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Mammalian Genome
Incorporating Mouse Genome

Mouse Chromosome 10

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Introduction

The 1998 Mouse Chromosome (Chr) 10 report includes information on newly mapped genes and other DNA variants, their positions in the linkage and/or cytogenetic maps, and new information about human-mouse linkage homology. In addition to the published Table, a cytogenetic map is available on the MGI Website for the Chromosome report. The locus position assignments have been adjusted to reflect new or previously overlooked information.

Table 1 lists known Chr 10 loci ordered by map position, with information on localization, method of mapping, and homologous human gene localization, if known. Due to space limitations, fewer references are given in the print version than the electronic version. Withdrawn locus symbols are not included, but are listed alphabetically at the end of this volume, together with the current locus symbol. Reference number refers to JAX reference numbers in the Mouse Genome Informatics Database (MGI). Also included in Table 1 are translocations, inversions, deletions, and Robertsonian fusions involving Chr 10.

The mouse Chr 10 map

The Chr 10 map is based primarily on data collected in numerous linkage crosses and recombinant inbred strains. Since many loci have been mapped in interspecific crosses involving *Mus spretus*, map distances tend to reflect recombination frequencies in interspecific hybrid females. A very large number of loci have been scored on the BSS (199 loci) and BSB (42) panels, a communal mapping resource (http://www.jax.org/resources/documents/cmdata). Information on mapping of most SSLP markers (those starting with *D10Mit* . . .) is also available on the MIT's own Website (http://www.genome.wi.mit.edu). The typing of microsatellite markers in many crosses greatly helps with the integration of these markers into the composite map. However, the number of such microsatellite markers or other common reference loci typed in most of the crosses is modest, so locus order inferred for loci mapped in different crosses is still based considerably on apparent map distances, and thus, subject to error.

Map positions were adjusted when new data became available. The map around *av* has refined not only the location of these phenotypes but also the position of MIT markers in the region (45743). At the distal end of the map, there continue to be some discrepancies between published reports, and especially this part of the map has to be used with caution. Three markers, *Tel-rs7, D10Rp1* and *D10Hgu1,* contain telomeric repeats. Of these, *D10Hgu1,* maps the most distal and might represent the actual telomere (26822).

Expressed sequences

Several groups are engaged in mapping expressed sequences in the mouse genome, and these are likely to contribute significantly to the future growth of the linkage map (44483, 49041, 50869). Many of these large scale EST mapping projects map these genes in the BSS or BSB panels, and make their data immediately available on these Websites (see above) where more up-to-date information may be available than in this report. ESTs that are part of an existing gene will be listed under the appropriate gene symbol, whereas anonymous ESTs that are not identical to known genes start with the symbols *D10Bwg, D10Ertd, D10Wsu* or *D10Xrf.*

New gene loci and traits

Over 70 newly identified genes defined by a DNA probe have been added to Chr 10. New QTLs were added whenever published, whether they fit criteria for proven, probable or tentative linkage. QTLs are generally mapped to very large intervals, and the position in the report is the peak, except when the area is broader than about 30 cM in which case they are listed as syntenic (S), as is a new QTL for Lupus, *Lmp4.* QTLs for fear-conditioning have been reported by Wehner et al. (43837) near 12–25 cM of Chr 10 but not yet been assigned locus names and are thus not listed in Table 1. A QTL affecting exploratory behavior, *Exq1,* has been mapped to the distal end of Chr 10 (41249). Some QTLs may turn out to be identical with already identified loci: one QTL for seizures (*El3*) maps near known Mendelian mutations with seizures (*mh=Ap3d, ji*), and a QTL affecting growth, *Bgeq8,* maps near two Mendelian loci (*hg, pg*) affecting growth. A modifier locus affecting severity of deafwaddler (*mdfw*), a deaf/circling mouse caused by mutation in the *Atp2b2* gene, has been mapped near the deafness mutation waltzer (*v*) and may be allelic with *v* (38429). The newly published age-related hearing loss locus *Ahl* also maps near several deafness mutations including *v* (44966).

The mouse mutation mocha (*mh*) has been identified as a null allele of the adaptor-related protein complex 3 delta subunit (*Ap3d*) (50662).

Once a gene is found mutant in a phenotype, the name usually changes to the gene symbol, so for example, the pygmy (*pg*) locus has been shown to be due to deletions of the high mobility group protein I, and is listed as *Hmgic,* with the addition of T in the trait column. Similarly, the mutants *Lop* and *Cat* were shown to be alleles of the *Mip* locus, and *mh* will now be withdrawn and is listed as an allele of *Ap3d.* An exception is *si,* which encodes the

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gene for Pmel17 which is mutant in silver mice, where the human symbol is *SILV* because of association with the mouse mutant, and to keep human and mouse loci consistent, the locus *si* was maintained. The *bpk* locus is likely to be allelic with *jcpk* but this symbol will not be withdrawn until the data are confirmed.

Human homologies

The proximal third of mouse Chr 10 is homologous to a segment of the long arm of human chromosome 6, q21-q24, while the distal half is homologous to a segment of the long human chromosome 12, q13-q24, but not necessarily in a continuous linkage group. In contrast, the central region of mouse Chr 10 has homologies to four different human chromosomes, each of which is only a few cM in size. The latter regions are, from the centromere to telomere, regions homologous to 10q21, 22q11, 21q22.3 and 19p13.3. In each case, several genes have been independently mapped to these segments of homology, and in the case of 22q11/21q22.3 and 21q22.3/19p13.3, confirmed by physical comparative mapping (48150 and MB, unpubl. data). *Prim1/PRIM1* may identify a homology between the most distal region of Chr 10 and human 1q44 but since there is only one gene, this synteny in the most distal region needs confirmation.

There are three exceptions to this general pattern. The potassium channel gene *Kcnc2* maps to 19q13.3 in human, and the tissue-inhibitor of metalloproteinase 3 (*Timp3*) maps to 22q12-q13. In both cases, the mouse homolog maps to the distal part of Chr 10 surrounded by genes homologous to human 12q. *Aco2* maps surprisingly far proximal on mouse Chr 10 for a gene with a human homolog on 22q, so this may represent an additional disruption of linkage conservation. Whether these are truly homologous loci that interrupt large regions of conserved homologies is still unknown. However, the K-channels and *Timp3* are members of gene families. When mapping members of large gene families, it is often hard to assign true homologies, compared to mapping another related orthologous member of the family. Indeed, *Kcnc3*, which previously had been assigned to mouse Chr 10 (16048 and previous reports), has now been mapped to mouse Chr 7 in a region of homology to 19p13.3 (46206). Probably, the same will be true for *Kcnc2* which is closely linked to *Kcnc3* (16048). Such linkage results and homologies thus have to be treated with caution until confirmed by the mapping of other genes. The reassignment of *Kcnc3* confirms that erroneous assignments are highly likely in the case of highly homologous genes.

Physical mapping

The Whitehead Institute/MIT Center for Genome Research has developed an extensive physical map of the mouse genome, with numerous, mostly short, YAC contigs, anchored with microsatellite markers. This information is accessible via the Internet: http://www.genome.wi.mit.edu. Only if mapping data in addition to these are available is a P mentioned in the mapping column. A physical map of the central region including the boundary of the human 21q22.3/22q11 syntenies has been established (48150).

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