10/W=B6.PL=B6/J=NON=DBA/2=AKR/J>>SPE
Publ	*Il-2*	ACTAGCAAGAGTTGGTCTCTG	ATTTTATATGTCTCTAGTTGCAC	232	NOD=B10/W=B6.PL=B6/J=NON=SPE=DBA/2
R78	*D3Nds5*	AGCATTATTTTAAACATCTGAATAG	TGGAGTCACCTTCTTGAGTTC	148	NOD>>DBA2/J=AKR/J=NON>B10.H-2g7=B6.PL=B6/J (SPE doublet)
	Cacy/Capl	CACAGTGAGACCAAACTC	CTTGGCTCTTATAGTGTTTG	117	SPR>>C57L/J>>SWR/J=C57BR=SJL/J=B10.H-2g7=NON> C3H/HeJ=A/J=AKR/J>>CBA=BALB/cByJ=NOD>>DBA=PL/J

	Adh-1	CTTACTGGGTGACATAGACG	CCTTTCATCCATGTACATATAC	330	B10/J=B10.BR>NOD>A=C58=MEV;SPE=B10/W.NOD.B6.PL>NON
L8	*D3Mit13*	CCTTTCTGATTATGTGGGCT	CCACTGAAGGATAACCACAG	220-240	LP=Spr>NOD=Cast>>OB=B6=DBA=C3H=BALB=AKR=NON /A;-
L37	*D3Mit13*	TTTCTGCATTATGTGGGCTT	AACCACAGATGACAATTGAA	220-237	LP>Spr>NOD>>Cast>>OB=B6=DBA=C3H=BALB=AKR=NON
L40	*D3Mit4*	TGTGCCTGCAAGTTGTTCTT	CTACAGTGGGGGCAGAAGGT	140-150	Cast>Spr>>OB=B6=DBA=A=C3H=BALB=AKR=NON=NOD=LP
M149	*D3Mit6*	AACTTCAACATGTGAGGGGC	CCTGAAACAAAGCAACAGCA	125-147	LP=B6>OB>>DBA=A>C3H=BALB=AKR=NON=NOD>Cast>>Spr
M141	*D3Mit19*	CAGCCAGAGAGGAGCTGTCT	GAACATTGGGGTGTTTGCTT	210-238	Cast=DBA=A=C3H=BALB=AKR=NOD>>OB=B6=NON>LP>>Spr
L38	*D3Mit11*	CCAACCACAGTAACACATGT	TGGAGACCAATGCGAACAAC	147-204	Cast>>AKR=BALB=C3H=A>NON>>Spr>>OB=B6=DBA=NOD=LP
M28	*D3Mit1*	TGTGCACAGGGGTACATACA	TCATTTTCTTCCTCCCCCTC	118-145	OB>LP>>NOD=BALB>B6=DBA=A=C3H=AKR=NON>Cast/Spr, -
M250	*D3Mit3*	CCTTTTGAGGCAAAGCTCC	CTAAGTCCTGCACCTGCCTC	88-200	Cast=DBA=BALB=AKR>>NOD>>NON=OB=B6>>LP=C3H>A>>Spr
M123	*D3Mit5*	AGCCCCTTCCAAGTGTCTCT	GGTTTCGGAATGAGATGAGC	178-188	OB=DBA=A=C3H=BALB=AKR=NON=NOD>>LP=Cast=B6>>Spr
M74	*D3Mit7*	ATGCAACTAACTTTATTGAAAATC	TACAATTATCCGGGAGCTA	142-147	OB=B6=SPR=DBA>>Cast=AC3h=BALB=Akr=NON=NOD=LP
A85	*D3Mit9*	AACTTCATTTGCTTGGAAACTACC	TGTTTTATATTGCCCTGTATGTGC	214-238	CAST>>OB=B6>>DBA>LP>NOD>A=BALB>Spr=AKR>>NOD /C3H;
D122	*D3Mit22*	AAGGATTGAAGAATGGTTGGG	AATCAGCGATTTCAGCACG	207-265	Cast>>A>>NOD>>NON=C3H=B6=OB>DBA=AKR>>LP=BALB>>Spr
A60	*D3Mit12*	TAGACCAATCTTGGGAGTGTCC	GGAAAAGCATAAGAAACAACCG	120-157	LP=AKR=A=>OB=B6=C3H=BALB..DBA=NON=NOD>>Cast /Spr;-
M206	*D3Mit14*	ATTGCGGTTAAAGTTTGCTT	TCCTGCAAATTGTCCTCTGA	140-147	DBA=A=C3H=BALB=AKR=NON=NOD>>LP=OB=B6>>Spr>Cast
A55	*D3Mit15*	AATTTGCATTCCAGGACCAC	AGGAAGTGACGTTGGGTTTG	212-145	DBA>>Cast>>Spr>>OB=B6=A=C3H=AKR=BALB=NON=NOD /LP;-
M159	*D3Mit16*	TGCTTGTCCTGTGTTAATGA	TGAGAATGGAGGTGAACAGC	186-220	Spr>>Cast>>OB=B6>A=C3H=BALB=NON=NOD=LP/AKR;-/DBA;-
M235	*D3Mit17*	CATGGCTCCATGGTTCTTG	CCACGGAGAACAACTGAAGA	180-208	OB=B6=NOD>>Cast>>LP>>DBA=A=C3H=BALB=AKR=NON /Spr
A96	*D3Mit18*	GAACAGTTCCCAGGTCCTCA	CTGCCTTTAAATTCTGTCACCC	192-242	Cast>>NOD=DBA=OB=B6>>LP=NON=AKR=BALB=C3H=A>>Spr
D122	*D3Mit21*	AAGCTCTACAGCGGAAGCAC	CTGGGGAGTTTCAGGTTCCT	208-236	OB=B6=NON=BALB>>LP=NOD=AKR=C3H=A=DBA>Cast>>Spr
A34	*D3Mit10*	CTGGCTTGGTGGAGTCCT	CCTAAGCCAGCTACCACCAC	121-158	Cast>>OB=B6>>DBA>LP>NON>BALB>Spr=AKR>>NOD /C3H;-

Locus	BXD Lines	Ref.
	11111111222222222333	
	12568912345689012345789012	
Car-2	DDDBDBDDDDBBDDBBBBBBDBDDBB	80
Ap2	DDDBDBDDDDBBD-BBBBBBDBDDDD	42
Il-2	DDBBDBDDDDDBDDBDBBBBDDBDDB	41a
Evi-1	DDBBDBBDBBBBBDBDBBBBDDDDDB	73
Cnp-2	BBDBBDDDBBDBBBBDDBBDDDBDBB	7
Xmmv-65	BBDBBBDBBBDBBBBDDBBDBDBDBB	106
Fgg	BBDBBBDBBBDBBBBDDBBDBDBDBB	9
Pmv-38	BBBBBBDBBBDBBBBDDBBDBDBDBB	36
Capl	BBBBBBDB-BDBBB--D-BDBDBDBB	28
Cal1l	BBBBBBDBBBDBBB--DBBDBDBDBB	87
D3Tu51	BBBBBB-BDBDBBB-DDBB-BDBD--	99
Amy	BDBBDBDDDBDBBBBDDBBDBDBDBB	80
Amy CB	BDBBDBDDDBDBBBBDDBBDBDBDBB	9
Adh-1ps	BDBBDBDDDBDBBBDDDBDDBDBBBD	15
Fabpi	BDBBDBDDDBDBB-DDDBB-BDBBBD	93
cdm	BDBBDBDDDDBBDBDDDBBDBDBBBB	95
Pmv-39	BDBBDBDDDDBDBDBDDDDBDBDBBD	36
Egf	BDBBDBDDDBBBDDDDBDBDBDBBBD	73
Adh-3	BDBBDBDD-BBBDDDDBDBDBDBBBD	73
Adh-3 RH	BDBBDBDD-BBBDD-DBDBDBDBBBD	52
Adh-1	BDBBDBDDDDBBBDDDDBDBDBDBBBD	15
D3Nds3	BDBBDBDDDBBBDDDDBDBDBDBBBD	21a
Bmn	BDBBDBDD-BBBDD-DB-BDBDB-BD	64
D3Jknl	BDBBDBDDDBBBDDDDBDBDBDBBBB	64a
Pmv-26	BDBBDDDDDBBBDDDDBBBDBDBBBD	36

Locus	AXB Lines	Ref.
	111111111222222	
	123456789012345789012345	
Car-2	BBAAABABABABAAAABBB-BBBA	73
Evi-1	BA-BABABABAA-A-AAAABABAA	73
Fgg	BBAABABBBBAB-AAABBBB-BBA	9
Ulb	ABAABABBBBAB-AABBBBB-BBA	9
UlT-13	ABAABABBBBAB-AABBBBB-BB-	9
mUlb3	AAAABABBBBABAAABBBBBABBA	63
Amy-1,2	AAAAAABABBAB-ABBBA-A-AB-	9
Egf	AAAAAABABBAAAA-AA-AAAABB	73
Adh-3	AAAABABAABAAAABBAAABAAB-	9
Mpmv-9	BAABAABAABAAAA--A-ABAABA	37

Locus	BXA Lines	Ref.
	1111111111222222	
	12345678901234567890123 45	
Car-2	AABB-ABAA-BAABBBAA---AABA	73
Evi-1	AA-B-B-AABBAAB---BB--AABB	73
mUlb3	AB-A-BABBABABB--BAAAA-ABB	63
Rnulb	A-AABB-BB-BA-B---AAA-B---	9
Fgg	A-ABBB-BBABA-B---AB------	9
U1T-13	A-AABB--B-BA-B---AAA-B---	9
Ulb	A-AABB-BBABA-B---AAA-B---	9
Amy-1,2	A-ABBB-BBABA-B---AAB-----	9
Egf	AA-A-BBBBAAABA---AA--A--B	73
Ahd-3	AAAAABABBAABBA---AAA-B--B	9
Mpmv-9	AB-A-AA-BAABBA--AAAA-ABAB	37

Locus	SXL Lines	Ref.
	11111	
	4724567	
Cal1l	SLLLSSL	87
Amy	LLLLSSL	80

Locus	AXD Lines	Ref.
	111111111222222222	
	123456789012345678012345678	
Mpmv-20	DDA--AAADAAADA-A-AADDDADADA	37
Il-2	ADA--AAADAAADADA-AAADADAADA	41a
Cnp-2	ADA--AADAAADAADA-AAADADAAAA	7
D3Nds1	ADA--AADAAADAADA-AAADADAAAA	21a
Pmv-28	DDA--AADDAADAADADAAADADDDAA	36
Pmv-38	DDA--AADDAADAADADAAADDDDDAA	36
Tshb	DDA--AADAAADADDA-AAAADDDDAA	1a
Pmv-39	DDD--DDDAADDADDADADDADDDDAD	36
D3Nds2	DDD--DADAADDADDA-ADDAADDDAD	21a
Egf	DDDADDADADDDADDADDDDAADDDAD	73

Locus	AXL Lines	Ref.
	1111112222233	
	567892346791458978	
Car-2	LALL-ALALAAALALLAA	80
Ap2	LALLLALALAAALALLLA	42
Evi-1	LLAALAAALALLLALLAL	73
Mpmv-20	LLAALALALLLLLALLLL	37
Xmmv-47	LLLLLAAALLALAALLLL	106
Xmmv-65	ALALLAAALLLLALLLAA	106
Pmv-28	ALALLAAALLLLALLLAA	36
Cal1l	ALALLAAA-LLLALLLAA	87
D3Tu51	LLALLAAALLLLA-LLAA	99
Amy	ALALLAAALLLLAAALLA	80
D3Tu33	AAL-AAAALLLLA-ALLA	99
Pmv-26	AAAAALALLLAAALALLA	36

Locus	BXH Lines	Ref.
	11111	
	2345678901249	
Car-2	HBH-BHBBBBBBB	80
Pgkps9	HBH-BHBBBBHBB	1
Evi-1	HBHBBHBBBHHBB	73
Rnu1b3	BBB-BHBBHHHBB	9
Cal1l	BBB-BHBBHHHBB	87
D3Tu51	BBB-BHBBHHHHB	99
Amy	BBB-BHBHHHBBB	80
Odc-3	HBH-BHBHBHBBB	82
Egf	BBBHBHBHHHBHB	73
Adh-3	BBB-BHBBHHBBB	81
Gbp-1	BBB-BHBBHHBBB	81
Mpmv-9	BBB-BBBBBHBHB	37

Locus	CXB Lines	Ref.
	1234567	
Car-2	CCBBCCB	34a
Xmmv-65	BCBBCBC	106
H-37	BCCBCBC	1b
Amy	CCCBCCB	80
H-23	CCCCCCB	1b
Adh-3	CCCBCCB	31
Ahr-1	CCCBCCB	31
Gbp-1	CCCBCCB	81
H-28	CCBBCCB	1b
If-1	CCBBCCB	26
Mpmv-9	BCBBCCB	37

Fig. 3. SDPs for Chr 3 loci in RI strains. Data were obtained from files maintained by B. Taylor at The Jackson Laboratory. Data for the AXB and BXA lines were provided by B. Paigen.

proximal Chr 3 are now known to have homologs in human chromosome region 3q21-28: *Evi-1, Fim-3, Glut-2, Mme,* and *Suc-1s*. These loci are divided into two groups by a region containing at least two genes with homologs on human chromosome 4q25-27, *Il-2* and *Fgfb*.

Acknowledgments. We thank the many individuals who contributed unpublished data so that this report could be as complete as possible. We would appreciate receiving information from readers regarding corrections and additions. We are grateful to Dr. Benjamin Taylor for providing the RI SDPs, and to Dr. Beverly Paigen for data on the AXB and BXA lines. Information on human homologs was contributed by Dr. Muriel Davisson. Jane Santoro provided invaluable assistance in preparation of the tables and figures.

References

1. Adra, C.N., Ellis, N.A., and McBurney, M.W.: The family of mouse phosphoglycerate kinase genes and pseudogenes. *Somatic Cell Mol Genet 14:* 69–81, 1988.

1a. Aitman, T.J., Hearne, C.M., McAleer, M.A., and Todd, J.A.: Mononucleotide repeats are an abundant source of length variants in mouse genomic DNA. *Mammalian Genome 1:* 206–210, 1991.

1b. Bailey, D.W.: Genetics of histocompatibility in mice. I. New loci and congenic lines. *Immunogenetics 2:* 249–256, 1975.

2. Bain, P., Meisler, M.H., and Payne, A.: Mapping of Amy-1, Tshβ and Hsd3β in an interspecific backcross. Unpublished observation.

3. Balak, K.J., Keith, R.H., and Felder, M.F.: Genetic and developmental regulation of mouse liver alcohol dehydrogenase. *J Biol Chem 257:* 15000–15007, 1982.

4. Bradbury, A., Milstein, C., and Kozak, C.A.: Chromosomal localization of *Cd1d* genes in the mouse. *Somatic Cell Mol Genet 17:* 93–96, 1991.

5. Beechey, C.V. and Searle, A.G.: Position of Va and ma on Chr 3. *Mouse News Lett 62:* 52, 1980.

6. Beechey, C., Tweedie, S., Spurr, N., Ball, S., Peters, J., and Edwards, Y.: Mapping of mouse carbonic anhydrase-3, Car-3; another locus in the homologous region of mouse chromosome 3 and human chromosome 8. *Genomics 6:* 692–696, 1990.

7. Bernier, L., Coleman, D.R., and D'Eustachio, P.: Chromosomal locations of genes encoding 2′, 3′ cyclic nucleotide 3′-phosphodiesterase and glial fibrillary acidic protein in the mouse. *J Neurosci Res 20:* 496–504, 1988.

8. Bessis, A., Simon-Chazottes, D., Devillers-Thiery, A., Guénet, J.-L., and Changeux, J.P.: Chromosomal localization of the mouse genes coding for alpha2, alpha3, alpha4, and beta2 subunits of neuronal nicotinic acetylcholine receptor. *FEBS Lett 264:* 48–52, 1990.

8a. Birkenmeier, E.H., Rowe, L.B., Leeper, L.L., and Henning, S.J.: Sucrase-isomaltase gene (*Suc-1s*) and a regulatory gene (*Suc-1r*) are closely linked to esterase 26 (*Es-26*) on mouse Chr 3. *American Gastroenterological Association.* Abstract, 1991.

9. Blatt, C., Saxe, D., Marzluff, W.F., Lobo, S., Nesbitt, M.N., and Simon, M.T.: Mapping and gene order of U1 small nuclear RNA, endogenous viral env sequence, amylase, and alcohol dehydrogenase-3 on mouse chromosome 3. *Somatic Cell Mol Genet 14:* 133–142, 1988.

10. Bloor, J.H. and Meisler, M.H.: Additional evidence for the close linkage of Amy-1 and Amy-2 in the mouse. *J Hered 71:* 449–451, 1980.

11. Bonhomme, F., Bemehdi, F., Britton-Davidian, J., and Martin, S.: Analyse genetique de croisement interspecifiques *Mus musculus L.* × *Mus spretus Lataste:* liaison de Adh-1 avec Amy-1 sur le chromosome 3 et de Es-14 avec Mod-1 sur le chromosome 9. *DR Acad Sci Paris 289:* 545–548, 1979.

12. Brooks, B., Johnson, B., Heinzmann, C., Mohandas, T., Sparkes, R., Jones, S., Bennett, P., Balacs, T., Moore, G., Conley, L., and Hankinson, O.: Localization of a gene required for the nuclear translocation of the dioxin receptor to human chromosome 1 and mouse chromosome 3 and a human RFLP with mSP I (abstract). *Am J Hum Genet 45:* 132, 1989.

13. Buchberg, A.M., Jenkins, N.A., and Copeland, N.G.: Localization of the murine macrophage colony-stimulating factor to chromosome 3 using interspecific backcross analysis. *Genomics 5:* 363–367, 1989.

14. Carter, T.C.: Genetics of the little and Bagg X-rayed mouse stock. *J Genet 54:* 311–326, 1956.

15. Ceci, J.D., Zheng, Y.-W., and Felder, M.R.: Molecular analysis of mouse alcohol dehydrogenase: nucleotide sequence of the *adh-1* gene and genetic mapping of a related nucleotide sequence to Chromosome 3. *Gene 59:* 171–182, 1987.

16. Chapman, V.M., Blaird, R.J., Murawski, M., and Quarantillo, B.A.: Electrophoretic variation for alcohol dehydrogenase ADH-1. *Mouse News Lett 61:* 60, 1979.

17. Chen, C.-Y., Salles, G., Seldin, M.F., Kister, A.E., Reinherz, E.L., and Shipp, M.A.: Murine common acute lymphoblastic leukemia antigen (CALLA, CD10 neutral endopeptidase 24.11): molecular characterization, chromosomal localization and modelling of the active site. *J Immunol* in press, 1992.

18. Cheng, I.C., Muralidharan, K., She, S.-X., Winter, W.R., and Wakeland, E.K.: Polymorphisms of the glucose transporter-2 gene are associated with susceptibility to insulitis and diabetes in NOD mice. Manuscript in preparation.

19. Clayton, L.K., Ramachandran, H., Pravtcheva, D., Chen, Y.-F., Diamond, D.J., Ruddle, F.H., and Reinherz, E.L.: The gene for T11 (CD2) maps to chromosome 1 in humans and to chromosome 3 in mice. *J Immunol 140:* 3617–3621, 1988.

20. Copeland, N.G., Buchberg, A.M., Gilbert, D.J., and Jenkins, N.A.: Recombinant inbred mouse strains: models for studying the molecular genetic basis of myeloid tumorigenesis. *Curr Top Microbiol Immunol 149:* 45–56, 1989.

21. Copeland, N.G. and Jenkins, N.A.: Retroviral integration in murine myeloid tumors to identify Evi-1, a novel locus encoding a zinc-finger protein. *Adv Cancer Res 54:* 141–157, 1990.

21a. Copeland, N.G. and Jenkins, N.A.: Development and applications of a molecular genetic linkage map of the mouse genome. *Trends Genet 7:* 113–118, 1991.

21b. Cornall, R.J., Aitman, T.J., Hearne, C.M., and Todd, J.A.: The generation of a library of PCR-analyzed microsatellite variants for genetic mapping of the mouse genome. *Genomics 10:* 874–881, 1991.

22. Curry, G.A.: Genetical and developmental studies on droopy-eared mice. *J Embryol Exp Morphol 7:* 39–65, 1959.

23. Czosnek, H., Nudel, U., Shani, M., Barker, P.E., Pravtcheva, D.D., Ruddle, F.H., and Yaffe, D.: The genes coding for the muscle contractile proteins, myosin heavy chain, myosin light chain 2, and skeletal muscle actin are located on three different mouse chromosomes. *EMBO J 1:* 1299–1305, 1982.

24. Czosnek, H., Nudel, U., Mayer, Y., Barker, P.E., Pravtcheva, D.D., Ruddle, F.H., and Yaffe, D.: The genes coding for the cardiac muscle actin, the skeletal muscle actin and the cytoplasmic b-actin are located on three different mouse chromosomes. *EMBO J 2:* 1977–1979, 1983.

25. Davisson, M.T., Eicher, E.M., and Green, M.C.: Genes on chromosome 3 of the mouse. *J Hered 67:* 155–156, 1976.

26. DeMaeyer, E., DeMaeyer-Guignard, J., and Bailey, D.W.: Effect of mouse genotype on interferon production. I. Lines congenic at the If-1 locus. *Immunogenetics 1:* 438–443, 1975.

27. Dietrich, W., Katz, H., Lincoln, S.E., Shin, H.-S., Friedman, J., Dracopoli, N., and Lander, E.S.: A genetic map of the mouse suitable for typing intraspecific crosses. *Genetics,* in press, 1992.

28. Dorin, J.R., Emslie, E., and van Heyningen, V.: Related calcium-binding proteins map to the same subregion of chromosome 1q and to an extended region of synteny on mouse chromosome 3. *Genomics 8:* 420–426, 1990.

29. Dower, N.A., Seldin, M.F., Pugh, S., and Stone, J.C.: Organization and chromosomal locations of Rap1a/Krev sequences in the mouse. *Mammalian Genome,* in press, 1992.

30. Dracopoli, N.C., Rose, E., Whitfield, G.K., Guidon, P.T., Jr., Bale, S.J., Chance, P.A., Kourides, I.A., and Housman, D.E.: Two thyroid hormone regulated genes, the beta-subunits of

nerve growth factor (NGFB) and thyroid stimulating hormone (TSHB), are located less than 310 kb apart in both human and mouse genomes. *Genomics 3:* 161–167, 1988.

31. Duley, J.A. and Holmes, R.S.: Biochemical genetics of aldehyde reductase in the mouse: *Ahr-1*—a new locus linked to the alcohol dehydrogenase gene complex on chromosome 3. *Biochem Genet 20:* 1067–1083, 1982.
32. Eicher, E.M., Stern, R.H., Womack, J.E., Davisson, M.T., and Roderick, T.H.: Evolution of mammalian carbonic anhydrase loci by tandem duplication: close linkage of *Car-1* and *Car-2* to the centromere region of chromosome 3 of the mouse. *Biochem Genet 14:* 651–660, 1976.
33. Eicher, E.M. and Lane, P.W.: Assignment of LGXVI to chromosome 3 in the mouse. *J Hered 71:* 315–318, 1980.
34. Eleftheriou, B.E.: A gene influencing hypothalamic norepinephrine levels in mice. *Brain Res 70:* 538–540, 1974.

34a. Elliott, R.W.: Use of two-dimensional electrophoresis to identify and map new mouse genes. *Genetics 91:* 295–308, 1979.

35. Fiorentino, L., Austen, D., Pravtcheva, D., Ruddle, F.H., and Brownell, E.: Assignment of the interleukin-2 locus to mouse Chromosome 3 in a region homologous to human chromosome 4q. *Genomics 5:* 651–653, 1989.
36. Frankel, W.N., Stoye, J.P., Taylor, B.A., and Coffin, J.M.: Genetic identification of endogenous polytropic proviruses by using recombinant inbred mice. *J Virol 63:* 3810–3821, 1989.
37. Frankel, W.N., Stoye, J.P., Taylor, B.A., and Coffin, J.M.: A linkage map of endogenous murine leukemia proviruses. *Genetics 124:* 221–236, 1990.

37a. Giri, P.R., Krug, J.F., Kozak, C., Moretti, T., O'Brien, S.J., Seuanez, H.N., and Goldman, D.: Cloning and comparative mapping of a human class III (chi) alcohol dehydrogenase cDNA. *Biochem Biophys Res Commun 164:* 453–460, 1989.

38. Gisselbrecht, S., Sola, B., Fichelson, S., Bordereaux, D., Tambourin, P., Mattei, M.-G., Simon, D., and Guénet, J.-L.: The murine M-CSF gene is localized on chromosome 3. *Blood 73:* 1742–1745, 1989.
39. Graves, R.A., Wellman, S.E., Chiu, I.-M., and Marzluff, W.F.: Differential expression of two clusters of mouse histone genes. *J Mol Biol 183:* 179–194, 1985.
40. Green, M.C.: Catalog of mutant genes and polymorphic loci. *In* M.F. Lyon and A.G. Searle (eds.); *Genetic Variants and Strains of the Laboratory Mouse,* 2nd edition, pp. 12–403, Oxford University Press, New York, 1989.
41. Haefliger, J.-A., Bruzzone, R., Jenkins, N.A., Gilbert, D.J., Copeland, N.G., and Paul, D.L.: Four novel members of the connexin family of gap junction proteins: molecular cloning, expression and chromosome mapping. Submitted, 1992.

41a. Hearne, C.M., McAleer, M.A., Love, J.M., Aitman, T.J., Cornall, R.J., Ghosh, S., Knight, A.M., Prins, J.-B., and Todd, J.A.: Additional microsatellite markers for mouse genome mapping. *Mammalian Genome 1:* 273–282, 1991.

42. Heuckeroth, R.O., Birkenmeier, E.H., Levin, M.S., and Gordon, J.I.: Analysis of the tissue-specific expression, developmental regulation, and linkage relationships of a rodent gene encoding heart fatty acid binding protein. *J Biol Chem 262:* 9709–9717, 1987.
43. Hoggan, M.D., O'Neill, R.R., and Kozak, C.A.: Nonecotropic murine leukemia viruses in BALB/c *Bxv-1* provirus and the single NFS endogenous xenotrope. *J Virol 60:* 980–986, 1986.
44. Holmes, R.S.: The genetics of alpha-hydroxy acid oxidase and alcohol dehydrogenase in the mouse: evidence for multiple gene loci and linkage between *Hao-2* and *Ahd-3*. *Genetics 87:* 709–716, 1977.
45. Holmes, R.S.: Genetics of hydroxyacid oxidase isozymes in the mouse. Localisation of *Hao-2* on linkage group XVI. *Heredity 41:* 403–406, 1978.
46. Holmes, R.S.: Genetics and ontogeny of alcohol dehydrogenase isozymes in the mouse: evidence for a cis-acting regulator gene (*Adt-1*) controlling C2 isozyme expression in reproductive tissues and close linkage of *Adh-3* and *Adt-1* on chromosome 3. *Biochem Genet 17:* 461–472, 1979.
47. Holmes, R.S., Albanese, R., Whitehead, F.D., and Duley, J.A.: Mouse alcohol dehydrogenase isozymes: products of closely localized duplicated genes exhibiting divergent kinetic properties. *J Exp Zool 217:* 151–157, 1981a.
48. Holmes, R.S., Andrews, S.J., and Beechey, C.V.: Genetic regulation of alcohol dehydrogenase C2 in the mouse. Developmental consequences of the temporal locus (*Adh-3t*) and positioning of Adh-3 on chromosome 3. *Dev Genet 2:* 89–98, 1981b.
49. Holmes, R.S., Andrews, S.J., and Beechey, C.V.: Alcohol dehydrogenase C2 (stomach enzyme). *Mouse News Lett 64:* 54, 1981c.
50. Holmes, R.S. and Duley, J.A.: Alcohol dehydrogenase isozymes (*Adh-1* and *Adh-3* on chromosome 3). *Mouse News Lett 66:* 60, 1982.
51. Holmes, R.S., Duley, J.A., and Imai, S.: Alcohol dehydrogenase temporal locus (Adh-1t). *Mouse News Lett 68:* 67, 1983.
52. Holmes, R.S., Mather, P.B., and Duley, J.A.: Gene markers for alcohol-metabolizing enzymes among recombinant inbred strains of mice with differential behavioural responses toward alcohol. *Anim Blood Groups Biochem Genet 16:* 51–59, 1985.
53. Jaenisch, R., Jahner, D., Nobis, P., Simon, I., Lohler, J., Harbers, K., and Grotkopp, D.: Chromosomal position and activation of retroviral genomes inserted into the germ line of mice. *Cell 24:* 519–529, 1981.
54. Kent, R.B., Fallows, D.A., Geissler, E., Glaser, T., Emanuel, J.R., Lalley, P.A., Levenson, R., and Housman, D.E.: Genes encoding alpha and beta subunits of Na, K-ATPase are located on three different chromosomes in the mouse. *Proc Natl Acad Sci USA 84:* 5369–5373, 1987.
55. Kingsmore, S.F., Moseley, W.S., Watson, M.L., Sabina, R.L., Holmes, E.W., and Seldin, M.F.: Long-range restriction site mapping of a syntenic segment conserved between human chromosome 1 and mouse chromosome 3. *Genomics 7:* 75–83, 1990.
56. Kourides, I.A., Barker, P.E., Gurr, J.A., Pravtcheva, D.D., and Ruddle, F.H.: Assignment of the genes for the alpha and beta subunits of thyrotropin to different mouse chromosomes. *Proc Natl Acad Sci USA 81:* 517–519, 1984.
57. Kozak, C.A., Fournier, R.E.K., Leinwand, L.A., and Ruddle, F.H.: Assignment of the gene controlling cellular ouabain resistance to *Mus musculus* chromosome 3 using human/mouse microcell hybrids. *Biochem Genet 17:* 23–34, 1979.
58. Lane, P.W.: Two new mutations in linkage group XVI of the house mouse. Flaky tail and vartint-waddler-J. *J Hered 63:* 135–140, 1972.
59. Lane, P.W. and Eicher, E.M.: Gene order in linkage group XVI of the house mouse. *J Hered 70:* 239–244, 1979.
60. Lane, P.W.: Chromosome 3 position of de. *Mouse News Lett 62:* 56, 1980.
61. Lane, P.W.: [Subtle gray (*sut*); small with kinky tail (*skt*).] *Mouse News Lett 80:* 165, 1988.
62. Lane, P.W., Bronson, R., and Spencer, C.: Rostral cerebellar malformation. *Mouse Genome 86:* 237, 1990.
63. Lund, E. and Nesbitt, M.N.: The embryonic and adult mouse U1 snRNA genes map to different chromosomal loci. *Somatic Cell Mol Genet 14:* 143–148, 1988.
64. Lundin, L.-G.: A gene (*Bmn*) controlling beta-mannosidase activity in the mouse is located in the distal part of chromosome 3. *Biochem Genet 25:* 603–610, 1987.

64a. Macleod D.T. and Jackson, I.J.: An insertion into ES cells defines a DNA segment, *D3Jknl,* mapping to distal chromosome 3. *Mouse Genome 89:* 277, 1991.

65. Marks, S.C., Jr. and Lane, P.W.: Osteopetrosis, a new recessive skeletal mutation on chromosome 12 of the mouse. *J Hered 67:* 11–18, 1976.

65a. Meisler, M.H. and Seldin, M.F.: Mouse Chromosome 3. *Mammalian Genome 1* (*Suppl*): S42–S50, 1991.

66. Melvold, R.W., Jokinen, D.M., Miller, S.D., Dal Canto, M.C., and Lipton, H.L.: Identification of a locus on mouse chromosome 3 involved in differential susceptibility to Theiler's murine encephalomyelitis virus-induced demyelinating disease. *J Virol 64:* 686–690, 1990.

66a. Milatovich, A., Travis, A., Grosschedl, R., and Francke, U.: Gene for lymphoid enhancer-binding factor 1 (LEF1) mapped to human Chromosome 4 (q23–q25) and mouse Chromosome 3 near *Egf. Genomics 11:* 1040–1048, 1991.

67. Mobraaten, L., Bunker, H.P., DeMaeyer-Guignard, J., DeMaeyer, E., and Bailey, D.W.: Location of histocompatibility and interferon loci on chromosome 3 of the mouse. *J Hered 75:* 233–234, 1984.
68. Moore, S.K., Appella, E., Villar, C.J., and Kozak, C.A.: Mapping of the mouse 86-kDa heat-shock protein expressed gene (*Hsp86-1*) on chromosome 12 and related genes on chromosome 3, 4, 9, and 1. *Genomics 10:* 1019–1029, 1991.
69. Moore, S.K., Kozak, C., Robinson, E.A., Ullrich, S.J., and Appella, E.: Murine 86 and 84 kDa heat shock proteins, cDNA sequences, chromosome assignments and evolutionary origins. *J Biol Chem 264:* 5343–5351, 1989.
70. Moseley, W.S. and Seldin, M.F.: Definition of mouse chromosome 1 and 3 gene linkage groups that are conserved on human chromosome 1: evidence that a conserved linkage group spans the centromere of human chromosome 1. *Genomics 5:* 899–905, 1989.
71. Moseley, W.S., Watson, M.L., Kingsmore, S.F., and Seldin, M.F.: CD1 defines conserved linkage group border between human chromosomes 1 and mouse chromosomes 1 and 3. *Immunogenetics 30:* 378–382, 1989.
72. Moseley, W.S., Morisaki, T., Sabina, R.L., Holmes, E.W., and Seldin, M.F.: *Ampd-2* maps to distal mouse chromosome 3 in linkage with *ampd-1*. *Genomics 6:* 572–574, 1990.
73. Mucenski, M.L., Taylor, B.A., Copeland, N.G., and Jenkins, N.A.: Chromosomal location of *Evi-1*, a common site of ecotropic viral integration in AKXD murine myeloid tumors. *Oncogene Res 2:* 219–233, 1988.
74. Munke, M., Harbers, K., Jaenisch, R., and Francke, U.: Chromosomal mapping of four different integration sites of Moloney murine leukemia virus including the locus for alpha(I) collagen in mouse. *Cytogenet Cell Genet 43:* 140–149, 1986.
75. Nadeau, J.H., Bedigian, H.G., Bouchard, G., Denial, T., Kosowsky, M., Norberg, R., Pugh, S., Sargeant, E., and Paigen, B.: Multilocus markers for mouse genome analysis: PCR amplification based on single primers of arbitrary nucleotide sequence. *Mammalian Genome 3:* 55–64, 1992.
76. Naylor, S.L., Sakaguchi, A.Y., McDonald, L., Todd, S., Lalley, P.A., Shows, T.B., and Chin, W.W.: Mapping thyrotropin beta subunit gene in man and mouse. *Somatic Cell Mol Genet 12:* 307–311, 1986.
77. Novak, E., Sweet, H.O., Prochazka, M., Parentis, M., Sobel, R., Reddington, M., Cairo, A., and Swank, R.T.: Cocoa: a new mouse model for platelet storage pool deficiency. *Br J Hematol 69:* 371–378, 1988.
78. O'Neill, R.R., Tokoro, T., Kozak, C.A., and Brady, R.O.: Comparison of the chromosomal localization of murine and human glucocerebrosidase genes and the deduced amino acid sequences. *Proc Natl Acad Sci USA 86:* 5049–5053, 1989.
79. Oakey, R.J., Howard, T.A., Hogarth, P.M., Tani, K., and Seldin, M.F.: Chromosomal mapping of the high affinity Fcγ receptor gene. *Immunogenetics*, in press, 1992.
80. Paul, P.R. and Elliott, R.W.: Analysis of the mouse Amy locus in recombinant inbred mouse strains. *Biochem Genet 25:* 569–579, 1987.
81. Prochazka, M., Staehelin, P., Holmes, R.S., and Haller, O.: Interferon-induced guanylate-binding proteins: mapping of the murine *Gbp-1* locus to chromosome 3. *Virology 145:* 273–279, 1985.
82. Richards-Smith, B. and Elliott, R.: Mapping of a family of repeated sequences in the mouse genome. *Mouse News Lett 71:* 46–47, 1984.
83. Ramesh, V., Cheng, S.V., Kozak, C.A., Herron, B.J., Shih, V.E., Taylor, B.A., and Gusella, J.F.: Mapping of ornithine aminotransferase gene sequences to mouse Chromosomes 7, X, and 3. *Mammalian Genome 3:* 17–22, 1992.
84. Ryan, J., Hart, C.P., and Ruddle, F.H.: Molecular cloning and chromosome assignment of murine N-ras. *Nucleic Acids Res 12:* 6063–6072, 1984.
84a. Seldin, M.F., Roderick, T.H., and Paigen, B.: Mouse Chromosome 1. *Mammalian Genome 1 (Suppl)*: S1–S17, 1991.
85. Siracusa, L.D., Rosner, M.H., Vigano, M.A., Gilbert, D.J., Staudt, L.M., Copeland, N.G., and Jenkins, N.A.: Chromosomal location of the octamer transcription factors, *Otf-1, Otf-2,* and *Otf-3,* defines multiple *Otf-3*-related sequences dispersed in the mouse genome. *Genomics 10:* 313–326, 1991.
86. Samuelson, L.C., Wiebauer, K., Snow, C.M., and Meisler, M.H.: Retroviral and pseudogene insertion sites reveal the lineage of human salivary and pancreatic amylase genes from a single gene during primate evolution. *Mol Cell Biol 10:* 2513–2520, 1990.
87. Saris, C.J.M., Kristensen, T., D'Eustachio, P., Hicks, L.J., Noonan, D.J., Hunter, T., and Tack, B.F.: CNDA sequence and tissue distribution of the mRNA for bovine and murine p11, the S100-related light chain of the protein-tyrosine kinase substrate p36 (Calpactin I). *J Biol Chem 262:* 10663–10671, 1987.
88. Sewell, W.A., Brown, M.H., Owen, M.J., Fink, P.J., Kozak, C.A., and Crumpton, M.J.: The murine homologue of the T lymphocyte CD2-antigen: molecular cloning, chromosome assignment and cell surface expression. *Eur J Immunol 17:* 1015–1020, 1987.
89. Siracusa, L.D., Rosner, M.H., Vigano, M.A., Gilbert, D.J., Staudt, L.M., Copeland, N.G., and Jenkins, N.A.: Chromosomal location of the octamer transcription factors, *Otf-1, Otf-2,* and *Otf-3,* defines multiple *Otf-3*-related sequences dispersed in the mouse genome. *Genomics 10:* 313–326, 1991.
90. Sola, B., Simon, D., Mattei, M.-G., Fichelson, S., Bordereaux, D., Tambourin, P.E., Guénet, J.-L., and Gisselbrecht, S.: *Fim-1, Fim-2/c-fms,* and *Fim-3,* three common integration sites of Friend murine leukemia virus in myeloblastic leukemias, map to mouse chromosomes 13, 18, and 3, respectively. *J Virol 62:* 3973–3978, 1988.
91. Southard, J.L.: (Soft coat and hemimelic extra toes.) *Mouse News Lett 45:* 29, 1971.
92. Sweet, H.O. and Prochazka, M.: Cocoa(coa). *Mouse News Lett 73:* 18, 1985.
93. Sweetser, D.A., Birkenmeier, E.H., Klisak, I.J., Zollman, S., Sparkes, R.S., Mohandas, T., Lusis, A.J., and Gordon, J.I.: The human and rodent intestinal fatty acid binding protein genes. A comparative analysis of their structure, expression, and linkage relationships. *J Biol Chem 262:* 16060–16071, 1987.
94. Tashian, R.E., Venta, P.J., Nicewander, P.H., and Hewett-Emmett, D.: Evolution, structure, and expression of the carbonic anhydrase multigene family. *In Isozymes: Structure, Function, and Use in Biology and Medicine,* pp. 159–175, Wiley-Liss, Inc., New York, 1990.
95. Taylor, B.A., Heiniger, H.J., and Meier, H.: Genetic analysis of resistance to cadmium-induced testicular damage in mice. *Proc Soc Exp Biol Med 143:* 629–633, 1973.
96. Taylor, B.A. and Rowe, I.: A mouse linkage testing stock possessing multiple copies of the endogenous ecotropic murine leukemia virus genome. *Genomics 5:* 221–232, 1989.
96a. Taylor, B.A.: Linkage of the cadmium resistance locus to loci on mouse Chromosome 12. *J Hered 67:* 389–390, 1976.
96b. Todd, J.A., Aitman, T.J., Cornall, R.J., Ghosh, S., Hall, J.R., Hearne, C.M., Knight, A.M., Love, J.M., McAleer, M.A., Prins, J.B., et al.: Genetic analysis of autoimmune type 1 diabetes mellitus in mice. *Nature 351:* 542–547, 1991.
97. van Heyningen, V., Emslie, E., and Dorin, J.F.: Related calcium binding proteins map to the same sub-region of chromosome 1q and to a probable region of homology on mouse chromosome 3. *Cytogenet Cell Genet 51:* 1095, 1989 (Abstr.).
98. Venta, P.J., Montgomery, J.C., Hewett-Emmett, D., Wiebauer, K., and Tashian, R.E.: Structure and exon to protein domain relationships of the mouse carbonic anhydrase II gene. *J Biol Chem 260:* 12130–12135, 1985.
99. Vincek, V., Kawaguchi, H., Mizuno, K., Zaleska-Rutczynska, Z., Kasahara, M., Forejt, J., Figueroa, F., and Klein, J.: Linkage map of mouse chromosome 17: localization of 27 new DNA markers. *Genomics 5:* 773–786, 1989.
100. von Deimling, O.H. and Otto, J.: Esterase-16 on chromosome 3. *Mouse News Lett 64:* 52, 1981.
100a. von Deimling, O.H., Schupp, P., and Otto, J.: Esterase-16 (*Es-16*): characterization, polymorphism and linkage to chromosome 3 of kidney esterase locus of the house mouse. *Biochem Genet 19:* 1091–1099, 1981.

101. von Deimling, O.H., Wassmer, B., and Muller, M.: Esterase-26 (*ES-26*): characterization and genetic location on chromosome 3 of an eserine-sensitive esterase of the house mouse (*Mus musculus*). *Biochem Genet 22:* 1119–1126, 1984.
102. von Deimling, O.H.: EST-A. *Mouse News Lett 73:* 15, 1985.
103. von Deimling, O.H.: Esterase 27. *Mouse News Lett 74:* 89, 1986.
104. Watson, M.L., D'Eustachio, P., Mock, B.A., Steinberg, A.D., Morse III, H.C., Oakey, R.J., Howard, T.A., Rochelle, J.M., and Seldin, M.F.: A linkage map of mouse chromosome 1 using an interspecific cross segregating for the *gld* autoimmunity mutation. *Mammalian Genome 2:* 158–171, 1992.
105. Watson, M.L. and Seldin, M.F.: Unpublished observation.
106. Wejman, J.C., Taylor, B.A., Jenkins, N.A., and Copeland, N.G.: Endogenous xenotro pic murine leukemia virus-related sequences map to chromosomal regions encoding mouse lymphocyte antigens. *J Virol 50:* 237–247, 1989.
107. Wiebauer, K., Gumucio, D.L., Jones, J.M., Caldwell, R.M., Hartle, H.T., and Meisler, M.H.: A 78-kilobase region of mouse chromosome 3 contains salivary and pancreatic amylase genes and a pseudogene. *Proc Natl Acad Sci USA 82:* 5446–5449, 1985.
107a. Wilkie, T.M., Gilbert, D.J., Olsen, A.S., Chen, X.N., Amatruda, T.T., Korenbog, J.R., Trask, B.J., de Jong, P., Reed, R.R., Simon, M.I., Jenkins, N.A., and Copeland, N.G.: Chromosomal evolution of the G protein alpha subunit multigene family. *Nature Genet,* in press, 1992.
108. Yoshida, H., Hayaski, S.-I., Kunisada, T., Ogawa, M., Nishikawa, S., Okamura, H., Sudo, T., Shultz, L.D., and Nishikawa, S.-I.: The murine mutation osteopetrosis is in the coding region of the macrophage colony stimulating factor gene. *Nature 343:* 442–443, 1990.
109. Zabel, B.U., Eddy, R.L., Lalley, P.A., Scott, J., Bell, G.I., and Shows, T.B.: Chromosomal locations of the human and mouse genes for precursors of epidermal growth factor and the beta subunit of nerve growth factor. *Proc Natl Acad Sci USA 82:* 469–473, 1985.
110. Zabel, B.U., Sakaguchi, A.Y., Lalley, P.A., Scott, J., and Naylor, S.L.: The nerve growth factor (*Ngf*) gene is on mouse chromosome 3 (abstract). *Cytogenet Cell Genet 37:* 614, 1984.