

Mouse Chromosome 11

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Introduction

A consensus linkage map of Chr 11 was constructed based on several multilocus genetic crosses, and the remainder of the loci were placed on this foundation (Buchberg et al. 1991). This report expands on the previous consensus map (Buchberg et al. 1991) and includes over 20 new loci that have been recently mapped on Chr 11. The cytogenetic characterization of mouse Chr 11 and the linkages of the human homologs of the genes mapping to mouse Chr 11 are summarized in this report. The resulting consensus linkage map is intended to be used as a guide for genetic, physical, and molecular analyses of Chr 11.

Locus list

In total, 167 loci are currently known to be assigned to mouse Chr 11 (Table 1). The new loci include the wobbler mutation (*wr*), insulin-dependent diabetes susceptibility-4 (*Idd-4*), and an imprinted gene (*Om*) associated with embryonic lethality. Additionally, several new molecular markers have been localized to Chr 11 including angiotensin-converting enzyme (*Ace*), a transplantation antigen (*AntP91a*), acid α glucosidase (*Gaa*), interferon regulatory factor-1 (*Irf-1*), UDP-N-acetylglucosamine: α -3-D-mannoside β -1,2-N-acetylglucosaminyltransferase I (*Mgat-1*), retinoic acid receptor α (*Rara*), sodium channel α subunit, skeletal

muscle (*Scn4a*), transcription factor 2 (*Tcf-2*), vacuolar (endomembrane) proton pump subunit-1 (*Vpp-1*). The largest class of new markers consisted of microsatellites, mononucleotide repeats, and anonymous DNA sequences (Table 1 and Table 7). Many of the new DNA markers were positioned by use of recombinant inbred (RI) lines.

The mouse gene symbols and official gene names are given with antiquated and alternate gene names. The human gene symbol and linkage are given where known. A reference is included for the mouse and human linkages. In the interest of space, an original reference either describing the gene or its localization to mouse Chr 11 was selected for inclusion in Table 1. Because many of the loci on Chr 11 have been mapped by several methods, interested readers are encouraged to refer to GBASE, OMIM, and the chapter on mouse-human comparative maps, which appears at the end of this issue, for additional references. Gene descriptions are provided for most of the phenotypic and biochemical markers in Green (1989).

Consensus map

Figure 1 shows the current consensus linkage map of mouse Chr 11. The map was originally constructed by first creating a skeleton map based on the multi-locus backcross analyses (Table 2 and Table 3; Buchberg et al. 1991). No significant differences in recombination distances were observed among the several backcrosses that have loci in common. These include Backcross A (*Mus spretus* \times C57BL/6J) \times C57BL/6J, Backcross B (CASA/Rk \times DF/B-*df/df*) \times DF/B-*df/df*, Backcross C (C3H/HeJ-*gld* \times *M. spretus*) \times C3H/HeJ

*Chair of Committee for Mouse Chromosome 11

Table 1. Locus list for mouse Chr 11.

New Locus	Gene name	A	M (cM)	T	Method	H. symbol	H. location	Reference
*	<i>Ace</i>		60	D	R	<i>ACE1</i>	17q23	57, 141
	<i>Acrb</i>		1 44	D	R,L	<i>CHRNB</i>	17p12-p11	91, 17
	<i>Adra-1</i>		1 25	D	S,L	<i>ADRA1</i>	5q32-q34	230
	<i>Ahd-4</i>		37	B	L	<i>ALDH3</i>	17	140, 191
	<i>Ahd-6</i>		30	B	L			186
	<i>Al</i>		56	V	L			54
*	<i>AntP91a</i>		53	D	R			57
	<i>Asgr-1</i>		41	D	R	<i>ASGR1</i>	17p13-p11	190, 189
	<i>Asgr-2</i>		41	D	R	<i>ASGR2</i>	17p	190, 100
	<i>Atp1b2</i>		44	D	S,R	<i>ATP1B2</i>	17p	171, 100
	<i>Bda</i>		62	V	L			68
	<i>Brp-8</i>		57	D	R			77
	<i>Bsk</i>		62	V	L			132
	<i>Cabm</i>		bt	D	S	<i>CBP68</i>	5q32-34	47
	<i>Chy</i>		30	B	L			133
	<i>Ck-5</i>		19	D	R			39
	<i>Cnp-1</i>		63	D	R	<i>CNP</i>	17q21	18
	<i>co</i>		bt	V	L			174
*	<i>Cod</i>		74	V	L			166
	<i>Cola-1</i>		60	D	L	<i>COL1A1</i>	17q21.3-q22	198, 215
	<i>Cryb1</i>		49	D	B	<i>CRYB1</i>	17q11.1-q12	28, 229
	<i>Csf8</i>		61	D	L	<i>CSF3</i>	17q11.2-q12	26, 217
	<i>Csfgm</i>		1 34	D	S,L,P	<i>CSF2</i>	5q23-q31	78, 175
	<i>Csfmu</i>		34		L			104, 102
*	<i>D11Bay1</i>		bt	D	S	<i>D17S28</i>	17p13.3	126
	<i>D11Bay2</i>		48	D	S,L	<i>D17S5</i>	17p13.3	126
	<i>D11Jkn1</i>		74	D	R			107
*	<i>D11Leh1</i>		44	D	L			42
*	<i>D11Leh2</i>		63	D	L			42
*	<i>D11Mit1</i>		4	D	R			57
*	<i>D11Mit2</i>		5	D	R			57
*	<i>D11Mit4</i>		41	D	R			57
*	<i>D11Mit5</i>		41	D	R			57
*	<i>D11Mit7</i>		45	D	R			57
*	<i>D11Mit8</i>		2 47	D	R			57
*	<i>D11Mit10</i>		59	D	R			57
*	<i>D11Mit11</i>		68	D	R			57
*	<i>D11Mit12</i>		72	D	R			57
*	<i>D11Nds1</i>		50	D	R			41
	<i>D11Nds2</i>		65	D	R,L			41
	<i>D11Pas1</i>		62	D	L			87
	<i>D11Pas2</i>		58	D	L			87
	<i>D11Sell</i>		28	D	L			169
	<i>D11Was70</i>		bt	D	I			58
	<i>D4S10h</i>		34	D	R	<i>D4S10</i>	4p16.3-p16.2	38, 88
	<i>df</i>		29	V	L			13
	<i>Dlb-1</i>		59	B	R			176
	<i>Edp-1</i>		42	D	R,L	<i>EDP</i>	17q22-q23	32
	<i>Empb3</i>		65	D	R,L	<i>EPB3</i>	17q21-q22	131, 197
	<i>Emv-14</i>		42	D	L,R			111
	<i>Emv-28</i>		58	D	L			212
	<i>Emv-30</i>		11	D	L			181
*	<i>Emv-33</i>		69	D	L			122
	<i>Erba</i>		61	D	S,L	<i>THRA1</i>	17q11.2-q21	53, 154
	<i>ErbB</i>		1 10	D	R,S,L,I	<i>EGFR</i>	7p14-p12.2	231, 201
	<i>ErbB-2</i>		61	D	L	<i>ERBB2</i>	17p11.2-q12	26, 177
	<i>Es-3</i>		74	B	R,L			179, 173
	<i>Evi-2</i>		49	D	R,L	<i>EV2A</i>	17q11.2	26
*	<i>Gaa</i>		bt	D	R	<i>GAA</i>	17q23	138, 137
	<i>Gabra-1</i>		28	D	L	<i>GABRA1</i>	5q34-q35	116, 30
	<i>Gas-3</i>		40	D	R,L			40
	<i>Gfap</i>		64	D	R	<i>GFAP</i>	17q21	18, 22
	<i>Gh</i>		66	D	S,R,L	<i>GHI</i>	17q22-24	108, 229
	<i>Glk</i>		78	B	S,R	<i>GALK</i>	17q	153, 229
	<i>Glns</i>		2 19	D	R	<i>GLNS</i>		131
	<i>Glut-4</i>		43	D	R	<i>GLUT4</i>	17p13	94, 99
	<i>H(js)</i>		bt	B	L			8
	<i>H(lt)</i>		bt	B	L			8
	<i>H(tn)</i>		bt	B	L			8
	<i>Hba</i>		19	B	R,L	<i>HBA</i>	16p13.3	178, 31
	<i>Hba-x</i>		19	B	L			224
	<i>Hox-2</i>		2 60	D	S,L,R	<i>HOX2</i>	17q21-q22	113, 129
	<i>Hox-2.1</i>		60	D	R,L,P			130
	<i>Hox-2.2</i>		60	D	R,P			130

Continued on next page

Table 1. Continued.

New Locus	Gene name	A	M (cM)	T	Method	H. symbol	H. location	Reference
	<i>Hox-2.3</i>		60	D	R,L,I,P			158
	<i>Hox-2.4</i>		60	D	P			59
	<i>Hox-2.5</i>		60	D	P			59
	<i>Hox-2.6</i>		60	D	R,P			130
	<i>Hox-2.7</i>		60	D	P			59
	<i>Hox-2.8</i>		60	D	P			79
	<i>Hsp86-PSI</i>		49	D	S,L			156
*	<i>Idd4</i>		47	B	L			214
	<i>Il-3</i>		33	D	I,R,S,L,P	<i>IL3</i>	5q23-q31	155, 102
	<i>Il-4</i>		32	D	R,S	<i>IL4</i>	5q31	45, 205
	<i>Il-5</i>		32	D	S,R,I	<i>IL5</i>	5q23-q31	127, 221, 204
*	<i>Irf-1</i>		33	D	L	<i>IRF1</i>	5q23-q31	32a, 106
	<i>js</i>		77	V	L			56
	<i>Krt-1</i>		62	D	S,L,R	<i>KRT15</i>	17q21-q23	150, 11
	<i>Krt-1.10</i>		62	D	R,L			163
	<i>Lif</i>		2	D	S,I,R,L	<i>LIF</i>	22q11.1-q13.1	202, 119, 206
	<i>lt</i>		bt	V	L			55
*	<i>Mgat-1</i>		34	D	L	<i>GLCT1</i>	5	121, 103
	<i>Mipla</i>		53	D	R	<i>SCYA3</i>	17q11-q21	226, 105
	<i>Miplb</i>		53	D	R	<i>SCYA4</i>	17q11-q21	226, 105
*	<i>Mmv-8</i>		bt	D	S			95
	<i>Mmv-11</i>		bt	D	S			95
	<i>Mmv-13</i>		bt	D	S			95
	<i>Mov-9</i>		48	D	I,L			109
	<i>Mpmv-2</i>		56	D	R,L			73
	<i>Mpmv-4</i>		52	D	R,L			72
	<i>Mpmv-8</i>		65	D	R,L			73
	<i>Mpmv-15</i>		71	D	R,L			73
	<i>Mpmv-18</i>		11	D	R,L			73
	<i>Mpo</i>	1	54	D	S,I,L	<i>MPO</i>	17q21.2-q23	27, 219
	<i>Mtv-3</i>		71	D	R,L			168
	<i>Myhs</i>		40	D	S,L,R	<i>MYH</i>	17p12-p13	43, 61
	<i>Myhs-e</i>		40	D	S,L,P			128
	<i>Myhs-f</i>		40	D	S,L,I,P			128
	<i>Myhs-p</i>		40	D	S,L,P			128
	<i>Myla</i>	1	66	D	R,L	<i>MYLA</i>	17q	183, 195
	<i>Nf-1</i>		49	D	L	<i>NF1</i>	17q11.2	28, 10, 196
	<i>Nfj</i>		4	D	I	<i>NFH</i>	22q12.1-q13.1	144, 143
	<i>Ngfr</i>		60	D	L	<i>NGFR</i>	17q21-q22	27, 101
	<i>nu</i>		48	V	L			69
	<i>oe</i>		49	V	L			135
*	<i>Om</i>		53	V	L			9
	<i>P4hb</i>		80	D	C,L	<i>P4HB</i>	17q25	28, 172
	<i>Pad-1</i>		28	D	L			27
	<i>Pdeg</i>		bt	D	S	<i>PDEG</i>	17	46, 120, 216
	<i>Pkca</i>		69	D	S,L	<i>PRKCA</i>	17q22-q24	27, 203
	<i>Pmv-2</i>		5	D	R,L			72
	<i>Pmv-22</i>		8	D	R,L			72
	<i>Pmv-46</i>		12	D	R			72
	<i>Pmv-56</i>		66	D	R			72
	<i>Re</i>		62	V	L			66
*	<i>Rara</i>		59	D	I,L	<i>RARA</i>	17q21.1	142
	<i>Rel</i>		14	D	S,L	<i>REL</i>	2p13-p12	25
	<i>Rnu1a-1</i>		62	D	S,R			151
	<i>Rnu3b</i>		bt	D	I			145
	<i>Rnu3b-1</i>		bt	D	I,P			145
	<i>Rnu3b-2</i>		bt	D	I,P			145
	<i>Rnu3b-3</i>		bt	D	I,P			145
	<i>Rnu3b-4</i>		bt	D	I,P			145
	<i>Rpo2-1</i>		41	D	S,L	<i>POLR2</i>	17p13.1	14, 33
*	<i>Scn4a</i>		65	D	L	<i>SCN4A</i>	17q23.1-q25	161, 76
	<i>sh-2</i>		37	V	L			60
	<i>Shbg</i>		40	D	S,L	<i>SHBG</i>	17p13-p12	112, 19
	<i>shm</i>		bt	V	L			80
	<i>Sigje</i>		53	D	S,R	<i>SCYA2</i>	17q11.2-q21.1	200, 148
	<i>Sparc</i>		34	D	R,L,I	<i>SPARC</i>	5q31-q33	139, 208
	<i>spd</i>		35	V	L			125
	<i>Syb-2</i>		bt	D	S	<i>SYB2</i>	17pter-p12	5
	<i>Tca-3</i>		52	D	R	<i>SCYA1</i>	17	226, 152
*	<i>Tcf-2</i>		47	D	S	<i>TCF2</i>	17cen-q21.3	113a, 1
	<i>Tcn-2</i>		0	B	L,R	<i>TCN2</i>	22q11.2-qter	74, 6
	<i>ti</i>		37	V	L			192
*	<i>Tk-1</i>		78	BD	S,C,I,L	<i>TK1</i>	17q23-q25	123, 161, 117
	<i>tn</i>		79	V	L			149

Continued on next page

Table 1. Continued.

New Locus	Gene name	A	M (cM)	T	Method	H. symbol	H. location	Reference
<i>Tr</i>	trembler		37	V	L			67
<i>Trp53</i>	transformation-related protein 53		44	D	S,L,I	<i>TP53</i>	17p13.1	232, 44, 147
<i>Ts</i>	tail-short		69	V	L			157
<i>Tse-1</i>	tissue specific extinction-1, of TAT		bt	B	S	<i>TSE1</i>	17q23-q24	117,
<i>Umph-2</i>	uridine monophosphatase-2		bt	B	S	<i>UMPH2</i>	17q23.2-q25.3	207, 225,
<i>vb</i>	vibrator		37	V	L			222, 124
* <i>Vpp-1</i>	vacuolar (endomembrane) proton pump subunit-1 (116kDa)		bt	D	S	<i>VPP1</i>	17q21-qter	170
<i>vt</i>	vestigial-tail		29	V	L			92
<i>wa-2</i>	waved-2		7	V	L			115
<i>Wnt-3</i>	wingless-related MMTV integration site-3 (Int-4)		64	D	L	<i>WNT3</i>	17q21-q22	27, 182
<i>Wnt-3A</i>	wingless-related MMTV integration site-3A(Int-4A)		bt	D				167
* <i>wr</i>	wobbler		12	V	L			114
<i>Xmv-4</i>	xenotropic murine leukemia virus-4		bt	D	S			95
<i>Xmv-5</i>	xenotropic murine leukemia virus-5		bt	D	S			95
<i>Xmv-20</i>	xenotropic murine leukemia virus-20		57	D	R,L			71
<i>Xmv-42</i>	xenotropic murine leukemia virus-42		56	D	R,L			71
<i>Xmv-63</i>	xenotropic murine leukemia virus-63		1	D	L			70
<i>Zfp-2</i>	zinc finger protein-2		48	D	S,L			164
<i>Zfp-3</i>	zinc finger protein-3 (Fnp-1)		44	D	R,L	<i>ZFP3</i>	17pter-p12	7

An asterisk in the column "New" represents new mapping information for those genes (29). Approved gene designation (in column labeled "Locus") is presented along with alternate or archaic locus designations (in column labeled "Gene name"). Recommended reference loci are indicated in the column labeled "A," with "1" indicating primary anchor and "2" indicating secondary anchor. The approximate map position of each locus relative to the centromere is given in cM in the column labeled "M," genes whose position is not known are listed at the bottom of Fig. 1 and are indicated here by "bt." The column labeled "T" indicates whether the locus is represented by a DNA

sequence or clone (D), a biochemical, protein, or immunological assay (B), or by a visible or other phenotype (V). The method by which the locus was mapped (shown in the column labeled "Method") are in situ hybridization (I), somatic cell genetics (S), radiation hybrid analysis (H), RI analysis (R), linkage analysis (L), cytogenetic analysis (C), deletion analysis (D), and physical mapping (P). Also presented are the human gene symbols and human gene location. Original references describing the human and mouse gene characterization and map locations are listed. More complete descriptions of some genes can be found in Green (81).

-*gld*, and Backcross F (NFS/N × *M.m. musculus*) × *M.m. musculus*.

Loci that were mapped in a single two-point linkage analysis where gene order is not known were not placed on the map. The information for these loci is listed in the bottom right of Fig. 1, including the gene name and distance from the known gene. Loci that were placed on Chr 11 only by analysis of recombinant inbred (RI) strains were included on the map, but in some cases gene order and distances are ambiguous. We encourage evaluation of the primary RI strain data included in Table 4.

The results of this compilation of data is shown in Fig. 1 as a linear map. An important note is that this map should be used as a guide for gene localization. Gene order is known with certainty only for those loci mapped in the same cross (Table 2).

Genes that have been localized by in situ hybridization (Table 5) are noted to the left of the chromosome with the regional localization in parentheses. The genes localized to mouse Chr 11 solely by in situ hybridization (Table 5) are listed at the bottom of Fig. 1. Genes whose human homologs have also been localized are underlined, and their human chromosomal locations are shown to the right of the chromosome. Genes that have been assigned to Chr 11 by somatic

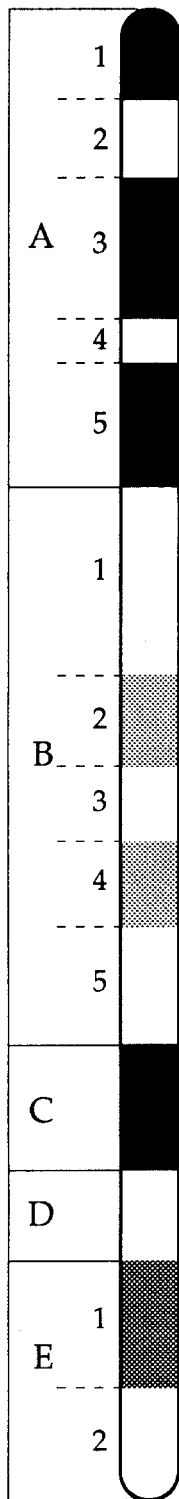
cell hybrid analysis or in situ hybridization are listed at the bottom of Fig. 1. Anchor loci are boxed.

Multilocus crosses

Table 2 and Table 3 contain the data derived from multilocus (three or more genes) crosses involving markers on mouse Chr 11. None of the multi-locus crosses present conflicting gene orders for loci mapped in common. A total of 88 loci have been mapped in the multi-locus crosses (Table 2), spanning 80 cM (the predicted length of Chr 11). Each column in this table (Table 2) represents a single cross involving three or more markers. The dots within the column denote the loci that were mapped in the cross. The shaded areas identify loci that were inseparable in the given cross. Some loci that were not separable in backcrosses were separated by recombination in the analysis of independent crosses or RI lines, permitting determination of gene order. Table 3 lists the experimentally determined map distance (± standard error) that was obtained in each of the multi-locus crosses. The utility of presenting the information in Table 2 is that it simplifies determining which genes have been mapped with respect to each other, hence allowing for identification of which loci are ordered unambiguously.

Fig. 1. Consensus linkage and cytogenetic map of mouse Chr 11. The chromosome on the right represents the consensus linkage map of mouse Chr 11. The genes mapping to mouse Chr 11 are presented on the right of the chromosome, and the distance from the centromere is indicated on the left of the chromosome. Genes that are listed along the left of the chromosome have also been localized on the cytogenetic map (on the left of the figure), with the cytogenetic location shown to the left of the chromosome (Table 5). Loci that are

underlined have also been localized to human chromosomes; their locations on human chromosomes are shown to the right of the chromosome (Table 1). Below the chromosome are those loci mapping to Chr 11 by somatic cell hybrid analysis or in situ hybridization methods; their cytogenetic and human locations are shown. Genes in the **lower right corner** have been mapped to Chr 11, but location could not be determined. Loci that are **boxed** represent anchor loci (Table 1, text).



	0	<i>Tcn-2</i>	22q11.2-qter
		<i>Xmv-63</i>	
A1-A5 (<i>Nfh</i>)	5	<i>Nfh</i> , <i>Lif</i> , <i>D11Mit1</i>	22q12.1-q13.1, 22q11-q12
A1-A2 (<i>Lif</i>)		<i>Pmv-2</i> , <i>D11Mü2</i>	
		<i>wa-2</i>	
A1-A4 (<i>ErbB</i>)	10	<i>Pmv-22</i>	7p14-p12
		<i>ErbB</i>	
A	15	<i>Mpmv-18</i> , <i>Emv-30</i>	2p13-p12
		<i>Pmv-46</i> , <i>wr</i>	
		<i>Rel</i>	
	20	<i>Hba</i> , <i>Hba-x</i> , <i>Glns</i> , <i>Ck-5</i>	16p13.3
	25	<i>Gabra-1</i> , <i>Adra-1</i>	5q34-q35, 5q32-q34
	30	<i>Pad-1</i> , <i>D11Sell</i>	
		<i>df</i> , <i>vi</i>	
		<i>Ahd-6</i> , <i>Chy</i>	
A5-B1 (<i>Il-5</i>)	35	<i>Il-4</i> , <i>Il-5</i>	5q31, 5q23-q31
A5-B1 (<i>Il-3</i>)		<i>Il-3</i> , <i>Csfm</i> , <i>Sparc</i> , <i>Lrf-1</i>	5q23-q31, 5q23-q31, 5q31-q33, 5q23-q31
B1 (<i>Sparc</i>)		<i>D4S10h</i> , <i>Mgat-1</i>	4p16.3-p16.2, 5
	40	<i>spd</i>	17
		<i>yb</i> , <i>sh-2</i>	17p13, 17p13-p12
B2-C (<i>Myhs</i>)		<i>Tr</i> , <i>Ahd-4</i>	
		<i>Myhs</i> , <i>Gas-3</i> , <i>Shbg</i>	
B1-C (<i>Rpo2-1</i>)	45	<i>Rpo2-1</i> , <i>Asgr</i> , <i>D11Mit4</i> , <i>D11Mü5</i>	17p13.1, 17p13-p11
		<i>Edp-1</i> , <i>Emv-14</i>	17q22-q23
B2-C (<i>Trp53</i>)		<i>Acrb</i> , <i>Atp1b-2</i> , <i>Trp53</i> , <i>Glut-4</i>	17p12-p11, 17p, 17p13.1, 17p13
		<i>Zfp-3</i> , <i>ti</i>	17pter-p12
	50	<i>H-3</i>	17cen-q21.3
		<i>Tcf-2</i> , <i>Idd-4</i>	17p13.3, 17p13-p12
B5 (<i>Mov-9</i>)		<i>D11Bay2</i> , <i>nu</i> , <i>Zfp-2</i> , <i>Mov-9</i>	17q11.1-q12, 17q11.2, 17q11.2
		<i>Crybl</i> , <i>Evi-2</i> , <i>NF-1</i> , <i>oe</i> , <i>Hsp86-ps1</i>	
		<i>D11Nds1</i> , <i>D11Mü7</i> , <i>D11Mü8</i>	
	55	<i>Tca-3</i> , <i>AntP91a</i>	17
		<i>Mpmv-4</i> , <i>Sigje</i> , <i>Mip1a</i> , <i>Mip1b</i> , <i>Om</i>	17q11.2-q21.1, 17q11-q21, 17q11-q21
C-E1 (<i>Mpo</i>)		<i>Mpo</i>	17q21.3-q23
	60	<i>Al</i>	17q21.1
D (<i>Rara</i>)		<i>Mpmv-2</i> , <i>Xmv-42</i> , <i>Brp-8</i>	17q21.31-q22, 17q21-q22, 17q21-q22
D (<i>Mov-13</i>)		<i>D11Pas2</i> , <i>Xmv-20</i> , <i>Emv-28</i>	17q21-q22, 17q11.2, 17q11.2-17q12
D (<i>Hox-2</i>)		<i>Dlb-1</i> , <i>Rara</i>	17q21-q23
		<i>Cata-1</i> , <i>Ngr</i> , <i>Hox-2</i>	17q21
		<i>ErbB-2</i> , <i>Erba</i> , <i>Csfj</i>	17q21, 17q21-q22, 17q23.1-q25, 17q23
		<i>Krt-1</i> , <i>Re</i> , <i>Bda</i> , <i>Bsk</i> , <i>Rnu1a-1</i>	17q21-q22
		<i>D11Pas1</i> , <i>Cnp-1</i>	17q, 17q22-q24
	65	<i>Glaf</i> , <i>Wnt-3</i> , <i>Scn4a</i> , <i>Ace</i> , <i>D11Mü10</i>	
		<i>Emph3</i> , <i>D11Nds2</i>	
		<i>Myla</i> , <i>Gh</i> , <i>Mpmv-8</i> , <i>Pmv-56</i>	
	70	<i>D11Mü11</i>	17q22-q24
		<i>Pkca</i> , <i>Ts</i>	
		<i>Emv-33</i>	
		<i>Miv-3</i> , <i>Mpmv-15</i>	
		<i>D11Mü12</i>	
	75	<i>Es-3</i> , <i>cod</i> , <i>D11Jkn1</i> , <i>Gaa</i>	17q23
		<i>js</i>	
B3-E2 (<i>Tk-1</i>)	80	<i>Glk</i> , <i>Tk-1</i>	17q21-q22, 17q23.2-q25.3
		<i>ln</i>	
		<i>P4hb</i>	17q25

Cabm 5q32-q34
co
D11Bay1 17q13.3
D11Was70 (cen)
Mmv-8
Mmv-11
Mmv-13
Pdeg 17q21
Rnu3b (C-D)
Syb-2 17pter-p12
Tse-1 17q23-q24
Umph-2 17q23.2-q25.2
Vpp-1 17q21-qter
Wnt-3A
Xmv-4
Xmv-5

shn - 1.5±.7 - *Re*
lt - 3.9±1.7 - *Re*
H(js) - 27±8 - *js*
H(lt) - 32±7 - *lt*
H(tn) - 30±8 - *tn*

Table 2. Continued.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ		
<i>Csf2</i>	●																																					
<i>Krt-1</i>									●	●	●	●																										
<i>Re</i>																		●	●	●	●	●	●															
<i>D11Pas1</i>					●																																	
<i>Gfap</i>	●			●	●																																	
<i>Wnt-3</i>	●					●																																
<i>Scn4a</i>											●																											
<i>Mpmv-8</i>																																						
<i>Myla</i>	●			●	●																																	
<i>Gh</i>		●						●	●																													
<i>Ts</i>																																						
<i>Pkca</i>	●			●																																		
<i>Mpmv-15</i>																																						
<i>Miv-3</i>																																						
<i>Es-3</i>					●				●		●						●	●	●		●	●	●	●	●	●												
<i>js</i>																																						
<i>Tk-1</i>											●																											
<i>Pdhb</i>	●																																					

The data presented in Tables 2 and 3 represent the basis of the linkage map (Fig. 1). Order for closely linked genes that have not yet been mapped with respect to each other was inferred on the basis of recombination distances. The presentation of a consensus linkage map is valuable and provides a basis for critical analysis of ambiguous areas. Unless genes are mapped relative to each other, inaccuracies may remain in the consensus map. These ambiguities can be minimized if more common anchor loci are utilized in the different crosses.

RI strain data

Table 4 is a compilation of the strain distribution patterns of genes mapped in RI strains. In the analysis of RI lines, the high frequency of double recombinants makes ordering of genes over long distances difficult. However, RI analysis can be extremely useful for determining gene order over short distances. Backcross analysis of Chr 11 markers revealed several clusters of genes in which gene order could not be determined, for example, *Sparc*, *Il-3*, *Il-4*, *Il-5*, and *Csfgm*. RI analysis showed recombination occurring between *Sparc* and *Il-5* and also between *Il-3* and (*Il-4*, *Il-5*), suggesting the gene order displayed on the consensus map.

Cytogenetics

Genes that have been cytogenetically localized to Chr 11 are listed in Table 5. The physical locations reported for these genes (Table 5) are consistent with their relative order in the consensus linkage map (Fig. 1).

The known chromosomal variants involving Chr 11 are listed in Table 6 along with the breakpoint regions. The chromosomal variants include inversions, trans-

locations, and Robertsonian fusions. As the breakpoints become better defined relative to molecular markers, it may be possible to utilize some of these chromosomal variants to gain access to different regions of the chromosome.

Comparative maps

Mouse Chr 11 contains at least seven homology segments, including genes whose human homologs map to human Chrs 2, 4, 5, 7, 16, 17, and 22 (Nadeau et al. 1991). Table 1 lists the locus designations and chromosomal locations of the human homologs of the corresponding mouse loci. This information is also shown in Fig. 1, facilitating the identification of regions of synteny conservation. The two most extensive regions of conserved synteny include the medial region of mouse Chr 11, which exhibits synteny conservation with human Chr 5q23-q34, and the distal half of mouse Chr 11, which displays synteny conservation with human Chr 17. To date, all of the genes that have been unambiguously localized to either the p or q arms of human Chr 17, when mapped in the mouse, have been assigned to mouse Chr 11 (Munke and Francke 1987; Buchberg et al. 1989, 1990; Nadeau et al. 1989, 1991; and Buckwalter et al. 1991). In contrast, genes from human Chr 5q22-q35 have also been localized to mouse Chr 18 (Nadeau et al. 1991). The localization of several new genes and genes that had previously been simply assigned to Chr 11 has augmented these evolutionary relationships and strengthened the suggestion of a region of synteny conservation including the most proximal region of mouse Chr 11 and human Chr 22q11-qter. Synteny conservation between mouse and humans was used successfully in the previous chromosome report to predict the localization of genes such as *Lif*, *Nfh*, *Glut-4*, *Syb-2*, and *Tk-1*, which were assigned to mouse Chr 11 by somatic cell hybrid analysis or in situ hybridization (Buchberg et al. 1991).

Table 3. This table presents the gene order (proximal to distal) and recombination distance (cM \pm standard error) for the multilocus crosses presented in Table 2.

Column	Gene order and recombination distance (cM)	Reference
A	<i>ErbB</i> -3.8 \pm 1.5- <i>Rel</i> -15.0 \pm 2.9- <i>Pad</i> -1-6.7 \pm 2.2-(<i>Il</i> -3, <i>Csfgm</i> , <i>Sparc</i>)-5.6 \pm 2.4- <i>Myhs</i> -4.8 \pm 1.8-(<i>Acrb</i> , <i>Atpb</i> -2, <i>Trp53</i> , <i>Zfp</i> -3, <i>Glut</i> -4, <i>D11Lehl</i>)-2.1 \pm 1.2-(<i>D11Bay</i> 2, <i>Mov</i> -9)-0.7 \pm 0.7-(<i>Cryb1</i> , <i>Evi</i> -2, <i>Nf</i> -1)-5.6 \pm 2.7- <i>Mpo</i> -6.3 \pm 2.0-(<i>Cola</i> -1, <i>Ngfr</i> , <i>Hox</i> -2)-0.7 \pm 0.7-(<i>ErbB</i> -2, <i>Erba</i> , <i>CsfG</i>)-2.6 \pm 1.5-(<i>Gfap</i> , <i>Wnt</i> -3, <i>Myla</i>)-3.2 \pm 1.4- <i>Pkca</i> -11.1 \pm 2.5- <i>P4hb</i> .	27, 28, 7, 42, 94
B	<i>ErbB</i> -14.5 \pm 3.3-(<i>Adral</i> , <i>Gabra</i> -1)-3.4 \pm 1.7-(<i>Pad</i> -1, <i>D11Sell</i>)-0.9 \pm 0.9- <i>df</i> -2.6 \pm 1.5-(<i>Il</i> -3, <i>Csfgm</i> , <i>Irf</i> -1, <i>Il</i> -5, <i>Il</i> -4, <i>Sparc</i>)-2.6 \pm 1.5- <i>Myhs</i> -1.7 \pm 1.2-(<i>Rpo</i> -2, <i>Asgr</i>)-0.9 \pm 0.9- <i>Edp</i> -1-5.8 \pm 2.5- <i>Tcf</i> -2-16.3 \pm 4.0- <i>Erba</i> -4.3 \pm 1.9- <i>Gh</i> .	32, 113a, Camper and Buckwalter, unpublished
C	<i>ErbB</i> -14.9 \pm 3.3- <i>Adral</i> -6.1 \pm 2.3- <i>D11Sell</i> -2.6 \pm 1.5- <i>Il</i> -3-7.0 \pm 2.4- <i>Gas</i> -3-4.4 \pm 1.9- <i>Trp53</i> -4.4 \pm 1.8-(<i>ErbB</i> -2, <i>Erba</i>)-7.9 \pm 2.5- <i>Pkca</i> .	169,40
D	<i>Glns</i> -24.4 \pm 2.5- <i>Acrb</i> -7.3 \pm 1.5- <i>D11Nds</i> 1-8.0 \pm 1.5- <i>Mpo</i> -16.4 \pm 2.2- <i>Gfap</i> -2.4 \pm 0.9- <i>Myla</i> .	214
E	<i>Tcf</i> -2-21.4 \pm 10.9- <i>Sparc</i> -3.4 \pm 2.4- <i>Csfgm</i> -28.8 \pm 5.9- <i>D11Pas</i> 2-2.3 \pm 2.3- <i>Hox</i> -2-1.9 \pm 1.9- <i>D11Pas</i> 1-1.4 \pm 1.4- <i>Gfap</i> -7.3 \pm 3.1- <i>Myla</i> -5.8 \pm 2.8- <i>Es</i> -3	87
F	<i>Rel</i> -9.8 \pm 3.3- <i>Gabra</i> -1-3.3 \pm 2.3-(<i>Il</i> -3, <i>Mgat</i> -1)-8.9 \pm 3.8- <i>Shbg</i> -11.6 \pm 3.9- <i>Hsp86-ps</i> 1-17.4 \pm 4.6- <i>Wnt</i> -3.	112, 116, 156,121
G	<i>ErbB</i> -9.5 \pm 3.7- <i>Hba</i> -20.6 \pm 5.1- <i>Evi</i> -2-25.4 \pm 5.5- <i>Gh</i> .	62, 63
H	<i>Sparc</i> -16.7 \pm 4.2- <i>Evi</i> -2-9.0 \pm 3.2- <i>Erba</i> -2.6 \pm 1.8- <i>Gh</i> -19.2 \pm 4.5- <i>Es</i> -3.	63
I	<i>Tr</i> -21.3 \pm 4.7- <i>Hox</i> -2-1.3 \pm 1.3-(<i>Krt</i> -1, <i>Re</i>).	163
J	<i>Hba</i> -20.3 \pm 4.5- <i>Tr</i> -27.7 \pm 3.6-(<i>Krt</i> -1, <i>Re</i>)-13.9 \pm 3.9- <i>Es</i> -3.	163
K	<i>Tr</i> -21.2 \pm 5.0- <i>Hox</i> -2-1.5 \pm 1.5-(<i>Krt</i> -1, <i>Re</i>)-2.6 \pm 1.8- <i>Scn4a</i> -12.8 \pm 3.8- <i>Tk</i> -1.	163, 161
L	<i>Tr</i> -20.6 \pm 4.7- <i>Hox</i> -2-1.4 \pm 1.4- <i>Re</i> .	89
M	<i>spd</i> -2.5 \pm 1.2- <i>Tr</i> -25.3 \pm 3.4- <i>Re</i> .	125
N	(<i>Il</i> -3, <i>Csfgm</i> , <i>Sparc</i>).	12
O	<i>Hba</i> -32.2 \pm 8.4- <i>Myhs</i> -26.2 \pm 6.8- <i>Myla</i> -8.1 \pm 4.5- <i>Es</i> -3.	223, 183
P	<i>Tcn</i> -2-6.9 \pm 2.2- <i>wa</i> -2-12.3 \pm 2.9- <i>Hba</i> .	75
Q	<i>Tr</i> -4.1 \pm 2.8- <i>Akv</i> -4-12.2 \pm 4.7- <i>Evi</i> -2-24.5 \pm 6.1- <i>Re</i> -10.2 \pm 4.3- <i>Es</i> -3.	213, 26
R	<i>oe</i> -13.3 \pm 6.2- <i>Re</i> -20.0 \pm 7.3- <i>Es</i> -3.	20
S	<i>Tr</i> -7.4 \pm 3.6- <i>nu</i> -11.1 \pm 4.3- <i>Re</i> .	69
T	<i>Re</i> -13.3 \pm 6.2- <i>Es</i> -3-3.3 \pm 3.3- <i>js</i> .	185
U	<i>wa</i> -2-22.2 \pm 1.7- <i>vt</i> -8.9 \pm 1.2- <i>ti</i> -20.2 \pm 1.5- <i>Re</i> .	192
V	<i>Re</i> -8.6 \pm 3.7- <i>Ts</i> -5.2 \pm 2.2- <i>Es</i> -3.	209
W	<i>Hba</i> -40.5 \pm 4.56 - <i>Dlb</i> -1-28.4 \pm 4.2- <i>Es</i> -3.	218
X	<i>Dlb</i> -1-2.3 \pm 1.3- <i>Re</i> -20.3 \pm 3.5- <i>Es</i> -3.	218
Y	<i>Hba</i> -20.4 \pm 2.9-(<i>Ahd</i> -4, <i>Tr</i>)-26.3 \pm 3.2- <i>Re</i> .	96
Z	<i>Hba</i> -13.8 \pm 3.9- <i>Ahd</i> -6-7.5 \pm 2.9- <i>Ahd</i> -4.	97
AA	<i>Hba</i> -29.6 \pm 4.6- <i>Hox</i> -2-23.5 \pm 4.3- <i>Es</i> -3.	220
AB	<i>Evi</i> -2-27.0 \pm 7.3- <i>Gh</i> -5.4 \pm 3.7- <i>Es</i> -3.	62
AC	<i>Tr</i> -4.7 \pm 3.2- <i>Trp53</i> -1.6 \pm 1.6- <i>Zfp</i> -3-8.1 \pm 3.5- <i>Zfp</i> -2-30.6 \pm 5.9- <i>Rara</i> -32.2 \pm 2.2- (<i>Hox</i> -2, <i>Krt</i> -1, <i>Re</i>).	164
AD	(<i>Mpmv</i> -18, <i>Emv</i> -30)-25.0 \pm 7.2- <i>Il</i> -3.	181
AE	<i>Pmv</i> -2-3.3 \pm 3.3- <i>Pmv</i> -22-3.7 \pm 3.6- <i>Mpmv</i> -18-51.8 \pm 9.6-(<i>Mpmv</i> -2, <i>Xmv</i> -42)-9.4 \pm 5.2- <i>Mpmv</i> -8.	73
AF	<i>Mpmv</i> -18-32.1 \pm 6.2- <i>Mpmv</i> -4-3.5 \pm 2.4- <i>Xmv</i> -42-14.0 \pm 4.6- <i>Mpmv</i> -8-15.8 \pm 4.8-(<i>Mpmv</i> -15, <i>Mtv</i> -3).	73
AG	<i>Xmv</i> -63-8.2 \pm 3.5- <i>Pmv</i> -2-4.5 \pm 3.2- <i>Pmv</i> -22-53.5 \pm 7.6-(<i>Mpmv</i> -15, <i>Mtv</i> -3).	73
AH	<i>Nfj</i> -5.6 \pm 3.1- <i>ErbB</i> -1.9 \pm 1.9- <i>wr</i> -1.9 \pm 1.9- <i>Rel</i> -4.4 \pm 2.1- <i>Hba</i> -17.8 \pm 4.0- <i>Il</i> -3.	114
AI	<i>Emv</i> -14- 23 \pm 9 - <i>Emv</i> -28 - 23 \pm 9 - <i>Es</i> -3.	212
AJ	(<i>Il</i> -5, <i>Csfgm</i>)-4.7 \pm 3.2- <i>Sparc</i> -30.2 \pm 7.0-(<i>Om</i> , <i>Sigje</i>)-20.9 \pm 6.2- <i>Es</i> -3.	9

Table 4. Continued. SDPs of Chr 11 loci typed in BXH RI strains. B and H represent alleles derived from C57BL/6J and C3H/HeJ, respectively.

Locus	2	3	4	5	6	7	8	9	10	11	12	14	15	18	19	20	Reference
<i>Pmv-22</i>	H	H	H	-	H	B	B	B	B	H	B	H	-	-	H	-	72
<i>Pmv-2</i>	H	H	H	-	H	B	B	B	B	H	B	H	-	-	H	-	72
<i>Hba</i>	x	x								x							38
<i>Sparc</i>	B	H	B	-	H	H	H	B	B	B	B	B	-	-	-	-	139
<i>D4S10h</i>	B	H	B	-	H	H	H	B	B	B	B	B	-	-	H	-	38
<i>Mpmv-2</i>	H	H	B	-	H	H	H	B	B	B	H	H	-	-	B	-	73
<i>Mpmv-4</i>	H	H	H	-	H	H	H	B	B	B	H	H	-	-	B	-	73
<i>Xmv-42</i>	H	H	H	-	H	H	H	B	B	B	B	H	-	-	B	-	71
<i>Krt-1</i>	B	H	H	-	H	H	H	B	B	H	B	H	-	-	B	-	163
<i>Gfap</i>	B	H	H	-	H	H	H	B	B	H	B	H	-	-	B	-	18
<i>Myla</i>	-	-	H	-	B	H	H	B	B	H	B	H	-	-	B	-	183
<i>Mpmv-8</i>	B	H	H	-	B	H	H	B	B	H	B	H	-	-	B	-	73
<i>Es-3</i>	B	B	H	H	B	H	H	B	B	H	B	B	B	B	B	B	153
<i>Tk-1</i>	B	B	H	-	B	H	H	B	B	H	B	B	-	-	B	-	138
<i>Gaa</i>	x	H	B	H	-	B	H	H	B	B	H	B	H	-	-	B	-
<i>Glk</i>	x	B	B	H	H	B	H	H	B	B	H	B	H	-	B	B	-

Table 4. Continued. SDPs of Chr 11 loci typed in SWXL RI strains. S and L represent alleles derived from SWR/J and C57L/J, respectively.

Locus	1	2	3	4	5	6	7	Reference
<i>Pmv-22</i>	C	C	B	B	B	B	C	72
<i>Pmv-2</i>	C	C	B	B	B	B	C	72
<i>Erbb</i>	C	B	B	C	B	B	C	199
<i>Mpmv-18</i>	C	B	B	C	B	B	C	73
<i>Hba</i>	C	B	B	C	B	B	C	187
<i>Mpmv-2</i>	C	B	C	C	B	C	C	73
<i>Xmv-42</i>	B	B	B	B	B	C	C	71
<i>Mpmv-8</i>	B	B	C	C	B	C	B	73

Table 4. Continued. SDPs of Chr 11 loci typed in AKXD RI strains. A and D represent alleles derived from AKR/J and DBA/2J, respectively.

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	20	21	22	23	24	25	26	27	28	Reference	
<i>Pmv-2</i>	D	A	A	-	-	A	A	D	A	D	D	D	D	D	A	A	A	A	D	D	D	D	A	A	D	A	D	72	
<i>Mpmv-18</i>	x	A	A	D	-	-	A	A	A	A	D	A	A	D	D	D	A	-	A	D	D	D	D	A	A	A	A	D	
<i>Hba</i>	A	D	D	A	D	A	A	A	A	D	A	A	D	D	A	D	A	A	D	D	D	A	A	D	A	A	A	D	38
<i>Sparc</i>	D	D	D	-	-	A	A	A	A	-	-	A	D	A	D	-	-	A	D	D	-	A	-	D	-	-	-	139	
<i>D4S10h</i>	D	D	D	-	-	-	A	A	A	D	D	A	D	A	D	D	D	A	D	D	D	A	D	-	A	A	D	38	
<i>Emv-14</i>	A	A	D	-	-	A	A	D	A	D	D	A	A	A	D	D	D	A	D	D	D	A	A	D	A	A	D	110	
<i>Atpb-2</i>	-	A	D	-	-	A	A	D	-	D	D	A	D	A	D	A	-	A	D	D	D	A	D	D	D	A	D	136	
<i>Acrb</i>	D	A	D	-	-	A	A	D	A	D	D	A	D	A	D	A	-	A	D	D	D	A	D	D	D	A	D	90	
<i>Glut4</i>	D	A	D	-	-	A	A	D	A	D	D	A	D	A	D	A	-	A	D	D	D	A	D	D	D	A	D	90	
<i>Evi-2</i>	D	A	D	A	D	A	A	D	A	D	D	A	D	A	D	A	D	A	D	D	D	A	D	D	D	D	D	26	
<i>Xmv-20</i>	-	-	-	-	-	A	A	-	-	D	-	-	D	A	D	A	-	A	A	D	D	-	D	A	D	-	-	71	
<i>Cola-1</i>	D	A	D	-	-	A	A	D	-	-	D	D	D	A	D	A	-	D	A	D	D	A	D	A	D	D	D	4	
<i>Hox-2</i>	D	A	D	-	-	A	A	D	A	D	D	D	D	A	D	A	D	D	A	D	D	A	D	A	D	D	D	89	
<i>Cnp-1</i>	D	A	D	-	-	A	A	D	A	D	D	D	D	A	D	A	D	A	D	D	D	A	D	D	D	D	D	18	
<i>Gfap</i>	D	A	D	-	-	A	D	D	A	D	D	D	D	A	D	A	A	A	D	D	D	A	A	D	D	D	D	18	
<i>Gaa</i>	x	A	D	A	-	-	D	D	D	A	-	D	D	D	A	A	A	-	A	A	D	D	A	A	-	D	D	138	
<i>Mpmv-15</i>	A	D	A	-	-	A	D	D	A	D	D	D	D	A	A	A	-	A	A	D	D	A	A	D	D	D	D	73	

Table 4. Continued. SDPs of Chr 11 loci typed in SWXL RI strains. S and L represent alleles derived from SWR/J and C57L/J, respectively.

Locus	4	7	12	14	15	16	17	Reference
<i>Sparc</i>	S	L	L	L	-	S	S	139
<i>Ahd-4</i>	S	-	L	L	S	S	-	96
<i>Dlb-1</i>	S	L	S	S	S	S	S	218

Table 4. Continued. SDPs of Chr 11 loci typed in OXA RI strains. O and A represent alleles derived from O20/A and AKR/FuRdA, respectively.

Locus	15	16	17	18	19	20	21	22	23	24	25	26	27	28	Reference
<i>Il-5</i>	O	O	A	A	A	A	O	O	A	A	A	A	A	O	226
<i>Il-4</i>	O	O	A	A	A	A	O	O	A	O	A	A	A	O	210
<i>Il-3</i>	O	O	A	A	A	A	O	O	A	O	A	A	A	O	210
<i>Tca-3</i>	x	x	x											x	226
	A	A	O	A	A	A	O	O	A	O	A	A	A	A	

Table 4. Continued. SDPs of Chr 11 loci typed in AXB RI strains. A and B represent alleles derived from A/J and C57BL/6J, respectively.

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	17	18	19	20	21	22	23	24	25	Reference	
<i>Pmv-2</i>	A	B	A	A	A	A	A	A	A	A	A	A	A	A	-	-	A	-	A	A	B	B	A	A	72	
<i>Pmv-22</i>	A	B	A	A	A	A	A	A	A	A	A	-	-	-	-	-	A	-	A	A	B	B	-	A	72	
<i>ErbB</i>	A	B	A	A	-	A	A	A	-	A	A	A	-	A	B	-	A	-	-	A	-	-	-	-	Blatt (unpublished)	
<i>Pmv-46</i>	A	B	A	A	A	A	A	A	A	A	B	A	A	B	-	-	A	-	A	A	B	A	-	B	72	
<i>Hba</i>	x	B	B	A	A	A	A	A	A	B	A	A	B	B	B	B	A	A	-	-	-	A	-	-	130	
<i>Il-3</i>	B	B	A	B	A	A	B	A	A	B	A	-	B	B	B	-	A	A	A	-	-	A	A	-	130	
<i>Mpmv-2</i>	B	B	A	B	B	B	A	A	A	B	B	B	B	B	-	-	A	-	A	B	B	A	A	A	73	
<i>Myhs</i>	B	B	A	B	A	A	-	A	-	B	B	A	B	B	A	A	B	A	A	A	B	A	A	-	130	
<i>Xmv-42</i>	B	B	A	B	A	A	A	A	B	B	A	A	A	B	-	-	A	-	A	B	A	A	A	B	71	
<i>Mpmv-4</i>	B	B	A	A	A	A	A	A	B	B	A	A	A	B	-	-	A	-	A	B	A	A	A	B	73	
<i>Hox-2.1</i>	B	B	A	B	A	A	A	A	B	B	A	B	B	B	B	B	B	B	B	B	B	A	A	A	-	130
<i>Hox-2.6</i>	B	B	A	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	B	A	A	A	-	130
<i>Mpmv-8</i>	B	B	B	B	A	A	A	B	B	B	A	B	A	B	-	-	B	-	B	B	B	A	A	B	73	
<i>Pmv-56</i>	B	B	B	B	A	A	A	B	B	B	A	B	A	B	-	-	B	-	B	B	B	A	A	B	72	
<i>Es-3</i>	B	B	A	A	A	B	A	B	A	B	A	A	A	B	B	B	B	B	B	B	B	-	A	A	-	130

Table 4. Continued. SDPs of Chr 11 loci typed in BXA RI strains. B and A represent alleles derived from C57BL/6J and A/J, respectively.

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	16	17	18	19	20	21	22	23	24	25	Reference	
<i>Pmv-2</i>	A	B	-	A	-	B	A	B	A	A	B	B	B	A	-	B	A	A	A	-	A	A	A	A	72	
<i>Pmv-22</i>	A	B	-	A	-	B	A	B	A	A	B	B	B	A	-	A	A	B	A	-	A	A	A	A	72	
<i>ErbB</i>	-	-	B	A	A	-	A	A	-	-	B	-	-	-	-	-	-	-	-	-	-	-	-	-	Blatt (unpublished)	
<i>Pmv-46</i>	A	B	-	A	-	A	A	A	A	A	B	A	A	A	-	A	A	A	A	A	A	A	A	A	72	
<i>Hba</i>	A	-	-	A	-	-	-	A	-	-	B	A	A	A	A	A	A	A	A	x	B	-	-	A	-	130
<i>Il-3</i>	A	B	B	B	-	A	A	-	B	-	B	-	A	A	-	-	A	B	-	-	A	-	A	-	130	
<i>Mpmv-2</i>	A	B	-	B	-	B	A	B	B	A	A	B	A	-	B	A	-	B	-	A	A	A	B		73	
<i>Myhs</i>	A	B	-	B	-	B	A	B	B	A	B	B	B	A	A	B	A	B	-	-	A	-	A	-	130	
<i>Xmv-42</i>	x	B	B	-	B	-	B	A	A	B	A	A	B	B	-	A	A	B	A	-	A	B	A	B	71	
<i>Mpmv-4</i>	B	B	-	B	-	B	A	A	B	A	A	B	B	B	-	A	A	-	A	-	A	B	A	A	73	
<i>Hox-2.1</i>	B	B	A	B	-	B	A	A	B	A	-	B	B	B	A	-	A	A	A	-	-	-	x	B	-	130
<i>Hox-2.6</i>	B	B	-	B	-	B	A	A	B	A	A	B	B	B	A	A	A	A	A	-	A	-	B	-	130	
<i>Hox-2.3</i>	B	B	B	B	-	B	A	A	B	-	A	B	B	B	A	A	A	A	A	-	A	-	B	-	130	
<i>Mpmv-8</i>	B	B	-	B	-	A	A	A	B	A	A	B	B	B	-	A	A	A	A	-	A	A	B	A	73	
<i>Pmv-56</i>	B	B	-	B	-	A	A	A	B	A	A	B	B	B	-	B	A	A	A	-	A	A	B	A	72	
<i>Es-3</i>	B	A	B	B	-	B	A	A	B	-	A	-	B	A	A	A	A	A	A	-	B	-	B	-	130	

Table 4. Continued. SDPs of Chr 11 loci typed in CXS RI strains. C and S represent alleles derived from BALB/cHeA and STS/A, respectively.

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	Reference
<i>Tcn-2</i>	C	S	S	C	S	C	S	C	C	S	C	C	C	S	75
<i>Hba</i>	C	S	C	C	C	S	S	C	C	S	C	C	C	S	75
<i>Il-5</i>	C	C	C	C	C	S	S	C	S	S	C	C	C	S	226
<i>Il-4</i>	C	C	C	C	C	S	S	C	S	S	C	C	C	S	45
<i>Il-3</i>	C	C	C	C	C	S	S	C	S	S	C	S	C	S	45
<i>Dlb-1</i>	C	C	S	S	S	S	S	C	S	S	S	S	C	S	93
<i>Hox-2</i>	C	C	S	S	S	S	S	C	S	S	S	S	C	S	226
<i>Tca-3</i>	C	C	S	S	S	S	S	C	S	C	S	S	C	S	226
<i>Rnu1a-1</i>	C	C	S	S	S	S	S	C	S	C	S	S	C	S	151
<i>Sigje</i>	C	C	S	C	S	S	S	C	S	C	S	S	S	S	226
<i>Mtv-3</i>	C	C	S	C	S	C	S	C	S	S	S	S	C	S	93
<i>Es-3</i>	C	S	S	C	S	C	S	C	S	S	S	S	C	S	75

Table 4. Continued. SDPs of Chr 11 loci typed in NXSM RI strains. N and S represent alleles derived from NZB/B1NRe and SM/J, respectively.

Locus	A	C	D	E	F	I	L	N	P	Q	T1	T2	U	V	W	X	Z	Reference
<i>Tcn-2</i>	S	S	N	S	S	S	N	N	S	N	S	S	S	N	S	S	N	62
<i>ErbB</i>	S	S	S	S	S	S	N	N	S	S	S	S	S	S	S	S	N	62
<i>Hba</i>	N	N	N	N	S	S	N	N	S	S	S	S	S	N	S	S	N	62
<i>Evi-2</i>	S	N	N	S	N	S	N	N	N	S	N	N	S	S	S	N	N	62
<i>Gh</i>	S	N	N	S	N	S	N	N	N	N	S	S	S	S	N	S	N	62
<i>Mtv-3</i>	S	N	N	S	N	S	N	N	N	S	S	S	S	N	S	N	N	62

Table 5. Cytogenetic localization of genes on mouse Chr 11.

Gene name	Band location	Reference
<i>Cola-1 (Mov-13)</i>	D	160
<i>D11Was70</i>	Chr 11	58
<i>ErbB</i>	A1-A4	159
<i>Hox-2</i>	D	158
<i>Il-3</i>	A5-B1	221
<i>Il-5</i>	A5-B1	221
<i>Lif</i>	A1-A2	119
<i>Mov-9</i>	B5	160
<i>Mpo</i>	C-E	184
<i>Myhs-f</i>	B2-C	159
<i>Nfya</i>	A1-A5	144
<i>Rara</i>	D	142
<i>Rnu3b</i>	C-D	146
<i>Rnu3b-1</i>	C-D	146
<i>Rnu3b-2</i>	C-D	146
<i>Rnu3b-3</i>	C-D	146
<i>Rnu3b-4</i>	C-D	146
<i>Rpo2-1</i>	B1-C	180
<i>Sparc</i>	B1	139
<i>Tk-1</i>	B3-E2	98
<i>Trp53</i>	B2-C	159

Table 6. List of variant chromosomes involving mouse Chr 11. NA means not applicable.

Variant name	Breakpoint	Reference
Robertsonian fusions		
Rb(1.11)2Mpl	NA	188
Rb(4.11)12Rma	NA	35
Rb(9.11)14Tu	NA	3, 23,24
Rb(10.11)8Bnr	NA	86, 35
Rb(10.11)5Rma	NA	34, 35, 82
Rb(11.13)4Bnr	NA	233, 84, 85, 83
Rb(11.13)6Lub	NA	82, 227, 228
Rb(11.13)6Tu	NA	3
Rb(11.14)1Dn	NA	50
Rb(11.16)2H	NA	134
Translocations		
T(X;11)38H	XA1, 11E1	194, 65, 193, 15
T(2;11)4Dn	2D,11B5	49
T(2;11)30H	2H1,11B1	36,15, 37
T(3;11)16Ad	3F1,11B5	49
T(5;11)17Ad	5B,11B1	49
T(9;11)9Ad	9B1,11D	2
T(11;16)53Dn	11D,16A	49
T(11;17)39Dn	11D,17A2	49
T(11;19)42H	11D, 19B	194, 64, 16, 118
Chromosomal inversions		
In(11)2Dn	11A4, 11B1	48
In(11)20Rk	11A2, 11D	52, 51

Table 7. Mouse Chr 11 loci defined by microsatellite sequences. Locus name is listed in the first column, DNA sequence of the primer pairs is given in the second and third columns in 5'-3' orientation. Columns 4, 5, and 6 provide information about the polymorphism detected for the microsatellites in intraspecific (I) backcrosses, intersubspecific (C) backcrosses involving *Mus castaneus*, and interspecific backcrosses (S) with *M. spretus*, respectively. (Y) indicates that a polymorphism was detected in only one out of six strains tested, N indicates no polymorphism was detected, and - indicates the primer pair was not tested.

Locus	Primer 1	Primer 2	Polymorphic			Reference
			I	C	S	
<i>Ace</i>	ATAACACCAACATTACCATAGAGGG	ATACTAAGTTCAGACTTTTCACCAATTTT	-	Y	-	57
<i>Acrb</i>	AGGCTACACAAAGAACTTTGACTTGA	GCTCAGGAATCCCTGGAACCTCA	Y	-	Y	90
<i>AntP91a</i>	CATGTGCGCGGATGAGACTT	TGACITGGCCTATCACCATGT	Y	-	Y	90
<i>AntP91a</i>	CCACTTAGTATATCTTGTCC	GCATGACTTGGCCTATCACC	Y	Y	Y	57
<i>AntP91a</i>	AGCCAGGGCTTGGTAGAGAGA	ATGTTTTCTCTCCTGTCTAGCG	Y	-	Y	90
<i>Atp1b2</i>	AGCATGGATTAACATATCTGG	ATTGAGGTCAGGAGITCAAGG	Y	-	Y	90
<i>Cola-1</i>	ATGGATAGGGACTTGTGTGAA	CTTCTTAAATAGCACCTTCAG	(Y)	-	Y	4
<i>Csfgm</i>	CTGTGCAACAGACTAAGCCT	CTGTAACACAATAACCAGGCA	Y	Y	Y	32a, 131, 90
<i>Csfgm</i>	TATTTTCTACTGATAGGGACC	TTATTTCTGGTAAGACATTCTC	N	-	N	90
<i>D11Mit1</i>	GGGTCTCTGAAGGCTTTGTG	TGAATACAGAAGCCACGGTG	(Y)	Y	Y	57
<i>D11Mit2</i>	TCCCAGAGGTCTCCAAGACA	CCACAGTGTGTGATGTCTTC	(Y)	Y	Y	57
<i>D11Mit4</i>	CAGTGGGTCATCAGTACAGCA	AAGCCAGCCCAGTCTTCATA	Y	Y	Y	57
<i>D11Mit5</i>	TTCTGTGAGCCTGGAGGAGT	TACAGGACTAGTTCCATTGGG	Y	Y	-	57
<i>D11Mit7</i>	AGGGTATTCTCTAGCCTCCACAC	TTTGAGGCAAGATGTCATGTATG	N	Y	Y	57
<i>D11Mit8</i>	CTTTTCATGGAGGCACAGGT	TGTGAACAGAGACACACATTCA	(Y)	Y	-	57
<i>D11Mit10</i>	GAACCGCAAGTCATGAATCA	TGGTTTATCTCTGAAGCTGC	(Y)	Y	Y	57
<i>D11Mit11</i>	TATTTCTCTCTCCCCCAC	TAGAGTTGGGACACCCAAGC	(Y)	Y	Y	57
<i>D11Mit12</i>	AGGGTTATGCTCTTGGCTGC	GATTTTCTAGGCTGGCTGG	Y	Y	(Y)	57
<i>D11Nds1</i>	TAAGAACCTTCTGTAGTIATT	ACCTTAGTTAGAGTTGGTCTC	(Y)	Y	Y	57
<i>D11Nds2</i>	TTATGTATGAATGTCCAC	AGGTTTCGATTCCCAACAC	(Y)	-	Y	90
<i>Empl-3</i>	GCTCAGACTCCTAGGTACTTAC	ACTCTGTGTCCTACTAGGTCTAG	N	-	Y	90
<i>Empb-3</i>	TCCTTATTTCTGTTGATTGGCAG	CTATAGAGAAATCCTGTCTTG	Y	-	Y	131, 90
<i>Gfap</i>	AACTGTTCAAAGCCATTTCG	CTATGGACTCACAGCCAGGCT	(Y)	-	Y	131
<i>Gfap</i>	TGAATTCFAGGACCAGCCAAGGCT	ACCTCTAAGATCCTGTGCGAGGCT	(Y)	-	Y	131
<i>Gfap</i>	CAGCTCTGCCCTTCTGAGTG	TTGGCCTTCTTTGGTGTCTTGC	(Y)	-	Y	131
<i>Gfap</i>	CCTAGGTCCTGGCTCTGTGTA	CAGAGTATCTCCTTGGAGCTC	(Y)	-	(Y)	90
<i>Gfap</i>	GTAATAAACGCTTACAAGTGG	GCGGATATATATGCAGCAGAG	Y	-	Y	90
<i>Glns</i>	AGCTTTGGAGACAACAATTAGATC	TGTTTCATCAGCTGAGGAATGGATG	Y	Y	Y	32a, 131, 90
<i>Glut-4</i>	GCGGAGCTAACGTGGGAACTA	AAGAATTGAGTGCAGCTGGTC	Y	-	Y	90
<i>Glut-4</i>	TGACATTTGGCGGAGCTAAC	ACATGTACTTGCAGGGTAC	Y	Y	Y	57
<i>Hox-2</i>	CCTTGCAITCTGAGGCTGAAGGAC	TCAGAAGTCTTGGCTGCATC	Y	-	Y	131, 90
<i>Il-3</i>	GAAATCTCAAATAGCAGGCACACT	TCTCCGAAAGCTCTTATTCTAAGA	N	Y	Y	32a, 90
<i>Il-4</i>	GTCTGCTGTGGCATATTCTG	GGCATTTCCTATTTCAGATTTC	(Y)	Y	Y	32a, 131
<i>Il-5</i>	CCTTTCTGAAAGTATTAAGAGT	ACAACCATCTGCATATCCAGC	(Y)	Y	Y	32a, 131
<i>Il-5</i>	GGCTACACAGAGAAACCCTGT	CATGCATACACAGGTAGTTCA	(Y)	-	Y	90
<i>Il-5</i>	AGCTTCTCATGTTTCGCGCAGTGGCACT	CATGTTTAAAAAACAATACTAAGGAGC	(Y)	-	Y	90
<i>Il-5</i>	TGATTGATATGCTTACITATG	GAAGTCAGCTACAGTGTATTTC	N	-	N	90
<i>Il-5</i>	CTTTAAATAGTGAATTATGGC	AATAGAGCTTATTTCAGGGCAT	N	-	Y	90
<i>Lif</i>	CAGCTAGAAATGGCAATGAGG	CTTGTCTACACCCAGCAAGC	Y	Y	Y	57
<i>Mpo</i>	GTGAGTTCTAGGACAGCCAGG	ACAACCCTTCTTACCCCATGG	(Y)	-	(Y)	90
<i>Myla</i>	ACTAGTCTTACCGTCTTCCA	TGCTGTGTTGCTTACTATGTGC	Y	-	Y	131, 90
<i>Rpo2-1</i>	TGCTGGAAGACAGCTACAGTGTAC	AGTGGCCAGGACACTCGGTCATGT	N	-	N	90
<i>Sigje</i>	GGATCAGAGATACTCATGAT	GAGAAGATTACCTGAGTACA	N	-	Y	4

Microsatellite markers

Polymorphisms detectable by the polymerase chain reaction (PCR) have several advantages over restriction fragment length polymorphisms (RFLPs) detected by Southern blot analyses in that less DNA is consumed, samples can be typed rapidly, and probes can be readily exchanged by publishing oligonucleotide primer sequences. In addition, microsatellites such as mono- and dinucleotide repeat sequences tend to exhibit more polymorphisms among closely related strains than do restriction fragments. Table 7 presents a summary of the oligonucleotide primer sequences that have been used to identify loci on Chr 11. For some loci there are several primer pairs available; not all of these have been tested in a wide variety of strains, but it is evident that some are more informative than others.

Reference mapping loci

To aid in incorporating new mapping information into the existing consensus map, a set of reference loci were suggested for use (Buchberg et al. 1991). The characteristics of these reference loci include: spacing every 5–15 cM, ease of use, universal availability, and useful polymorphisms. The original set of reference loci proposed by the Chr 11 mapping committee has been expanded as follows, with the estimated distance (cM) between neighboring markers:

Lif-5-*ErbB*-10-*Glns*-5-*Adra*-1-9-*Csfgm*-
10-*Acrb*-7-*D11Mit8*-5-*Mpo*-6-
Hox-2-6-*Myla*-14-*P4hb*.

The underlined loci are primary anchors and have been confirmed in independent crosses (Buchberg et al. 1991). The newly proposed reference loci have not been mapped relative to one another in multilocus crosses; therefore, they are listed as secondary anchors. Nonetheless, this set of 12 loci spans 76 cM of the 80 cM of Chr 11, providing complete coverage of Chr 11. The community is encouraged to incorporate the use of these loci as markers in their genetic mapping experiments.

DNA probes corresponding to these genes have been requested to be deposited in ATCC. Polymorphisms can be detected by PCR for nine of the anchors: *Lif*, *Glns*, *Csfgm*, *Acrb*, *D11Mit8*, *Mpo*, *Hox*-2, and *Gfap* (Table 7). Ideally, it will be possible to type each reference locus with a probe that is informative in both intraspecific as well as interspecific backcrosses by both conventional Southern blotting and PCR analysis.

Conclusions

Part of the objective of this report is to provide a mechanism for routine review of the mapping data that have been published and to generate a consensus map that corrects errors and omissions in previous reports. We apologize for any references or data that may have

been excluded in this report. We welcome the receipt of additional information and suggestions concerning the consensus linkage map. We appreciate authors' sending us reprints of new papers that report the mapping of genes to mouse Chr 11.

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