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The gene encoding the thrombin receptor (*Cf2r*) maps to mouse Chromosome 13

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Species: Mouse
Locus name: Thrombin receptor
Locus symbol: *Cf2r*
Map position: cen-*As1*–2.4 (0–5.4)–*Cf2r*–2.4 (0–5.4)–*Pmv9* at the 5% risk level.
Method of mapping: AKXL RIS, 218 progeny from the interspecific backcross (C57BL/6 × SEG)F_1 × C57BL/6 of the EUCIB resource [1].
Molecular reagents: A $(GA)_{26}$ microsatellite has been found in exon 2 of the mouse thrombin receptor gene, and oligonucleotides flanking this microsatellite were designed with the following sequence:

forward: 5'.....GTACGCAAGGTTTAACTCCAGCAGC....3'
reverse: 5'.....CAAGTCGGGCTCAGTTACCCTACACC.....3'

Annealing temperature, 55°C; 1.75 mM $MgCl_2$.
Allele detection: The primers allow the amplification of a 310-bp-long fragment with AKR/J and SEG genomic DNA and 320 bp with C57L/J and C57BL/6J genomic DNA.
Previously identified homologs: Human F2R mapped to human 5q13.
Discussion: The serine protease α-thrombin (mouse gene symbol: *Cf2*) plays an important role in the hemostatic response. Its activation is the last step in the coagulation cascade, where it catalyzes fibrin clot formation.

With the AKXL recombinant inbred strains, we found tight linkage of the *Cf2r* locus with several markers of mouse Chr 13 (Fig. 1). This assignment was confirmed with the data obtained with the EUCIB resource; we found no recombinant between *Cf2r* and *D13Mit28* [2] out of 218 backcross progeny. We conclude that these two loci map in a genetic interval of 1.36 cM or less (5% risk level). The data obtained from the AKXL RIS have been analyzed with the help of RI Manager Software [3], and the data obtained from the interspecific backcross have been analyzed with the help of Gene-Link [4] and MBx [1] softwares.

	05	06	07	08	09	12	13	14	16	17	19	21	24	25	28	29	37	38
As1	A	A	L	A	L	L	L	A	A	A	L	A	A	L	L	L	A	A
Cf2r	A	A	L	A	L	L	L	A	L	A	L	A	A	L	L	L	A	A
Pmv9	A	A	L	A	L	L	L	A	L	A	A	A	A	L	L	L	A	A

Fig. 1. Strain distribution pattern for the *Cf2r* alleles among the 18 strains (05–38) of the AKXL set of Recombinant Inbred Strains.

Because of the weak sensitivity to thrombin of the platelets collected from mice homozygous for the pearl mutation (*pe*) [5] and considering the localization of the *pe* locus in the segment of Chr 13 [6] where the thrombin receptor-encoding gene was found to map, *Cf2r* was regarded as a candidate gene for *pe*. In order to test this hypothesis, we mapped *Cf2r* on the panel used to map *pe* [6] and found two recombinants out of 1,100 backcross progeny (0.18 cM, 0–0.43 at the 5% risk level). We then conclude that *pe* and *Cf2r* are two different loci closely linked on Chr 13.

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Chromosomal assignment of the porcine gene for apolipoprotein C3 (APOC3) to Chromosome 9 by somatic cell hybrids

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Species: Pig (*Sus scrofa domestica*)
Locus name: Apolipoprotein C3
Locus symbol: *APOC3*
Map position: 9
Method of mapping: PCR analysis with 21 somatic cell hybrids which have been characterized by QFQ, FISH, and PCR as described earlier [1,2].
Molecular reagents: Porcine specific PCR primers have been selected from the partial genomic porcine DNA sequence of *APOC3* in intron 3 (accession no. M84134). Primer sequences *APOC3*vers: 5' CAC TCA GCC CGC ACT TCG TTT CCT T 3' and *APOC3*rev: 5' GAT GAT TAG CTG CAG GAG CTG GGG C 3' were used at an annealing temperature of 56°C for 1 min in a standard PCR as described earlier [1,2]. Primers amplify a porcine specific product of 407-bp size. After PCR screening of the 21 somatic cell hybrids, correlation ϕ and concordance c for apoli-

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