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Mouse Chromosome 3

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Introduction

During the past year, more than 80 new loci have been assigned to Chromosome (Chr) 3, including 15 genes and a large number of anonymous DNA markers. This wealth of markers makes it increasingly difficult to represent the genetic maps of mouse chromosomes in traditional formats. In this report, map positions for Chr 3 loci are presented in tabular form. A traditional graphic representation of Chr 3 is available in the first and second committee reports (103, 103a).

This report provides an updated locus list and map, updated strain distribution patterns for recombinant inbred lines, recombination data from seven large multilocus crosses, a new map entirely based on PCR-based microsatellite loci that span Chr 3, and primer sequences for a large number of markers that can be detected by the PCR.

Locus list and chromosome map

The main features of Chr 3 loci are presented in Table 1. Map positions were calculated by Seldin using the methods previously described (103, 103a). Entries that have been added or changed since the previous report are marked with an asterisk. The map positions 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 are greater than 5 cM. As discussed in the previous reports, there may be errors in the indicated gene orders for closely linked loci that have not been mapped in the same cross.

The map positions that are listed alphabetically in Table 1 are also listed in order of increasing distance from the centromere in Table 2, providing a tabular representation of the Chr 3 map.

Data on gene order obtained from seven multilocus crosses are summarized in Fig. 1A. Unambiguous gene order can be determined only for loci that were mapped within the same cross. The data from the seven crosses generate a consistent gene order. The quantitative data from these crosses are presented in Fig. 1B.

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 primers that detect (CA)n repeat length variation have been developed from anonymous genomic clones by the Mouse Genome Center at the Massachusetts Institute of Technology (MIT) (37). Primer sequences for 72 Chr 3 loci of both types are presented in Table 3.

Microsatellite map of Chr 3

During the past year, microsatellite markers have been widely adopted by many investigators as convenient and reliable genetic markers. The presence of variation among inbred strains, the reproducibility of as-

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Table 1. Locus list for mouse Chr 3.

New	Symbol	Name	A	Map	T	Method	H. symbol	H. location	Notes	References
	Acrb-2	acetylcholine receptor beta 2 neural		43.0	D	L			8	11
	Acts	skeletal alpha actin		X	D	S,R	ACTA1	1p21-qter	8,12	33
	Adh-1	alcohol dehydrogenase-1	1	68.1	B,D	L,R	ADH1	4q21-q23	4,5	13,15,20,22,54, 68,150,159
	Adh-1ps	alcohol dehydrogenase-1 pseudogene		52.0	D	R				20
	Adh-1t	alcohol dehydrogenase-temporal		68.1	B	L			13	6,71
	Adh-3	alcohol dehydrogenase-3		68.1	B	R,L	ADH3	4q21-q23	12	43,67,68,69,72, 112,124
	Adh-3t	alcohol dehydrogenase-3-temporal		68.1	B	L			12	66,69
	Adh-5	alcohol dehydrogenase-5		X	B	S	ADH5	4q21-q25		53
	Ahr-1	aldehyde reductase-1		68.1	B	R,L			12	43
	Ampd-1	AMP deaminase-1 (muscle form)		47.4	D	L	AMPD1	1p13	1	79
	Ampd-2	AMP deaminase-2 (nonmuscle form)		50.2	D	L			1	79,111,118
	Amy-1	amylase, salivary	1	49.6	B,D	L,R	AMY1	1p21	8,10,12	13,15,45,52, 59,86,121, 137,138,156
	Amy-2	amylase, pancreatic	1	49.6	B,D	L,R	AMY2	1p21	1,2	13,14,109,121
*	*Ank-2*	brain specific ankyrin-2		58.4	D	L			12	122
	Ap2	adipocyte protein aP2		9.7	B,D	R,L			4	61,150
	Arnt	aryl hydocarbon receptor nuclear translator		X	B	S	ARNT	1pter-q12		17
	Atp1a1	Na, K ATPase alpha-1		47.3	D	L	ATP1A1	1p13	1,13	77,79,81,109
	Atpa-1	see Atp1al								
*	*Bglap*	bone matrix Gla protein			D	S	BGLAP			76
	Bmn	Beta-mannosidase activity (liver, kidney)		68.1	B	R				97
	BRS-3	see Odc-rs3								
	Cacy	calcyclin		42.9	D	L	CACY	1q21-q25	1,12	39,79,109,118
	Call1	calpactin I light chain		42.9	D	R				131,151
	Calla	see Mme								
	Capl	calcium binding protein, placental		42.9	D	R	CAPL	1q12-q22		39,151
	Car-1	carbonic anhydrase-1		6.3	B	L	CA1	8q13-q22	13	44
	Car-2	carbonic anhydrase-2	1	6.3	B,D	L,R	CA2	8q13-q22	1,7,8,13	15,23,28,44, 47,109, 117,121,156,161
	Car-3	carbonic anhydrase-3		7.5	D	L	CA3	8q13-q22	13	9
*	*Ccna*	Cyclin a		15.0	D	L			1,2	92,129,134
	Cd1	cluster designation 1		43.9	D	L	CD1	1q22-23	1	23,110,111,118
	Cd2	cluster designation 2		46.4	D	L	CD2	1p13	1	78,79,109,118
	Cd10	see Mme								
*	*Cd53*	cluster designation 53		47.4	D	L			1	168
	cdm	cadmium resistance		61.6	V	R				145,146
*	*Cf-3*	coagulatioon factor 3		49.6	D	R	F3	1p22-p21		98
	Cnp-2	cyclic nucleotide phosphodiesterase-2		38.8	D	R				10
	Cnx40	connexin (see Gja-5)								
	coa	cocoa		8.3	V	L			13	117,142
	Csfm	colony stimulating factor, macrophage (alternative for op)		48.4	B,D,V	L	CSF1	1p13-21	2,8	18,54,86,93,169
*	*D3Byu1*	DNA segment, Brig Young Univ. 1 (RAPD)		6.9	D	R				167
*	*D3Byu2*	DNA segment, Brig Young Univ. 2 (RAPD		6.9	D	R				167
*	*D3Byu3*	DNA segment, Brig Young Univ. 3 (RAPD)		8.1	D	R				167
*	*D3Byu4*	DNA segment, Brig Young Univ. 4 (RAPD)		45.3	D	R				167
*	*D3Byu5*	DNA segment, Brig Young Univ. 5 (RAPD)		34.4	D	R				167
*	*D3Byu6*	DNA segment, Brig Young Univ. 6 (RAPD)		42.3	D	R				167
*	*D3Byu17*	DNA segment, Brig Young Univ. 17 (RAPD)		30.1	D	R				167
*	*D3Dol*	P40-4 clone ? high affinity laminin		76.4	D	R				40
*	*D3Hun1*	DNA segment, Chr 3, Hunter 1		56.1	D	L			1	73
*	*D3J1*	DNA segment, Chr 3, Jackson Lab 1		33.1	D	R				114
	D3J2	DNA segment, Chr 3, Jackson Lab 2		65.6	D	R				114
	D3J3	DNA segment, Chr 3, Jackson Lab 3		54.7	D	R				114
*	*D3Jfr1*	DNA segment, Chr 3, MJeffers-1		47.4	D	P				75
*	*D3Jkn1*	DNA segment, Chr 3, Ian Jackson 1		69.0	D	R				99
*	*D3Leh1*	DNA segment, Chr 3, Lehrach 1		17.6	D	L			2	31
*	*D3Leh2*	DNA segment, Chr 3, Lehrach 2		10.2	D	L			2	31
*	*D3Ler1*	DNA segment, Chr 3, Leroy 1		41.5	D	L			8	91
*	*D3Ler2*	DNA segment, Chr 3, Leroy 2		41.5	D	L			8	91
*	*D3Mit1*	DNA segment, Chr 3, MIT 1		7.0	D	L			3,4,5	37,150,159
*	*D3Mit3*	DNA segment, Chr 3, MIT 3		20.0	D	L			3	37
*	*D3Mit4*	DNA segment, Chr 3, MIT 4		20.0	D	L			3	37
*	*D3Mit5*	DNA segment, Chr 3, MIT 5	1	24.0	D	L			3,4	37,150
*	*D3Mit6*	DNA segment, Chr 3, MIT 6		22.0	D	L			3	37,150
*	*D3Mit7*	DNA segment, Chr 3, MIT 7		30.0	D	L			3	37
*	*D3Mit9*	DNA segment, Chr 3, MIT 9		38.6	D	L			3	37
*	*D3Mit10*	DNA segment, Chr 3, MIT 10		48.6	D	L			4,5	37,159
*	*D3Mit11*	DNA segment, Chr 3, MIT 11		48.6	D	L			3,4	37,150
*	*D3Mit12*	DNA segment, Chr 3, MIT 12		50.3	D	L			3	37
*	*D3Mit13*	DNA segment, Chr 3, MIT 1		57.7	D	L			3	84
*	*D3Mit14*	DNA segment, Chr 3, MIT 14		61.0	D	L			3	37
*	*D3Mit15*	DNA segment, Chr 3, MIT 15		63.1	D	L			3	37
*	*D3Mit16*	DNA segment, Chr 3, MIT 16		63.1	D	L			3	37
*	*D3Mit17*	DNA segment, Chr 3, MIT 17		68.7	D	L			3	37
*	*D3Mit18*	DNA segment, Chr 3, MIT 18		73.0	D	L			1,3	37,134,161
	D3Mit19	DNA segment, Chr 3, MIT 19	1	81.0	D	L			1,3,4	134,150,159
	D3Mit21	see Il-2								
*	*D3Mit22*	DNA segment, Chr 3, MIT 22	1	35.0	D	L			3,4	84,150
*	*D3Mit23*	DNA segment, Chr 3, MIT 23		0.0	D	L			3	84
*	*D3Mit24*	DNA segment, Chr 3, MIT 24		20.0	D	L			3	84

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Table 1. *Continued.*

*	*D3Mit25*	DNA segment, Chr 3, MIT 25		30.0	D	L			3	84
*	*D3Mit26*	DNA segment, Chr 3, MIT 26		38.6	D	L			3	84
*	*D3Mit28*	DNA segment, Chr 3, MIT 28		44.9	D	L			3	84
*	*D3Mit31*	DNA segment, Chr 3, MIT 31		73.0	D	L			3,4	84,150
*	*D3Mit32*	DNA segment, Chr 3, MIT 32		77.0	D	L			3,4	84,150
*	*D3Mit36*	DNA segment, Chr 3, MIT 36		53.4	D	L			3	84
*	*D3Mit38*	DNA segment, Chr 3, MIT 38		67.2	D	L			3	84
*	*D3Mit39*	DNA segment, Chr 3, MIT 39		53.4	D	L			3	84
*	*D3Mit40*	DNA segment, Chr 3, MIT 40		40.1	D	L			3	84
*	*D3Mit41*	DNA segment, Chr 3, MIT 41		46.1	D	L			3	84
*	*D3Mit42*	DNA segment, Chr 3, MIT 42		56.1	D	L			3	84
*	*D3Mit45*	DNA segment, Chr 3, MIT 45		75.3	D	L			3	84
*	*D3Mit46*	DNA segment, Chr 3, MIT 46		9.6	D	L			3	84
*	*D3Mit49*	DNA segment, Chr 3, MIT 49		40.1	D	L			3	84
*	*D3Mit51*	DNA segment, Chr 3, MIT 51		36.2	D	L			3	84
*	*D3Mit53*	DNA segment, Chr 3, MIT 53		35.0	D	L			3	84
	D3Nds1	DNA segment, Chr 3, Nottingham Dept. Surgery 1		27.0	D	L			4,5,9	150,159
*	*D3Nds2*	DNA segment, Chr 2, Nottingham Dept. Surgery 2		61.0	D	L,R			3	84
*	*D3Nds3*	DNA segment, Chr 2, Nottingham Dept. Surgery 3		63.0	D	R				30
	D3Nds6	see Il-2								
	D3Nds8	see Tshb								
	D3Nds9	see Adh-1								
*	*D3Pas1*	DNA segment, Chr 3, Pasteur Institute-1		20.9	D	R				135
*	*D3Pas2*	DNA segment, Chr 3, Pasteur 2		13.2	D	L			8	123
*	*D3Pas501*	DNA segment, Chr 3, Pasteur 501-temporary designation		8.2	D	L			8	26
*	*D3Pas502*	DNA segment, Chr 3, Pasteur 502-temporary designation-FP25		42.9	D	L			8	123
	D3Sel1	DNA segment, Chr 3, Seldin 1		48.1	D	L			1	162
	D3Sel2	DNA segment, Chr 3, Seldin 2		30.1	D	L			1	162
	D3Tu33	DNA segment. Chr 3 Tubingen-33		57.9	D	R			3	153
	D3Tu51	DNA segment, Chr 3 Tubingen-51		42.9	D	L,R			1	118
*	*D3Ufl*	DNA segment, Chr3 Wakeland 1 (RAPD)		43.5	D	L			5	159
*	*D3Uf2*	DNA segment Chr 3 Wakeland 2 (RAPD)		52.3	D	L			5	159
	de	droopy ear		48.4	V	L			12,13	32,68,86,87
	Egf	epidermal growth factor	1	62.1	D	L,R	EGF	4q25	1,2,7	52,109,112,137, 161,170
	Emv-27	endogenous ecotropic MuLV-27		49.6	D	L			13	148
	Es-16	esterase-16		10.1	B	L			12	154,156,158
	Es-26	esterase-26		33.3	B	L			12	117,154,156,158
	Es-27	esterase-27, serum cholinesterase		23.3	B	L			12	157,158
	Evi-1	ecotropic viral integration site-1		10.2	D	L,R	EVI1	3q24-q28	1,2,6	21,23,27,28, 31,54,62, 92,109,112,141
	Fabpi	fatty acid binding protein intestinal		54.7	D	R	FABP2	4q28-q31		143
	Fcgr1	high affinity FC gamma receptor		42.9	D	L	FCGR1	1q		1,12,118,120
	Fgf2	fibroblast growth factor basic		15.7	D	I,L	FGF2	4q25-27	1,2	23,31,62,92, 102,141
	Fgg	gamma fibrinogen		42.3	D	L,R	FGG	4q28	2	13,31,59,92, 93,94
	Fim-3	Friend MuLV integration site-3		10.2	D	L	FIM3	3q27	2,8	7,27,54,139
	Fpsl-rs1	farnesyl pyrophosphate synthetase - like 1		43.9	D	L	FPSL	1q24-q31	1	134
	ft	flaky tail		42.4	V	L				85,86
	Gba	beta glucocerebrosidase	1	42.6	B,D	L	GBA	1q21	1,12	109,118
	Gbp-1	guanine nucleotide-binding protein-1		64.3	D	L,R			12	124
*	*Gja-5*	gap junction protein - connexin 40		45.5	D	L			2	59,94
*	*Glur-2*	glutamate receptor 2		34.9	D	L	GLUR2	4q25-34	1	58
	Glut-2	glucose transporter 2		10.2	D	L	GLUT2	3q26	2,5	62
*	*Gnai-2*	guanine nucleotide binding protein, alpha inhibiting activity-2		48.4	D	L			2	166
	Gnai-3	guanine nucleotide binding protein, alpha inhibiting activity-3		48.4	D	L	GNAI3	1p13	2,4	166
*	*Gsl-4*	globoglycolipid expression-4		X	V	R				115
	H-23	histocompatibility-23		59.6	B	L,R			12	4,106
	H-28	histocompatibility-28		79.3	B	L,R			12	4,106
	H-37	histocompatibility-37		(X)	B	R				4
*	*H3f2*	histone 3 , family 2		44.9	D	R	H3F2	1q21-21		132
	Hao-2	hydroxyacid oxidase-2 (kidney)		40.0	B	L			8,12	54,64,65
*	*Hc3*	heterochromatin, Chr 3		0.0		L			6	21
	Hist2	histone gene (2)		X	D	S				56
	Hnl	hypothalamic norepinephrine level		59.6	V	L				46
	Hsd3b	3-beta-hydroxy steroid dehydrogenase		45.0	D	L	HSDB3	1p11-p13		5
	Hsp86-ps2	heat shock protein 86- pseudogene 2		19.3	D	S,L				107,108
*	*Iap1a1-7*	Intracisternal A-particle a1-7		42.3	D	R				95
*	*Iap1a2-9*	Intracisternal A-particle a2-9 (near Fgg)		X	D	R				94
*	*Iap1a2-14*	Intracisternal A-particle a2-14		74.6	D	R				94
*	*Iap1a3-13*	Intracisternal A-pariticle a3-13		28.0	D	R				95
	Idd-3	insulin dependent diabetes 3		X	V	L				149
	If-1	interferon inducibility locus		84.6	V	L,R			12	36,106
	Il-2	interleukin 2	1	15.0	D	S,L	IL2	4q26-q27	1,3,4,9	49,134,149,150, 159,162,163
	Il-7	interleukin 7		2.0	B,D	L			2,6	21,62,137
*	*Kv1.2*	potassium channel gene		48.2	D	L			2	93

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Table 1. *Continued.*

*	*Kv1.3*	potassium channel gene	48.2	D	L			2	93
*	*Kv1.3rs3*	potassium channel gene 1.3 related sequence	48.4	D	L			2	93
	Lef-1	lymphoid enhancer-binding factor 1	X	D	R,S	LEF1	4q23-q25		105
*	*M6pr-ps*	cation-dependent mannose 6-phosphate receptor pseudo gene	45.5	D	L			2	94
	ma	matted	40.4	V	L			10,12	85,86,87,106
	Mme	membrane metallo-endo peptidase (neutral endopeptidase)	30.1	D	L	MME	3q21-27	1,7	23,161
	Mmv-2	MCF endogenous virus-2	X	D	S				63
	Mmv-12	MCF endogenous virus-12	X	D	S				63
	Mov-10	Moloney leukemia virus-10	X	D	S				74,113
	Mpmv-9	modified polytropic murine leukemia virus-9	88.2	D	L,R			11	51
	Mpmv-20	modified polytropic murine leukemia virus-20	9.6	D	R				51
	my	blebs	30.4	V	L			10	19,35,45
	Ngfb	nerve growth factor beta	47.4	D	L	NGFB	1p13	1,2	18,42,52,59,79,94, 109,118,166,171
	Nras	Nras oncogene	47.4	D	L	NRAS	1p13	1,2	18,93,118,128
*	*Nscl-2*	see Tau-1							
	Oat-rs2	ornithine aminotransferase related sequence 2	52.4	D	L				125
	Odc-rs3	ornithine decarboxylase-3	X	D	R				126
	op	osteopetrosis (Csfm mutation see Csfm)							
	Otf-3rs3	octamer transcription factor -3 related sequence 3	0.0	D	L			2,7	137,161
	Otf-3rs4	octamer transcription factor-3 related sequence 4		62.1	D	L			1,2,7,137,161
*	*Otf-3rs9*	octamer transcription factor-3 related sequence 9		16.4	D	L			7,161
	Oua-1	ouabain resistance-1	X	V	S				83
	Pgk-1ps3	phosphoglycerate kinase-1 pseudogene 3	8.7	D	S,R				1
	Pk-1	pyruvate kinase (may be the same as Pklr)	33.6	B	L			8	54,139
	Pklr	pyruvate kinase liver, red blood cells (see Pk-1)		42.6	D	L	PKLR	1q21	1,118
*	*Pmp-1*	peroxisomal membrane protein (70k)	54.6	D	L	PMP1	1p21-22	2	52
	Pmv-26	polytropic murine virus-26	71.8	D	R				50
	Pmv-28	polytropic murine virus-28	42.9	D	R				50
	Pmv-38	polytropic murine virus-38	43.1	D	R				50
	Pmv-39	polytropic murine virus-39	53.8	D	R				50
	Rap1a	member of RAS oncogene family	47.4	D	L	RAP1A	1p12-p13	1	41
	rcm	rostral cerebellar malformation	65.4	V	L			12	89,90
*	*Rn7s-3*	7s RNA related sequence -3	63.0	D	R				147
	Rnu1b-1	U1b1 small nuclear RNA	42.7	D	R	RNU1			96
	Rnu1b-3	U1b3 small nuclear RNA	42.9	D	R				13,96
	soc	soft coat	43.4	V	L			10	45,140
	spa	spastic	37.4	V	L			10	85,86
	suc-1	see Suc-1r							
	Suc-1r	sucrase-isomaltase, regulatory	33.3	B	L				12
	Suc-1s	sucrase-isomaltase, structural	33.3	D	R	SI	3q25-26		12
	sut	subtle gray	12.2	V	L			12	88
	Tau-1	basic domain helix-loop-helix (bHLH)	50.6	D	L			12	55
*	*Thbs3*	thrombospondin 3	43.9	D	L			1	38
*	*Tkr*	tyrosine kinase receptor (Ngf is ligand)	43.9	D	L			1	80
	Tmevd-2	TMEV induced demyelinating disease susceptibility	8.4	V	R				104
*	*Tpi-2*	triosephosphate isomerase related sequence-2	36.4	D	L			2	138
	Tshb	thyrotropin stimulating hormone beta subunit 1	47.4	D	L	TSHB	1p13	1	13,42,79,82,109, 116,118,150,159
	Va	varitint-waddler	71.6	V	L			10,12	32,43,45,67,68, 86,87,106
	Xmmv-22	xenotropic-MCF leukemia virus - 22	42.3	D	R				13
	Xmmv-47	xenotropic-MCF leukemia virus - 47	31.0	D	R				164
	Xmmv-65	xenotropic-MCF leukemia virus - 65	42.3	D	L,R			12	164
*	*Ybld*	YB-1 DNA binding protein related sequence d	14.6	D	L			2	141

The Chr 3 map positions are an estimate of distances, in cM, from the centromere. The position of the centromere is determined by heterochromatin mapping data (21, 101). 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. For a fuller discussion of the generation of map positions, see text and (133). In addition to the references cited for each locus, data used to derive map positions are described in the following "Notes:" (1) Duke University cross: complete haplotypes in 114 and incomplete haplotypes in 338 interspecific [(C3H/HeJ-*gld* × *M. spretus*)F_1 × C3H/HeJ-*gld*] backcross mice (134); (1a) same cross as above, but fewer than 40 meiotic events examined; (2) Frederick cross: complete haplotypes in 83–198 interspecific [(C57BL/6J × *M. spretus*)F_1 × C57BL/6J] backcross mice; (2a) same cross as 2, but fewer than 50 meiotic events examined; (3) Rockefeller University cross and MIT microsatellite mapping panel: complete haplotype data in 40–48 (C57BL/6J-*ob* ×CAST/Ei)F_2 intersubspecific intercross mice; (4) European Collaborative Interspecific Backcross [(C57BL/6 × SPR)F_1 × SPR] produced by the UK's Human Genome Mapping Project, with the support of the Medical Research Council (15); (5) data from the cross [(NOD/*Uf* × C57BL/6J)F_1 × NOD/*Uf*] from the laboratory of E.K. Wakeland. The RAPD polymorphism *D3Uf1* was detected with the primer GTGCCTAACC, and *D3Uf2* with the primer TGCTCACTGA; (6) RPMI cross: complete haplotypes in 130–140 [(C57BL/6 × *M. spretus*)F_1 × *M. spretus*]; (7) Duke University cross #2: complete haplotype data in 100–182 [(MRL/MpJ-*lpr* × CAST/Ei)F_1 × MRL/MpJ-*lpr*] intersubspecific backcross mice (161); (8) Pasteur cross: incomplete haplotypes in 38–74 interspecific backcross mice (J.-L. Guénet, unpublished data); (9) same as 4 with complete haplotype data in 92–299 mice; (10) included in nine overlapping three- or four-point crosses that derive from analysis of 125–500 meiotic events in each of multiple individual crosses; (11) haplotype data in 75 interspecific backcross mice (W.N. Frankel, unpublished data); (12) three-point mapping data; (13) two-point mapping data.

Table 2. Tabular map of Chr 3. Loci described in Table 1 are arranged in order of increasing distance from the centromere. The 95% confidence intervals for these composite data are greater than 5 cM. Unambiguous gene order can only be determined for loci which were mapped within the same cross (Fig. 1B).

Map	Locus	Map	Locus	Map	Locus
0.0	*D3Mit23*	28.0	*Iapla3-13*	42.9	*Capl*
0.0	*Hc3*	30.0	*D3Mit25*	42.9	*D3Pas502*
0.0	*Otf-3rs3*	30.0	*D3Mit7*	42.9	*D3Tu51*
2.0	*Il-7*	30.1	*D3Byu17*	42.9	*Fcgrl*
6.3	*Car-1*	30.1	*D3Sel2*	42.9	*Pmv-28*
6.3	*Car-2*	30.1	*Mme*	42.9	*Rnu1b-3*
6.9	*D3Byu1*	30.4	*my*	43.0	*Acrb-2*
6.9	*D3Byu2*	31.0	*Xmmv-47*	43.1	*Pmv-38*
7.0	*D3Mit1*	33.1	*D3J1*	43.4	*soc*
7.5	*Car-3*	33.3	*Es-26*	43.5	*D3Uf1*
8.1	*D3Byu3*	33.3	*Suc-1r*	43.9	*Cd1*
8.2	*D3Pas501*	33.3	*Suc-1s*	43.9	*Fpsl-rs1*
8.3	*coa*	33.6	*Pk-1*	43.9	*Thbs3*
8.4	*Tmevd-2*	34.4	*D3Byu5*	43.9	*Tkr*
8.7	*Pgk-1ps3*	34.9	*Glur-2*	44.9	*D3Mit28*
9.6	*D3Mit46*	35.0	*D3Mit22*	44.9	*H3f2*
9.6	*Mpmv-20*	35.0	*D3Mit53*	45.0	*Hsdb3b*
9.7	*Ap2*	36.2	*D3Mit51*	45.3	*D3Byu4*
10.1	*Es-16*	36.4	*Tpi-2*	45.5	*Gja-5*
10.2	*D3Leh2*	37.4	*spa*	45.5	*M6pr-ps*
10.2	*Evi-1*	38.6	*D3Mit26*	46.1	*D3Mit41*
10.2	*Fim-3*	38.6	*D3Mit9*	46.4	*Cd2*
10.2	*Glut-2*	38.8	*Cnp-2*	47.3	*Atp1a1*
12.2	*sut*	40.0	*Hao-2*	47.4	*Ampd-1*
13.2	*D3Pas2*	40.1	*D3Mit40*	47.4	*Cd53*
14.6	*Ybld*	40.1	*D3Mit49*	47.4	*D3Jfr1*
15.0	*Ccna*	40.4	*ma*	47.4	*Ngfb*
15.0	*Il-2*	41.5	*D3Ler1*	47.4	*Nras*
15.7	*Fgf2*	41.5	*D3Ler2*	47.4	*Rap1a*
16.4	*Otf-3rs9*	42.3	*D3Byu6*	47.4	*Tshb*
17.6	*D3Leh1*	42.3	*Fgg*	48.1	*D3Sel1*
19.3	*Hsp86-ps2*	42.3	*Iapla1-7*	48.2	*Kv1.2*
20.0	*D3Mit24*	42.3	*Xmmv-22*	48.2	*Kv1.3*
20.0	*D3Mit3*	42.3	*Xmmv-65*	48.4	*Csfm*
20.0	*D3Mit4*	42.4	*ft*	48.4	*de*
20.9	*D3Pas1*	42.6	*Gba*	48.4	*Gnai-2*
22.0	*D3Mit6*	42.6	*Pklr*	48.4	*Gnai-3*
23.3	*Es-27*	42.7	*Rnu1b-1*	48.4	*Kv1.3rs3*
24.0	*D3Mit5*	42.9	*Cacy*	48.6	*D3Mit10*
27.0	*D3Nds1*	42.9	*Call1*	48.6	*D3Mit11*
49.6	*Amy-1*	68.1	*Ahr-1*		
49.6	*Amy-2*	68.1	*Bmn*		
49.6	*Cf-3*	68.7	*D3Mit17*		
49.6	*Emv-27*	69.0	*D3Jkn1*		
50.2	*Ampd-2*	71.6	*Va*		
50.3	*D3Mit12*	71.8	*Pmv-26*		
50.6	*Nscl-2*	73.0	*D3Mit18*		
52.0	*Adh-1ps*	73.0	*D3Mit31*		
52.3	*D3Uf2*	74.6	*Iapla2-14*		
52.4	*Oat-rs2*	75.3	*D3Mit45*		
53.4	*D3Mit36*	76.4	*D3Dol*		
53.4	*D3Mit39*	77.0	*D3Mit32*		
53.8	*Pmv-39*	79.3	*H-28*		
54.6	*Pmp-1*	81.0	*D3Mit19*		
54.7	*D3J3*	84.6	*If-1*		
54.7	*Fabpi*	88.2	*Mpmv-9*		
56.1	*D3Hun1*	X	*Idd-3*		
56.1	*D3Mit42*	(X)	*H-37*		
57.7	*D3Mit13*	X	*Acts*		
57.9	*D3Tu33*	X	*Adh-5*		
58.4	*Ank-2*	X	*Arnt*		
59.6	H-23	X	*Bglap*		
59.6	Hnl	X	*Gsl-4*		
61.0	*D3Mit14*	X	*Hist2*		
61.0	*D3Nds2*	X	*Iapla2-9*		
61.6	*cdm*	X	*Lef-1*		
62.1	*Egf*	X	*Mmv-12*		
62.1	*Otf-3rs4*	X	*Mmv-2*		
63.0	*D3Nds3*	X	*Mov-10*		
63.0	*Rn7s-3*	X	*Odc-rs3*		
63.1	*D3Mit15*	X	*Oua-1*		
63.1	*D3Mit16*				
64.3	*Gbp-1*				
65.4	*rcm*				
65.6	*D3J2*				
67.2	*D3Mit38*				
68.1	*Adh-1*				
68.1	*Adh-1t*				
68.1	*Adh-3*				
68.1	*Adh-3t*				

says, and the availability of the MIT primers from Research Genetics (Birmington, Ala.) make these markers extremely useful. Additional microsatellite markers have been developed by J. A. Todd and coworkers at the Nuffield Department of Surgery, Oxford, U.K. (Nds). Table 4 presents recombination data for 21 microsatellite markers spanning Chr 3, obtained from the European Interspecific Backcross [(C57BL/6J × Spretus) F_1 × Spretus].

Recombinant inbred 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 RI lines are presented in Fig. 2.

Anchor loci

In the last report we recommended use of six anchor loci to facilitate integration of new genetic data with the current map. It is too early to judge the effectiveness of this recommendation, that is, the degree to which investigators will type these loci in new crosses. To fill in the gaps in the previous anchor map, we recommend two additional microsatellite markers. Either *D3Mit5* or *D3Mit27* will divide the 28-cM interval between *Il-2* and *Gba* approximately in half. *D3Mit19* provides a marker for the distal end of Chr 3; it is located approximately 20 cM distal to *Adh-1*. A subset of these well-mapped anchor markers can be selected to divide Chr 3 into convenient intervals: *centromere* – 6 – *Car-2* – 9 – Il-2 – 9 – *D3Mit5*, *D3Mit27* – 11 – *D3Mit22* – 8 – *Gba* – 5 – *Tshb* – 2 – *Amy-1* – 12 – *Egf* – 6 – *Adh-1* – 13 – *D3Mit19*.

Conserved linkage relationships

Mapping of genes has identified syntenic relationships between mouse Chr 3 and four human chromosomes: 1, 3, 4, and 8. The position of these mouse Chr 3 genes and their relationships to the chromosomal positions of the human homologs are shown in Table 5. These data suggest that rearrangements of chromosomal segments during mouse evolution have resulted in three separate homology groups with human Chr 4 and two separate homology groups with human Chr 3. In addition, the conserved linkage relationship with human Chr 1 spans the centromere of this chromosome. Long-range restriction site analysis has also indicated very strong conservation of some of these relation-

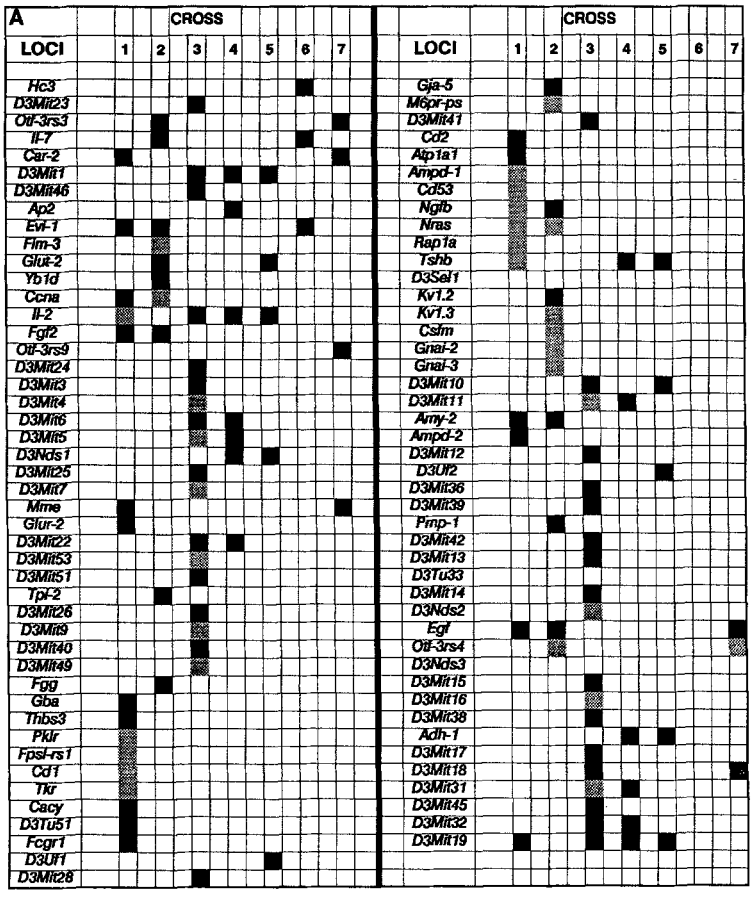

Fig. 1. (A) Gene order in seven multilocus crosses. Loci are listed from proximal to distal on the chromosome. The **filled boxes** represent the loci that were typed in each cross. The **shaded boxes** represent loci that did not recombine with the locus listed directly above. The observed recombination frequencies from each of these crosses are presented in Fig. 1B. See Table 1 and Fig. 1B for additional information about the crosses.

B

CROSS 1: (C3H/HeJ-*gld* x *M. spretus*)F_1 x C3H/HeJ-*gld* (n = 117 to 338)

Car-2 - 3.5 - *Evi-1* - 2.6 - *Il-2* - 0 - *Cyca* - 0.9 - *Fgf2* - 13.5 - *Mme* - 4.4 -*Glur-2* - 7.10 - *Gba* - 0.9 - *Thbs3* - 0 - *Pkir* - 0 - *Fspl-rs1* - 0 - *Cd1* - 0 - *Trk* - 0.6 -*D3Tu51* - 0 - *Cacy* - 0.9 - *Fcgr1* - 2.6 - *Cd2* - 0.9 - *Atp1a1* - 0.3 - *Nras* - 0 - *Cd53* - 0 - *Ngfb* - 0 - *Tshb* - 0 - *Ampd-1* - 1.8 - *Amy-2* - 0.6 - *Ampd-2* - 13.4 - *Egf* - 11.7 - *D3Mit18* - 9.3 - *D3Mit19*

CROSS 2: (C57BL/6J x *M. spretus*)F_1 x C57BL/6J (n = 83 to 198)

Otf-3rs3 - 2.0 - *Il-7* - 7.3 - *Evi-1* - 0 - *Fim-3* - 0 - *Glut2* - 7.6 - *Ybld* - 0 -*Ccna* - 0 - *Fgf2* - 21.8 - *Tpi-2* - 6.0 - *Fgg* - 6.8 - *Gja-5* - 0 - *M6pr-ps* - 5.2 - *Ngfb* - 0 - *Nras* - 2.2 - *Kv1.2* - 0 - *Kv1.3* - 0.6 - *Csfm* - 0 - *Kv1.3-rs3* - 0 - *Gnai-2* - 0 - *Gnai-3* - 1.5 - *Amy-2* - 4.9 - *Pmp-1* - 5.5 - *Egf* - 0 - *Otf-3rs4*

CROSS 3: (C57BL/6J-*ob* x CAST/Ei)F_2 (n = 40 to 48)

D3Mit23 - 6.8 - D3Mit1 - 1.4 - D3Mit46 - 2.4 - Il-2 - 2.2 - D3Mit4 - 0 - D3Mit3 - 0 - D3Mit24 - 1.1 - D3Mit5 - 0 - D3Mit6 - 4.7 - D3Mit7 - 0 - D3Mit25 - 3.4 - D3Mit22 - 0 - D3Mit53 - 1.1 - D3Mit51 - 2.3 - D3Mit26 - 0 - D3Mit9 - 1.4 - D3Mit40 - 0 - D3Mit49 - 4.6 - D3Mit28 - 1.1 - D3Mit41 - 2.3 - D3Mit10 - 0 - D3Mit11 - 1.1 - D3Mit12 - 1.8 - D3Mit39 - 0.5 - D3Mit36 - 1.8 - D3Mit42 - 1.1 - D3Mit13 - 2.2 - D3Nds2 - 0 - D2Mit14 - 1.1 - D3Mit16 - 0 - D3Mit15 - 3.5 - D3Mit38 - 1.2 - D3Mit17 - 4.3 - D3Mit31 - 0 - D3Mit18 - 3.1 - D3Mit45 - 2.4 - D3Mit32 - 7.3 -D3Mit19

CROSS 4: C57BL/6J x SPR)F_1 x SPR: D3Mit1 - 7.6 - Ap2 - 10.8 - Il-2 - 7.6 - D3Mit6 - 2.0 - D3Mit5 - 3.0 - D3Nds1 - 8.6 - D3Mit22 - 8.6 - Tshb - 1.0 - D3Mit11 - 1.9 - Adh-1 - 10.8 - D3Mit31 - 4.3 - D3Mit32 - 3.0 - D3Mit19

CROSS 5: (NOD/Uf x C57BL/6J)F_1 x NOD/Uf

D3Mit1 - 19.0 - Glut-2 - 4.0 - Il-2 - 6.1 - D3Nds1 - 18.8 - D3Uf1 - 7.3 - Tshb - 4.3 - D3Mit10 - 3.2 - D3Uf2 - 14.1 - Adh-1 - 20.5 - D3Mit19

CROSS 6: (C57BL/6J x *M. spretus*)F_1 x *M. spretus* (n = 130 to 140)

Hc3 - 0.7 - Il-7 - 6.9 - Evi-1

CROSS 7: (MRL/MpJ-*lpr* x CAST/Ei)F_1 x MRL/MpJ-*lpr:* Otf-3rs3 - 6.3 - Car-2 - 10.6 - Otf-3rs9 - 14.4 - Mme - 24.3 - Otf-3rs4 - 0 - Egf - 26.8 - D3Mit18

Fig. 1. (B) Recombination frequencies in multilocus crosses. Crosses 1–7 are described in Table 1 and Fig. 1A. The approximate lengths, in cM, of the intervals observed in each cross are presented here. We included only crosses with at least six markers analyzed in at least 80 meiotic events, with the exception of cross 6, which provides data for anchoring the composite maps with respect to the centromere. (Note: Cross 4, n = 92)

Table 3. PCR primers for amplification of polymorphic loci on Chr 3.

Locus	Sequence	Primer forward (5'-3')	Primer reverse (5'-3')	Product size	Conditions	Size variation
D3Nds1		GGATCTGGCACCTCCAGGG	TATGTTGCCTTGGCAAATAGATG	90	1mM/55	NOD=NON>>AKR/J>B10/W=B6.PL=B6/J=DBA/2J; SPE:-
D3Nds2		ACACATTGGAGATGCACAGCG	TCTGCATGCCAGGGTTGTGAT	128	3mM/55	SPE>>DBA/2J>>NOD=NON=B10/W=B6.PL=B6/J=AKR/J
D3Nds3		CTGTGAAATTTGCCATCAACT	CATAATATTCATATATAATGC	165	3mM/55	NOD=NON=B10/W=B6.PL=B6/J=AKR/J>>DBA/2J>>SPE
D3Nds4		ATTTTAAATATTCATTCATTTGGG	CTCACAAATACCTTCAGAGGA	110	1mM/55	NON>B6/J=B10/W=B6PL>DBA/2J>NOD
D3Nds5		AGCATTATTTTAAACATCTGAATAG	TGGAGTCACCTTCTTGAGTTC	148		NOD>>DBA/2J=AKR/J=NON>B10/W=B6.PL=B6/J (SPE doublet)
D3Nds6	*Il-2*	GTGGGAGTGTGTGCAAAAGAC	AAGTATGGGTCAGATTGTGTGGG	170	2mM/58	SPE>B6.PL=B10/W=B6/J>NON>AKR/J>DBA/2J>NOD
D3Nds7	*Cacy/Capl*	CACAGTGAGACCAAACTC	CTTGGCTGTTATAGTGTTTG	117	1.5mM/55	SPE>>C57L/J>>SWR/J=C57BR=SJL/J=B10/W=NON>C3H/HeJ=A/J=AKR/J>>CBA=BALB/cByJ=NOD>>DBA=PL/J
D3Nds8	*Tshb*	TCTGAAGAGTTTGTCCTCATC	TGAATAAAGGACTCCTGAGCT	145	2mM/55	NOD=AKR/J>>NON=B10/W=B10/J=B6/J=DBA/2J>>SPE
D3Nds9	*Adh-1*	CTTACTGGGTGACATAGACG	CCTTTCATCCATGTACATATAC	330	2mM/55	B10/J=B10.BR>NOD>A=C58=MEV; SPE=B10/W>NOD>B6.PL>NON
D3Nds11	*Fcgr1*	GTCCCCAGTCATCAGCTCCTG	CGCTTCTAACTTGCTGAAAGGAA	184-188	1.5mM/63	C3H=DBA=A=B6=AKR=BALB=B10=CAST=SPE=NON>>NOD
D3Nds12	*Glut-2*	GGGCGCTGGAAAGCTAATACC	CATAAGAGAGGGAGGGAGATC	120	1mM/55	B6=B6.PL=DBA=B10=AKR=SPE>NON=NOD
D3Nds13	*Glut-2*	GTCTCCTTTCTAGTTTCTGAGGC	CTTCACAGATGGTATTTGAAACAG	113	1mM/55	B6=B6.PL=DBA=B10=AKR=SPE=NON=NOD
D3Nds14	*Ap2*	TCCATAGCATTCATGCGTGCA	GTCTGTTGCTTACTATGTGC	146	2mM/55	NON>CBA>B10/W=B6.PL=NOD=SPE=B6/J>DBA/2J
D3Nds15	*Ap2*	TATAAGATTCCAGAACACATT	GATAAGAGCATGGATTTAACT	133	2mM/55	NOD=B10/W=B6.PL=B6/J=DBA/2J=NON>SPE
D3Nds16	*Il-2*	TGTACCTCCTGCTTACAACAC	TACCTACACATGATATTTAAC	224	2mM/55	NOD=B10/W=B6/J=NON=DBA/2J=SPE
D3Nds17	*Il-2*	ACTAGCAAGAGTTGGTCTCTG	ATTTTATATGTCTCTAGTTGCAC	232	2mM/55	NOD=B10/W=B6.PL=B6/J=NON=SPE=DBA/2J
D3Nds18	*Ngfb*	AGGTTCATCCGGATAGACACA	TTCGGTATACAGGATGCTTTG	232	1.5mM/55	NOD=B10/W=NON=SPE=B6/J=DBA/2J
D3Nds19	*Amy-1*	ATGAACATATGTGTAAGTAAAATG	AAATAAAAAGGCCACTATTTGAAG	153	2mM/45	CBA=MOLD=YBR=C3H=NOD>BRcdJ>AKR>SPE
D3Nds20	*Gba*	GAAGGAAAGGACTTAGTCTACC	GGCCTTGGCTCTGTTATTCTGT	190	1.5mM/55	SPE (doublet)>>NOD=B10.W=B6.PL=B6/J=DBA/2J
D3Nds21	*Ly-38*	GTGTAAAATCAACACCAACAGTAT	GGCAGGTTTGATTCTAAGGTAG	166	1mM/55	NOD=B10/W=B6.PL=B6/J=NON=DBA/2J=AKR/J=SPE
D3Nds22	*Ly-38*	GGGGTTTTGTTTGCTGGTTAGT	GGACAGCCAGGACTATACAGA	164	1mM/61	NOD=B10/W=B6.PL=B6/J=NON=DBA/2J=AKR/J>>SPE
*D3Nds23**	*Hsp86-ps2*	AGTGCCCAATCACATTCTGC	GATCCTGTAATCTGTCCATAG	1100	2mM/55	RFLP; HinfI NOD=+; B10, B6, NON=-
*D3Nds24***	*Cd-10*	GTCCTGGAGGTTCATAATG	GGGAGAGAAAACGCAACAT	1200	1mM/55	RFLP; MspI SPE=+; B6=-
*D3Nds25****	*Gba*	GATGCAGTACAGTCACAGCAT	CCATCCAGTTACGTGGTAAAG		1.5mM/58	SPE>>B6
*D3Nds26*****	*Gpi-irs*	GTCCCCGTGTCTGGTTTGTCTCTAACATT	TGACCACAGCGAATAGCGGCAACCTACCC	280	2mM/60	NOD=+; B10=-
D3Nds27	*Il-2*	GTGCTCCTTGTCAACAGCGCA	CTCCTGTAGGTCCATCAACAGC	129	1mM/55	NOD=B10/W=B6/J=B6.PL=NON=DBA/2J=AKR>>SPE
D3Mit1	*M28*	TGTGCACAGGGGTACATACA	TCATTTTCTTCCTCCCCCTC	118-145	3mM/55	OB>LP>>BALB=NOD>>A=B6=C3H=DBA=AKR=NON>CAST; SPE:-
D3Mit3	*M250*	CCTTTTGAGGCAAAGCTCC	CTAAGTCCTGCACCTGCCTC	88-200	1mM/55	CAST>>A=BALB=LP>OB=B6=DBA=AKR=NOD>>C3H=NON>>SPE
D3Mit4	*L40*	TGTGCCTGCAAGTTGTTCTT	CTACAGTGGGGGCAGAAGGT	140-150	1.5mM/55	CAST>>SPE>>OB=A=B6=C3H=DBA=BALB=AKR=NON=NOD=LP
D3Mit5	*M123*	AGCCCCTTCCAAGTGTCTCT	GGTTTCGGAATGAGATGAGC	178-188	1mM/55	OB=A=C3H=DBA=BALB=AKR=NON=NOD>>CAST=B6=LP>>SPE
D3Mit6	*M149*	AACTTCAACATGTGAGGGGC	CCTGAAACAAAGCAACAGCA	125-145	1.5mM/55	B6=LP>OB>>A=C3H=DBA=BALB=AKR=NON=NOD>>CAST>>SPE

Continued on next page

Table 3. *Continued.*

D3Mit7	*M74*	ATGCAACTAACTTTATTGAAAATC	TACAATTATCCGGGAGCTA	142-147	1mM/55	OB=SPE=B6=DBA>>CAST=A=C3H=BALB=AKR=NON=NOD=LP
D3Mit9	*A85*	AACTTCATTTGCTTGGAAACTACC	TGTTTTATATTGCCCTGTATGTGC	214-238	1mM/55	CAST>>OB=B6>>DBA>LP>NOD>A=BALB>SPE=AKR>>NOD; C3H:-
D3Mit10	*A34*	CTGGCTTGGTGGAAGTCCT	CCTAAGCCAGCTACCACCAC	121-158	1mM/55	CAST>>B6=OB>>DBA>LP>NON>BALB=A>AKR=SPE>>NOD; C3H:-
D3Mit11	*L38*	CCAACCACAGTAACACATGT	TGGAGACCAATGCGAACAAC	146-204	1mM/55	CAST>>A=C3H=BALB=AKR>NON>>SPE>>OB=B6=DBA=NOD=LP
D3Mit12	*A60*	TAGACCAATCTTGGGAGTGTCC	GGAAAAGCATAAGAAACAACCG	120-157	1mM/55	LP=AKR=A>BALB=C3H=B6=OB>>NOD=NON=DBA>>CAST; SPE:-
D3Mit13	*L8*	CCTTTCTGATTATGTGGGCT	CCACTGAAGGATAACCACAG	228-240	1mM/55	SPE=LP>CAST=NOD>>OB=B6=C3H=DBA=BALB=AKR=NON; A:-
D3Mit13	*L37*	TTTCTGCATTATGTGGGCTT	AACCACAGATGACAATTGAA	220-237	1mM/55	LP>SPE>NOD>>CAST>>OB=B6=DBA=C3H=BALB=AKR=NON
D3Mit14	*M206*	ATTGCGGTTAAAGTTTGCTT	TCCTGCAAATTGTCCTCTGA	127-198	1mM/55	NOD=NON=AKR=BALB=DBA=C3H=A>>LP=B6=OB>>SPE>>CAST
D3Mit15	*A55*	AATTTGCATTCCAGGACCAC	AGGAAGTGACGTTGGGTTTG	145-212	1mM/55	DBA>>CAST>>SPE>>NOD=NON=AKR=BALB=C3H=B6=A=OB; LP:-
D3Mit16	*M159*	TGCTTGTCCTGTGTTAATGA	TGAGAATGGAGGTGAACAGC	186-220	1mM/55	SPE>>CAST>>B6=OB=LP=NOD=NON=BALB=C3H=A; AKR, DBA:-
D3Mit17	*M235*	CATGGCTCCATGGTTCTTG	CCACGGAGAACAACTGAAGA	180-208	1mM/55	NOD=B6=OB>>CAST>>LP>>NON=AKR=BALB=DBA=C3H=A; SPE:-
D3Mit19	*M141*	CAGCCAGAGAGGAGCTGTCT	GAACATTGGGGTGTTTGCTT	210-238	1.5mM/55	CAST=A=C3H=DBA=BALB=AKR=NOD>>OB=B6=NON>LP>>SPE
D3Mit21	*D31*	AAGCTCTACAGCGGAAGCAC	CTGGGGAGTTTCAGGTTCCT	208-236	1mM/55	NON=BALB=B6=OB>>LP=NOD=AKR=DBA=C3H=A>CAST>>SPE
D3Mit22	*D122*	AAGGATTGAAGAATGGTTGGG	AATCAGCGATTTCAGCACG	207-265	1mM/55	CAST>>A>>NOD>>OB=B6=C3H=NON>DBA=AKR>>BALB=LP>>SPE
D3Mit23	*D102*	GATTCCAGAACACATTGTGGG	TCAATCAGAGAGATAAGAGCATGG	138-162	1mM/55	CAST>>LP=NOD=NON=AKR=BALB=DBA=C3H=B6=A=OB>>SPE
D3Mit24	*A636*	AGTTTCTAGCCTCAGTGTTCTTCA	GTCATTGTTTATCATACCCACAGG	130-168	1mM/55	CAST>>SPE>>NON>>LP=NOD=AKR=BALB=DBA=B6=OB>>C3H=A
D3Mit25	*A726*	GTCTGGGTCGTCAGTGGC	TGGAGGCTACCATCTCCAAG	114-134	1mM/55	B6=OB>LP=NOD=AKR=BALB=C3H=A>>129>NON>DBA>>SPE
D3Mit26	*B332*	TTGGATTCATATCAGGACTGTACA	CTGGAATCAAGTGGTTTAGTCAA	130-156	1mM/55	CAST>>B6=OB>>LP=NON>>NOD=AKR=BALB=DBA=SPE; C3H, A:-
D3Mit28	*D627*	GATGAGAGATTCTGATGTGGAGG	CCAGCCTCAGTATCTCAAAACC	150-202	1mM/55	BALB>>CAST>>DBA>>SPE>>OB>NON=AKR=C3H=B6=A; LP, NOD:-
D3Mit29	*D566*	GATGAGAGATTCTGATGTGGAGG	CCAGCCTCAGTATCTCAAAACC	144-200	1mM/55	BALB>>CAST>>DBA>>SPE>>B6=A=OB>LP=AKR=C3H>NON>NOD
D3Mit31	*A629*	ACAACCCGAGTTCAGTCCC	GTGCTGCCAGTTAAGCCTG	222-242	1mM/55	CAST>SPE>>LP=NOD=NON=AKR=BALB=DBA=C3H=A>B6=OB
D3Mit32	*B128*	CACCCTGGTTAACTCAGAAAGG	GCACTTGTGTTTCATGTCACTG	164-178	1mM/55	LP=NOD=NON=AKR=BALB=DBA=C3H=A=SPE>>B6=OB>>CAST
D3Mit36	*D501*	GATTTTAATTCATTAAATAAGGGTTAG	GAACATATGTGTAAGTAAAATGTAC	138-226	1mM/55	NOD>>CAST>>SPE; LP, NON, AKR, BALB, DBA, C3H, B6, A, OB:-
D3Mit38	*A674*	CTGAACCAGAAAGTTGTTTTTCTG	ACCATGGCCAGCTTCTAATG	122-142	1mM/55	CAST>>LP=BALB=C3H=A=SPE>>NOD=NON=AKR=DBA>B6=OB
D3Mit39	*A869*	CTGCCACAGAGCTATAGCCC	AATGGAGCTTGCTTTCGATG	226-242	1mM/55	SPE=CAST>>LP=NOD=NON=AKR=DBA=C3H=B6=A=OB>>BALB
D3Mit40	*AI110*	CAGCTGGTCTAACTATCCCCC	CCTTATTAAGTGCATGACCTTGC	110-140	1mM/55	B6=OB>>CAST>>SPE>>LP=NOD=NON=AKR=BALB=DBA=C3H=A
D3Mit41	*B235*	AATTTCTTCCTGTTACACTGAGCC	CATGAGAGAACTCCTTCCATCC	210-236	1mM/55	CAST>>NOD>>SPE>>LP=NON=AKR=BALB=DBA=C3H=B6=A=OB
D3Mit43	*B391*	TGACCTCCAGAGAGTCTTCCA	CTGTGCATGAGACCACTACCA	114-146	1mM/55	CAST>>BALB=C3H=A>>LP=NOD=NON=AKR=B6=OB>>DBA>SPE
D3Mit44	*B439*	CCTGACTCATTTATTTAACTCCCC	CCCTATCACATAGGGCAACC	124-148	1mM/55	NOD=DBA>B6=OB>NON>>AKR>>LP=BALB=C3H=A>>CAST>>SPE
D3Mit46	*D534*	ATCCCCCACCCAACTCTAAC	TTCCCCAGGGAAATCTCTCT	152-194	1mM/55	SPE>>CAST>>C3H=A>>B6=OB>BALB>LP=NOD>DBA>NON>>AKR
D3Mit48	*D535*	TCTGTACCCCTTTCCCCC	GTTGACACAAAACTAGCCAGTACA	247	1mM/55	
D3Mit49	*D567*	CTTTTCTCGCCCCACTTTC	TCCTTTTAGTTTTTGATCCTCTGG	108-148	1mM/55	BALB=DBA>>LP=B6=OB>>NON=C3H>CAST; NOD, AKR, A, SPE:-

Continued on next page

Table 3. *Continued.*

Locus	Sequence	Primer forward (5'-3')	Primer reverse (5'-3')	Product size	Conditions	Size variation
D3Mit50	*F107*			168-198	1mM/55	CAST>>LP=AKR=BALB=DBA>C3H=A>NOD=NON=B6=OB; SPE:-
D3Mit51	*J8*	GGCACTGATAGCAGGCCTAG	TCTCTTCTGGTATTTCCTTCCG	230-258	1mM/55	AKR=BALB=DBA>NOD=NON>>LP>>C3H=B6=A=OB>>CAST; SPE:-
D3Mit52	*A1081*	AGCCAGGATATGGAATATGCC	TGACCAGATTGCATGCATTT	196-204	1mM/55	A=SPE>OB>NOD=NON=AKR=DBA=C3H>LP>BALB=B6; CAST:-
D3Mit54	*B572*	TTGGTTCCACAGCAACTACG	CAGGGAATGTATGTCAATGAGG	122-148	1mM/55	NOD=BALB=C3H=B6=A=OB>CAST>NON>>LP=AKR=DBA>>SPE
D3Mit55	*B536*	CTGGGACCACCAGTAGTACCA	TCAGGACTGCAACTGAGGC	116-144	1mM/55	C3H=A>>LP=NOD=B6>AKR=BALB=DBA=CAST>>NON>>SPE; OB:-
D3Mit56	*B713*	TCTAGCTATGTGATGAGTGTGTCG	CAGGATTTCCAAAAACATCCA	138-148	1mM/55	A>LP=NOD=NON=AKR=DBA=C3H=B6=OB>BALB>>CAST; SPE:-
D3Mit57	*B493*	TCCAGTTACTTGGTGAACTCCA	ATATGTGTACATGTTCATGGTGTG	148-176	1mM/55	CAST>>SPE>>LP>B6>NON=AKR=BALB=C3H=A=OB>>NOD; DBA:-
D3Mit58	*B527*	ACATCAGAAGAGTCATTCATTTCA	GCTCTTCAGTCACAGCTCTGC	140-152	1mM/55	CAST>>NOD=NON=BALB=DBA=C3H=B6=A=OB>>LP=AKR; SPE:-
D3Mit59	*B543*	GTTGATGCCCAAGGAATGAT	CTACTGCATCCTGGCACAGA	204-212	1mM/55	OB>CAST>LP=AKR=B6=NON=BALB=DBA=C3H=A=SPE>NOD

Recommended magnesium concentrations and annealing temperatures are indicated for most loci. **D3Nds23: Hsp86-ps2,* unpublished sequence was kindly provided by S. Moore, Food and Drug Administration, Division of Metabolism and Endocrine Drug Products, Rockville, Md.; the STS and polymorphism are from N. Rodrigues. ***D3Nds24: CD10,* clone obtained from M. Shipp, Dana-Farber Cancer Institute, Boston, Mass.; the STS and polymorphism are from N. Rodrigues. ****D3Nds25: Gba,* (ref. 119). *****D3Nds26: Gpi-irs,* unpublished STS from J. Jones, MRC Radiobiology Unit, UK.

Table 4. Microsatellite map of Chr 3.

Loci	RF	Distance
D3Mit1-D3Nds15	7/92	7.65 cM
D3Nds15-D3Nds27	10/92	11 cM
D3Nds27-D3Mit6	7/92	7.65 cM
D3Mit6-D3Mit5	2/92	2.1 cM
D3Mit5-D3Mit7	3/92	3.2 cM
D3Mit7-D3Nds1	0/92	0
D3Nds1-D3Nds24	3/92	3.2 cM
D3Nds24-D3Mit22	5/92	5.4 cM
D3Mit22-D3Mit51	3/92	3.2 cM
D3Mit51-D3Mit9	1/85	1.1 cM
D3Mit9-D3Nds25	0/85	0
D3Nds25-D3Nds22	0/92	0
D3Nds22-D3Nds8	4/92	4.3 cM
D3Nds8-D3Mit11	1/91	1 cM
D3Mit11-D3Mit42	7/91	7.7 cM
D3Mit42-D3Nds9	12/92	13.3 cM
D3Nds9-D3Mit38	3/92	3.2 cM
D3Mit38-D3Mit31	7/90	7.8 cM
D3Mit31-D3Mit32	4/90	4.4 cM
D3Mit32-D3Mit19	3/92	3.2 cM

Data from the laboratory of J.A. Todd from the European Collaborative Interspecific Backcross [(C57BL/6 × SPR)F_1 × SPR] produced by the UK's Human Genome Mapping Project, with the support of the Medical Research Council. Distances were calculated with the Kosambi mapping function. RF, recombinant fraction (recombinants/total analyzed).

Table 5. Relationships between mouse Chr 3 genes and homologous human genes.

Map	Locus	Name	Human	Human position
6.3	*Car-1*	carbonic anhydrase-1	CA1	8q13-q22
6.3	*Car-2*	carbonic anhydrase-2	CA2	8q13-q22
7.5	*Car-3*	carbonic anhydrase-3	CA3	8q13-q22
10.2	*Evi-1*	ecotropic viral integration site-1	EvI1	3q24-q28
10.2	*Fim-3*	Friend MuLV integration site-3	FIM3	3q27
10.2	*Glut-2*	glucose transporter 2	GLUT2	3q26
15.0	*Il-2*	interleukin 2	IL2	4q26-q27
15.7	*Fgf2*	fibroblast growth factor basic	FGF2	4q25-27
30.1	*Mme*	membrane metallo-endo peptidase	MME	3q21-27
33.3	*Suc-1s*	sucrase-isomaltase, structural	SI	3q25-26
34.9	*Glur-2*	glutamate receptor 2	GLUR2	4q25-34
42.3	*Fgg*	gamma fibrinogen	FGG	4q28
42.6	*Pklr*	pyruvate kinase liver, red blood cells	PKLR	1q21
42.6	*Gba*	beta glucocerebrosidase	GBA	1q21
42.9	*Cacy*	calcyclin	CACY	1q21-q25
42.9	*Capl*	calcium binding protein, placental	CAPL	1q12-q22
42.9	*Fcgr1*	high affinity FC gamma receptor	FCGR1	1q
43.9	*Cd1*	cluster designation 1	CD1	1q22-23
43.9	*Fpsl-rs1*	farnesyl pyrophosphate synthetase-like 1	FPSL	1q24-q31
44.9	*H3f2*	histone 3, family 2	H3F2	1q12-21
45.0	*Hsd3b*	3-beta-hydroxy steroid dehydrogenase	HSDB3	1p11-13
46.4	*Cd2*	cluster designation 2	CD2	1p13
47.3	*Atp1a1*	Na, K ATPase alpha-1	ATP1A1	1p13
47.4	*Ampd-1*	AMP deaminase-1 (muscle form)	AMPD1	1p13
47.4	*Ngfb*	nerve growth factor beta	NGFB	1p13
47.4	*Nras*	Nras oncogene	NRAS	1p13
47.4	*Rap1a*	member of RAS oncogene family	RAP1A	1p12-p13
47.4	*Tshb*	thyrotropin stimulating hormone beta subunit	TSHB	1p13
48.4	*Csfm*	colony stimulating factor, macrophage	CSF1	1p13-21
48.4	*Gnai-3*	guanine nucleotide binding protein, alpha inhibiting activity-3	GNAI3	1p13
49.6	*Amy-1*	amylase, salivary	AMY1	1p21
49.6	*Amy-2*	amylase, pancreatic	AMY2	1p21
49.6	*Cf-3*	coagulation factor 3	F3	1p22-p21
54.6	*Pmp-1*	peroxisomal membrane protein (70k)	PMP1	1p21-22
54.7	*Fabpi*	fatty acid binding protein intestinal	FABP2	4q28-31
62.1	*Egf*	epidermal growth factor	EGF	4q25
68.1	*Adh-1*	alcohol dehydrogenase-1	ADH1	4q21-q23
68.1	*Adh-3*	alcohol dehydrogenase-3	ADH3	4q21-q23
X	*Acts*	skeletal alpha actin	ACTA1	1p21-qter
X	*Adh-5*	alcohol dehydrogenase-5	ADH5	4q21-q25
X	*Arnt*	aryl hydocarbon receptor nuclear translator	ARNT	1pter-q12
X	*Lef-1*	lymphoid enhancer-binding factor 1	LEF1	4q23-q25

Locus	AXL Lines	Ref.
	1111112222233	
	5678923467914589 78	
Car-2	LALL-ALALAAALALLAA	121
Ap2	LALLLALALAAALALLLA	61
Mpmv-20	LLAALALALLLLLALLLL	51
Evi-1	LLAALAAALALLLALLAL	112
Xmmv-47	LLLLLAAALLALAALLLL	164
Xmmv-65	ALALLAAALLLLALLLAA	164
Pmv-28	ALALLAAALLLLALLLAA	50
Cal1l	ALALLAAA-LLLALLLAA	131
D3Tu51	LLALLAAALLLLA-LLAA	153
Amy	ALALLAAALLLLAAALLA	121
D3Tu33	AAL-AAAALLLLA-ALLA	153
Pmv-26	AAAAALALLLAAALALLA	50

Locus	BXD Lines	Ref.
	11111111222222222333	
	12568912345689012345789012	
Car-2	DDDBDBDDDDBBDDBBBBBDBDDBB	121
Ap2	DDDBDBDDDDBBD-BBBBBBDBDDDD	61
D3Byu2	DDDBDBDDDDBBDDBBBBBBDBDDDB	167
D3Byu1	DDDBDBDDDDBBDDBBBBBBDBDDDB	167
D3Byu3	DDBBDBBDDDBBDDBBBBBBDBDDDB	167
Evi-1	DDBBDBBDBBBBBDBDBBBBDDDDDB	112
Il-2	DDBBDBDDDDBDDBDBBBBDDBDDB	37
D3Mit5	-DBBDDDDBDBBDDBDBBBBDDB---	37
D0Byu17	BBDBDDDDBBDBBBBDDBBDDBDDBB	167
Cnp-2	BBDBBDDDBBDBBBBDDBBDDDBDBB	10
D3J1	BBDBBBDBBBDBBB-DBBDBDBDBB	114
D3Byu5	BBDBBDDDBBDBBBBDDBBDBDBDBB	167
D3Mit22	-BDBBBDDBBDBBBBDDBBDBDB---	37
Xmmv-65	BBDBBBDBBBDBBBBDDBBDBDBDBB	164
D3Mit9	-BDBBBDBBBDBBBBDDBBDBDB---	37
Fgg	BBDBBBDBBBDBBBBDDBBDBDBDBB	13
D3Byu6	BBDBBBDBBBDBBBBDDBBDBDBDBB	167
Pmv-38	BBBBBBDBBBDBBBBDDBBDBDBDBB	50
D3Mit10	-BBBDBDBBBDBBBBDDBBDBDB---	37
Capl	BBBBBBDB-BDBBB--D-BDBDBDBB	39
Cal1l	BBBBBBDBBBDBBB--DBBDBDBDBB	131
D3Tu51	BBBBBB-BDBDBB-DDBB-BDBD--	153
D3Byu4	BBDBBBDBBBDBBBBDBBDBDBDBB	167
Amy	BDBBDBDDDBDBBBBDDBBDBDBDBB	121
Amy CB	BDBBDBDDDBDBBBBDDBBDBDBDBB	13
Fabpi	BDBBDBDDDBDBB-DDDBB-BDBBBD	143
D3J3	BDBBDBDDDBDBBBD--BBDBDBBBD	114
Adh-1ps	BDBBDBDDDBDBBBDDDBDDBDBBBD	20
cdm	BDBBDBDDDDBBDBDDDBBDBDBBBB	145
Pmv-39	BDBBDBDDDBDBDBDDDDBDBDBBBD	50
Oat-rs2	BDBBDBDDDBDBDBDDDDBDBDBBBD	125
Egf	BDBBDBDDDBBBDDDDBDBDBDBBBD	112
D3Mit15	-DBBDBDDDBBBDDDDBDBDBDB---	37
Adh-3	BDBBDBDD-BBBDDDDBDBDBDBBBD	112
Adh-3 RH	BDBBDBDD-BBBDD-DBDBDBDBBBD	72
Adh-1	BDBBDBDDDBBBDDDDBDBDBDBBBD	20
D3Nds3	BDBBDBDDDBBBDDDDBDBDBDBBBD	30
D3Nds2	-DBBDBDDDBBBDDDDBDBDBDB---	37
Emn	BDBBDBDD-BBBDD-DB-BDBDB-BD	97
D3Jknl	BDBBDBDDDBBBDDDDBDBDBDBBBB	99
Pmv-26	BDBBDDDDDBBBDDDDBBBDBDBBBD	50
P40-4	DDBBBDDDDBBBDDDBDBBDDDBBBD	40
D3Mit19	-DBDBBDDDBDBDBDBDBBBDDB---	37
D3Mit17	-BBDDDDBDBBBDDDDBBBDBDB---	37

Locus	AXB Lines	Ref.
	111111111222222	
	123456789012345789012345	
Car-2	BBAAABABABABAAAABBB-BBBA	73,112
Evi-1	BA-BABABABAA-A-AAAABABAA	112
D3Mit6	BA-ABB-A-BA-BAA-AAA--BB-	73
D3Mit7	BB-ABA-B-BA-AAA-AAA--BB-	73
Fgg	BBAABABBBBAB-AAABBBB-BBA	13
Thbs3	BB-ABA-B-BA-AAA-BBB--BB-	73
Rnu1b-1	ABAABABBBBAB-AABBBBB-BBA	13
Rnu1b-3	AAAABABBBBABAAABBBBB-BB-	13
D3Mit14	AA-AAA-A-BA-AAB-AAA--AB-	73
Amy-1,2	AAAAAABABBAB-ABBBA-A-AB-	13
Egf	AAAAAABABBAAAA-AA-AAAABB	112
Adh-3	AAAABABAABAAAABBAAABAAB-	13
Mpmv-9	BAABAABAABABAAABAAABAABA	51,100a
D3Mit18	AA-BAA-A-BA-AAB-A-A--AB-	73
D3Mit19	AA-AAA-A-AA-AAB-AAA--AB-	73

Locus	BXA Lines	Ref.
	1111111111222222	
	12345678901234567890123 45	
Car-2	AABB-ABAA-BAABBBAA---AABA	73,112
Evi-1	AA-B-B-AABBAAB---BB--AABB	112
D3Mit6	AB-B--BBB-BAAB-BB------BA	73
D3Mit7	AB-B--BBB-BAAB-BB------BA	73
Fgg	A-ABBB-BBABA-B---AB------	13
Tsp3	AB-A--ABB-BAAB-BB------BA	73
Rnu1b-1	A-AABB-BB-BA-B---AAA-B---	13
Rnu1b-3	ABAABBABB-BABB--BAAA-B-BB	13
D3Mit14	AA-A--ABB-AABB-BB------BB	73
Amy-1,2	A-ABBB-BBABA-B---AAB-----	13
Egf	AA-A-BBBBAAABA---AA--A--B	112
Adh-3	AAAAABABBAABBA---AAA-B--B	13
Mpmv-9	AB-A-AA-BAABBA-AAAAA-ABAB	51,100a
D3Mit18	AA-A--AAB-ABBA-AA------AB	73
D3Mit19	AB-B--AAB-ABB8-AA------AA	73

Locus	AXD Lines	Ref.
	1111111112222222	
	12345678901234567 8012345678	
Mpmv-20	DDA--AAADAAADA-A-AADDDADADA	51
Il-2	ADA--AAADAAADADA-AAADADAADA	60
Cnp-2	ADA--AADAAADAADA-AAADADAAAA	10
D3Nds1	ADA--AADAAADAADA-AAADADAAAA	30
Pmv-28	DDA--AADDAADAADADAAADADDDAA	50
Pmv-38	DDA--AADDAADAADADAAADDDDAA	50
Tshb	DDA--AADAAADADDA-AAAADDDDAA	2
Pmv-39	DDD--DDDAADDADDADADDADDDDAD	50
Oat-rs2	DDD--AADAADDADDADADDADD-DAD	125
D3Nds2	DDD--DADAADDADDA-ADDAADDDAD	30
Egf	DDDADDADADDDADDADDDDAADDDAD	112

Locus	BXH Lines	Ref.
	11111	
	2345678901249	
Car-2	HBH-BHBBBBBBB	121
Pgkps3	HBH-BHBBBBHBB	1
Evi-1	HBHBBHBBBHHBB	112
Rnu1b3	BBB-BHBBHHHBB	13
Cal1l	BBB-BHBBHHHBB	131
D3Tu51	BBB-BHBBHHHHB	153
Amy	BBB-BHBHHHBBB	121
Odc-rs3	HBH-BHBHBHBBB	126
Oat-rs2	BBB-BHBHHHBBB	125
Egf	BBBHBHBHHHBHB	112
Adh-3	BBB-BHBBHHBBB	124
Gbp-1	BBB-BHBBHHBBB	124
H3f2	BBB-BHBBHHHBB	132
Mpmv-9	BBB-BBBBBHBHB	51

Locus	CXB Lines	Ref.
	1234567	
Car-2	CCBBCCB	47
Car-2 RE	CCBBBCB	121
Xmmv-65	BCBBCBC	164
H-37	BCCBCBC	4
Amy	CCCBCCB	121
H-23	CCCCCCB	4
Adh-3	CCCBCCB	43
Ahr-1	CCCBCCB	43
Gbp-1	CCCBCCB	124
H-28	CCBBCCB	4
If-1	CCBBCCB	36
Mpmv-9	BCBBCCB	51

Locus	NXO Lines	Ref.
	11	
	125702	
Xmmv-65	NONOOO	164
Gbp-1	NNOONO	124

Locus	SXL Lines	Ref.
	11111	
	4724567	
Cal1l	SLLLSSL	131
Amy	LLLLSSL	121

Fig. 2. Strain distribution patterns for recombinant inbred strains. Data from Benjamin Taylor and Beverly Paigen (The Jackson Laboratory).

ships in both gene order and approximate physical length (79).

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