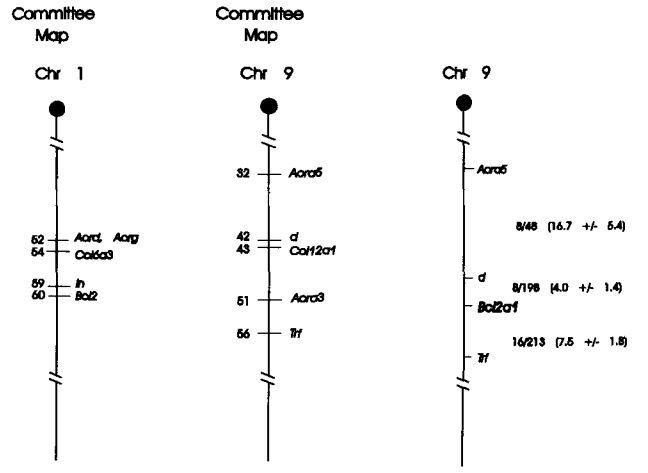

Fig. 1. Abbreviated maps of mouse Chr 1 and Chr 9. The map on the far right was derived from analysis of the two crosses described in this study. Recombination fractions are given to the right for each adjacent locus pair; percentage recombination and standard error were calculated according to Green [12]. *Acra5* was typed only in the musculus cross. The map in the center was derived from the Chr 9 committee map [10] and shows the map locations in cM from the centromere for the previously mapped loci used to position *Bcl2a1* in our crosses. The Chr 9 committee map and the Chr 1 committee map given to the extreme left [11] also show map locations for paralogous genes that map to these chromosomes.

Data were stored and analyzed with the program LOCUS. Percent recombination and standard errors between specific loci were calculated from the number of recombinants according to Green [12]. Loci were ordered by minimizing the number of double recombinants.

[10,11]. These observations suggest that these regions of mouse Chr 9 and Chr 1 may have been generated by duplication of some ancestral chromosome or subchromosomal region.

The region of Chr 9 to which we mapped the A1 gene contains genes with homologs on three human chromosomes: Chr 3, 6, and 15. Therefore, we used the same A1 gene probe to type a panel of human/rodent somatic cell hybrids (BIOS, New Haven, Conn.) to determine the human map location of this gene. Digestion with *Eco*RI identified A1 probe reactive fragments of 6.2 and 1.8 kb in mouse and 4.4 kb in human. Analysis of 18 hybrids identified the human fragment gene in two hybrids, and correlation with the chromosome content of these hybrids showed perfect correspondence with human Chr 15 (data not shown). At least two discordancies were identified for all other chromosomes. These data indicate that the human homolog of the A1 gene maps to Chr 15. Comparative analysis of human Chr 15 and mouse Chr 9 indicates that the mouse chromosome contains two regions of homology to this human chromosome. Most of the genes with human Chr 15 homologs map to a region proximal to the dilute locus, although previous studies had identified two human Chr 15 homologs, *Acra3* and *Grf1*, distal to *d*. Our data now place another gene in this more distal region of homology.

Acknowledgments: This work was supported by funds from Yeshiva University Grant 9-526-0522 to M.B. Prystowsky, who is a recipient of an American Cancer Society Faculty Research Award. We thank Dr. Lois Maltais (Jackson Laboratory) for providing nomenclature assistance.

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Mouse angiotensin receptor genes *Agtr1a* and *Agtr1b* map to Chromosomes 13 and 3

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Received: 13 September 1996 / Accepted: 9 November 1996

Species: Mouse
Locus names: angiotensin receptor 1a and angiotensin receptor 1b
Locus symbols: *Agtr1a* and *Agtr1b*
Map positions: 13 centromere–*Pll*–(3.2 ± 1.8)–*Mf4, D13Bir8, Agtr1a*–(1.1 ± 1.1)–*D13Bir9, D13Mit4;* and 3 centromere–*D3Mit60*–(1.1 ± 1.1)–*Agtr1b*–(1.1 ± 1.1)–*D3Bir3*.
Method of mapping: Determined from 94 interspecific backcross progeny of the BSS panel (C57BL/6JEi × SPRET/Ei) × SPRET/Ei of The Jackson Laboratory Backcross DNA Panel Mapping Resource as described [1].
Database deposit information: MGD accession numbers: MGD-CREX-689 for Chromosome (Chr) 13 data and MGD-CREX-690 for Chr 3 data.
Molecular reagents: The mouse *Agtr1a* and *Agtr1b* genes were cloned from a strain 129 genomic library, using a probe generated by PCR from primers based on the rat *Agtr1a* sequence [2]. These genes were mapped for restriction enzyme sites and partially sequenced (unpublished data). This information was used to design the following probes. Probe 1: A 450-bp *Apa*I to *Bgl*II fragment derived from the 5′ flanking region of the *Agtr1a* gene. Probe 2: A 318-bp PCR product corresponding to a portion of the single coding exon of *Agtr1b*. This probe was generated with primers 5′ CC GTC ATC CAC CGA AAT GTG TA 3′ and 5′ CAG CTG AAT GAG CAC ATC CAG A 3′.
Allele detection: Both probes recognized restriction fragment length variation between *M. spretus* and C57BL/6J DNA digested with *Eco*RI. For *Agtr1a*, the *M. spretus* fragment was approximately 7.0 kb while the C57BL/6J fragment was approximately 7.3 kb. For *Agtr1b*, the *M. spretus* and C57BL/6J fragments were approximately 6.2 kb and 1.8 kb respectively.
Previously identified homologs: The human angiotensin II type I receptor gene (AGTR1) has been mapped to Chr 3q21-q25 [3]. The rat *Agtr1a* gene is on Chr 17, while the rat *Agtr1b* gene is on Chr 2 [4].
Discussion: The renin-angiotensin system plays a primary role in cardiovascular homeostasis. Many of the biological effects of this system are mediated by the octapeptide angiotensin II, which interacts with specific cell surface receptors [5]. There are two pharmacologically distinct types of angiotensin II receptors, designated type 1 (AT1) and type II (AT2). Two subtypes of type I receptor have been identified in rodents (AT1a and AT1b) [6,7]. AT1a and

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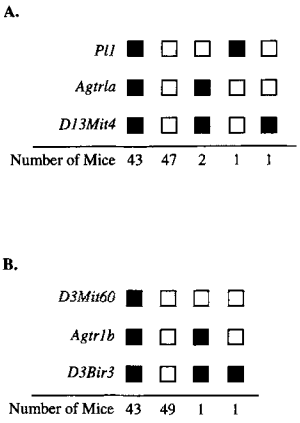

Fig 1. (**A**) Localization of *Agtr1a* to proximal Chr 13. The markers *Mf4* (mesoderm/mesenchyme fork head 4) and *D13Bir8* had not recombined with *Agtrla*. They were, therefore, placed at the same location as *Agtr1a*, and are not shown. (**B**) Localization of *Agtr1b* to proximal Chr 3. The filled boxes indicate the presence of both C57BL/6J and SPRET/Ei alleles. The open boxes indicate the presence of only SPRET/Ei alleles. The number of offspring carrying each type of chromosome is indicated at the bottom. Complete raw data for the Jackson BSS backcross are available on The World Wide Web at the URL address http://www.jax.org/resources/documents/cmdata.

AT1b are encoded by separate genes, *Agtr1a* and *Agtr1b* respectively.

In this study, we used probes specific to the mouse *Agtr1a* and *Agtr1b* genes to follow allelic segregation in an interspecific backcross panel. Comparison of the haplotype distribution pattern located *Agtr1a* to proximal Chr 13, and *Agtr1b* to proximal Chr 3. Map Manager [8] was used to determine linkage, to calculate marker distances, and to draw haplotypes. The most likely marker order was determined by inspection of the data and minimization of double recombinants (Fig. 1). Three recombinants were found between *Agtr1a* and the placental lactogen-1 gene (*Pl1*), and one recombinant was found between *Agtr1a* and *D13Mit4*. These data place *Agtr1a* 3.2 cM distal to *Pl1* and 1.1 cM proximal to *D13Mit4* on Chr 13. One recombinant was identified between *Agtr1b* and *D3Mit60* and between *Agtr1b* and *D3Bir3* respectively. Thus, *Agtr1b* was placed 1.1 cM distal to *D3Mit60*, and 1.1 cM proximal to *D3Bir3* on Chr 3.

The human AGTR1 gene has been mapped to Chr 3q21-25. The mouse *Agtr1b* gene maps to proximal Chr 3. Proximal Chr 3 contains other genes that map to human 3q21-25, such as carboxypeptidase A3 (*Cpa3*) [9,10]. This study, therefore, extends the relationship between these chromosomes.

Acknowledgments: We thank Lucy Rowe for her advice and for critical reading of the manuscript. We also thank Achim Gossler for manuscript review and Sylvia Hiller for her assistance.

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An MMTV integration site maps near the distal end of mouse Chromosome 11

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Received: 13 October 1996 / Accepted: 9 November 1996

Species: Mouse
Locus name: A somatically acquired MMTV integration site from a T-cell lymphoma
Locus symbol: *Pad3*
Map position: *Pad3* is located on mouse Chromosome (Chr) 11: Centromere–(//)–*D11Hun20*–(1.09 ± 1.08)–*D11Hun21*–(2.13 ± 1.49)–*Fasn*–*Hfh4*–*Pad3*–*D11Xrf16*–*D11Xrf107* (upper 95% confidence limit is 3.8 cM).
Method of mapping: Southern blot analysis of DNAs from 94 backcross (N2) progeny from the cross (C57BL/6JEi × SPRET/Ei) × SPRET/Ei (The Jackson laboratory BSS panel).
Database deposit information: MGD accession number MGD-CREX-706
Molecular reagents: The *Pad3* probe is a 0.7-kb *PstI* unique cellular DNA fragment 3′ to an acquired MMTV provirus from the RL♂1 T-cell lymphoma.
Allele detection: By Southern blot analysis, the *Pad3* probe hybridized to an *EcoRI* fragment of approximately 10 kb in C57BL/6J (*Mus musculus*) DNA and 5 kb in SPRET/Ei (*Mus spretus*) DNA.
Previously identified homologs: None.
Discussion: Mouse mammary tumor virus (MMTV) is a type B retrovirus that induces breast cancer and, at a lower frequency, T-cell tumors in mice [1]. MMTV-induced breast cancers result from the transcriptional activation of cellular oncogenes located in the vicinity of proviral integration sites. Activation of transcription at nine different loci—namely, *Int1*/*Wnt1*, *Int2*/*Fgf3*, *Int3*/Notch-like, *Int4*/*Wnt3*, *Fgf-4*/*Hst*/*K-FGF*/*Int5*/*IntH*/aromatase, *Fgf8*, *Int6*, and *Wnt10b*—has been observed in MMTV-induced mammary tumors in mice [2–4]. However, the mechanism of T-cell tumor induction by MMTV is still unclear. TBLV, a T-cell tropic infectious variant of MMTV, has been shown to integrate on the mouse X Chr and to activate transcription of one or more nearby genes [5].

To determine if the *Pad3* MMTV integration site maps close to any known cellular gene, we used RFLPs for the *Pad3* locus to screen the BSS panel [6]. Digestion of each of the 94 BSS panel DNAs with *EcoRI* detected a 5-kb band in the homozygous animals and both 5- and 10-kb bands in the heterozygous animals. Thus, the allelic segregation of the *Pad3* locus in the BSS panel was determined. This pattern was compared with the patterns of segregation of the approximately 2000 other loci previously mapped in the cross, and linkage was found to distal Chr 11 [6]. The *Pad3* locus cosegregated with at least four other markers, namely, *Fasn*, *Hfh4*, *D11Xrf16*, and *D11Xrf107* (see Fig. 1). The proximity of the *Pad3* integration to *Hfh4* (HNF-3/forkhead homolog 4) is intriguing, since members of the HNF-3/forkhead or "winged helix" proteins are transcription factors with diverse biological functions [7–9]. At least two members of the forkhead family have been shown to participate in translocation-mediated oncogenesis in human malignancies. Translocations to FKHR (also designated ALV) have been observed in alveolar rhabdomyo-

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