

ers and consumers. As a first step in characterizing the role of OBS protein in controlling fat metabolism in ruminants, we have mapped the bovine homolog of the *obese* gene to a linkage group previously assigned to bovine Chr 4 [1]. The obese gene has been mapped to mouse Chr 6 [9] and human Chr 7 [15], which shares synteny with bovine Chr 4 [16].

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Radiation hybrid mapping of SNAP, PCSK2, and THBD (human Chromosome 20p)

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Species: Human

Locus names: synaptosomal-associated protein (25kDa), proprotein convertase subtilisin/kexin type 2, thrombomodulin

Locus symbols: SNAP (EST00925, D20S140E), PCSK2 (NEC2), THBD

Map position: 20p: telomere . . . D20S192–[27.9 cR]–D20S115–[25.2 cR]–D20S175–[68.6 cR]–(D20S188–[7.4 cR]–SNAP)–[23.6 cR]–D20S186 . . . PCSK2–[17.8 cR]–D20S112–[13.5 cR]–

D20S182 . . . D20S190–[69.0 cR]–THBD–[26.9 cR]–D20S184 . . . centromere

Method of mapping: PCR from radiation hybrid panel 3 (Research Genetics, Inc., Huntsville, Ala., USA) and two-point linkage analysis (RH2PT ver. 2.01 [1]) with Chr 20 markers by use of available radiation hybrid scores (anonymous ftp from shgc.stanford.edu).

Database deposit information: Primers 135S/A: GDB probe: GDB: 198854

Molecular reagents: primers (all 5'-3', with the sense primer listed first): SNAP (135S/A): caaacaccaggggaaatg, gatggctactgtttg-gagag; PCSK2--gcatcaagcacagacctaca, cttggaagcagcgaatc; THBD--gccttaatcaggtctca, tcataaactggatggggg.

Previously identified homologs: Snap (2, 78 cM), Pcsk2 (2, 80 cM), Thbd (2, 84 cM)

Discussion: To characterize gene products highly expressed in the human brain, we have been determining the subregional chromosome localization and expression patterns of expressed sequence tags or ESTs. After mapping EST00925 to human Chr 20 by PCR [2], we studied it and related ESTs (EST00669, EST01078) in more detail because BLAST analysis [3] showed that EST00925 matched several other independently isolated ESTs--suggesting derivation from a relatively abundant brain transcript. Northern analysis with hybridization membranes from Clontech (human 7760-1, human brain 7755-1, and mouse 7762-1) and the insert from ATCC 77877 (EST00669) demonstrated a 2.2-kb transcript only in human and mouse brain and in all human brain regions tested (not shown). EST00925 matched the published sequence of SNAP (GenBank D21267 [4]), with nucleotides 53–312 of EST00925 corresponding to nucleotides 1695–1954 of D21267 with 99% identity. The size of the transcript, the sequence conservation, and the brain specificity we observed for this set of ESTs were consistent with what has previously been observed for SNAP [4,5], confirming the identification of EST00925 as the 3' untranslated region of SNAP.

SNAP is not reported as mapped in the human in the Genome Data Base (date searched 8/31/95), but *Snap* has been assigned to Chromosome (Chr) 2 in the mouse [6], in a region that is syntenic with human 20p [7]. We therefore used the comparative map to identify sequenced human genes that might be used in a PCR approach to corroborate placing SNAP on human 20p. PCSK2 and THBD were selected, both with cytogenetic locations of 20p11.2 [8–11]. These genes are ordered *cen-Snap-PCSK2-Thbd* in the mouse [7].

PCR reaction conditions were as previously reported [2]. Patterns of amplification from the radiation hybrid panel were submitted to the radiation hybrid server at the Stanford Human Genome Center (rhserver@shgc.stanford.edu). Because linkage with CEPH framework markers was indicated by this analysis [12], the raw radiation hybrid mapping scores for the linked markers, as well as others in the region [12], were retrieved from the ftp site at Stanford and used in two-point linkage analyses.

Centirad 8000 distances between the markers D20S192, D20S115, D20S175, D20S188, D20S186, D20S98, D20S112, D20S182, D20S190, D20S184 (ordered according to CEPH average map C20M21, GDB5.6-G00-354-610) and SNAP, PCSK2, and THBD were determined. Those marker pairs with two-point LOD scores >3.0 are presented in Table 1. The RH data show SNAP to be most closely linked to D20S188, with the order given above in Map position. Although the retention patterns of D20S188 and SNAP were not identical, the cR distances between them and the flanking markers D20S175 and D20S186 were indistinguishable. These data also show PCSK2 linked to D20S112, and THBD linked to D20S184. Based on the marker order of the CEPH consensus map, a gene order of *pter-SNAP-PCSK2-THBD-cen* is indicated on human 20p, corroborating the order in the mouse. Also, the placement of D20S112, D20S182, and

Table 1. CentiRad-8000 distances between marker pairs.

Marker 1	Marker 2	cR 8000	LOD
<i>SNAP</i>	<i>D20S188</i>	7.4	14.93
<i>SNAP</i>	<i>D20S186</i>	23.6	9.01
<i>SNAP</i>	<i>D20S175</i>	35.2	7.62
<i>SNAP</i>	<i>D20S115</i>	68.6	3.63
<i>SNAP</i>	<i>D20S192</i>	73.7	3.63
<i>PCSK2</i>	<i>D20S112</i>	17.8	10.55
<i>PCSK2</i>	<i>D20S182</i>	30.0	7.72
<i>THBD</i>	<i>D20S184</i>	26.9	9.69
<i>THBD</i>	<i>D20S190</i>	69.0	3.92
<i>D20S112</i>	<i>D20S182</i>	13.5	11.32
<i>D20S115</i>	<i>D20S175</i>	35.2	7.62
<i>D20S115</i>	<i>D20S188</i>	68.6	3.98
<i>D20S115</i>	<i>D20S192</i>	27.9	9.32
<i>D20S175</i>	<i>D20S186</i>	42.5	5.92
<i>D20S175</i>	<i>D20S188</i>	35.2	7.62
<i>D20S175</i>	<i>D20S192</i>	63.9	4.30
<i>D20S184</i>	<i>D20S190</i>	69.3	3.87
<i>D20S186</i>	<i>D20S188</i>	23.6	9.01
<i>D20S188</i>	<i>D20S192</i>	73.7	3.63

D20S190 between *PCSK2* and *THBD* indicates that the cytogenetic localization of these markers is also 20p11.2.

Although not explicitly identified as such, all three of these genes have been converted to STS markers [13]. Sequence alignments show that WI-7829 and WI-6063 are derived from *SNAP*, WI-9181 from *PCSK2*, and WI-7085 from *THBD*. These STS markers have been mapped to distinct contigs on Chr 20, WC-252, WC-539, and WC-1436 respectively. The physical linkage indicated by the two-point RH mapping is mirrored in the STS mapping. Several YACs are reported to contain both *SNAP* and *D20S188* (881-H-2, 1.4 Mb; 953-A-2, 1.63 Mb), *PCSK2* and *D20S112* (804-B-8, 0.7 Mb), and *THBD* and *D20S184* (893-F-3, 0.81 Mb; 916-A-4, 0.82 Mb; 786-C-3, 1.45, 1.77 Mb). If none of these YACs has an internal deletion, these data provide some indication of the physical distance between these markers.

Note added in proof: After this paper was submitted, it was reported that *SNAP* maps to human chromosome 5q11.2 based on fluorescence *in situ* hybridization. Our chromosome 20 localization was established using 3 independently constructed mapping resources and is consistent with the mouse comparative map. (Korenberg, J., Chen, X.N., Adams, M.D., Venter, J.C. 1995. *Genomics* 29, 364-370.)

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