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Assignment of eight loci to bovine syntenic groups by use of PCR: extension of a comparative gene map

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Abstract. The polymerase chain reaction (PCR) has been combined with hybrid somatic cell technology to extend the bovine physical map. Eight bovine loci—glycoprotein hormone alpha (*CGA*), coagulation factor X (*F10*), chromogranin A (*CHGA*), low-density lipoprotein receptor (*LDLR*), human prochymosin pseudogene (*CYM*), oxytocin (*OXT*), arginine-vasopressin (*ARVP*), and cytochrome oxidase c subunit IV pseudogene (*COXP*)—were assigned to bovine syntenic groups with this approach. *CGA* was assigned to bovine syntenic group U2, *F10* to U27, *CHGA* to U4 [bovine Chromosome (Chr) 21], *LDLR* to U22, *CYM* to U6, *OXT* and *ARVP* to U11, and *COXP* to U3 (bovine Chr 5). Seven of these genes, *CGA, F10, CHGA, LDLR, OXT, ARVP,* and *CYM,* further delineate regions of chromosomal conservation on human Chrs 6, 13, 14, 19, 20, 20, and 1, respectively. *CHGA, OXT,* and *ARVP* are unmapped in the mouse. Comparative mapping predicts the mouse *CHGA* will map to Chr 12, and mouse *OXT* and *ARVP* will map to mouse Chr 2. Furthermore, human *CYM* is predicted to be sublocalized to 1p32-q21. The primers developed for these eight loci will be useful for the development of hybrid somatic cell panels in the future as well as establishing a collection of bovine expressed sequence tags.

Introduction

Syntenic comparisons among distantly related species suggest that large chromosomal regions are conserved within mammals (Womack and Moll 1986; Brubacher et al. 1990; Copeland and Jenkins 1991; Nadeau 1989; Levan et al. 1991). Because of this chromosomal conservation, it is possible to use the extensive gene maps of human and mouse to speed the development of gene maps in other species. Inferences can be made about information derived from the mapping of loci in one species to their location in another. The development of the domestic cow gene map has benefited from a comparative mapping approach (Threadgill and Womack 1990; Threadgill et al. 1990a, 1991; Skow et al 1988). If the borders of the evolutionarily conserved regions can be determined, then mapping information from mouse and human will be immediately useful in the bovine gene map. Likewise, syntenic information from cattle can be used to make predictions regarding syntenic organization in human and mouse.

The syntenic characterization of cattle has been primarily through Southern analysis of bovine–rodent DNAs. Recently, PCR has been used extensively in the development of physical and linkage maps of mouse and man (Cornall et al. 1991; Dionne et al. 1990; Trapani et al. 1990; Iggo et al. 1989; Rose, 1991). Here we demonstrate its value as a tool in bovine gene mapping.

Materials and methods

Bovine leukocytes were fused with hypoxanthine phosphoribosyltransferase-deficient rodent CHO, E-36, and thymidine kinase-deficient ($LMTK^-$) cell lines, and the hybrid cell lines were developed as described previously (Womack 1990; Womack and Moll 1986). Genomic DNA was extracted from bovine, rodent, and bovine-rodent cells according to established protocols (Blinn and Stafford 1976).

Primers were designed from published bovine sequences (Table 1) and synthesized in the Department of Biology (Texas A&M University). A PCR cocktail consisting of 1.0 μM upper and lower primers and 0.2 mM dNTPs, 10 mM Tris pH 9.0, 50 mM KCl, 1.5 mM $MgCl_2$, 0.01% gelatin (w/v), 0.1% Triton X-100, and 1–1.25 units of *Taq* polymerase (Promega, Madison, Wis.). The cocktail was aliquoted into tubes with 100 ng of bovine CHO, E36, $LMTK^-$, or hybrid cell DNA per reaction and overlaid with approximately 100 μl of sterile mineral oil. The reaction cycled for 1 min at 94°C, 2 min at an optimized annealing temperature, and 2 min at 72°C for 25–35

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Table 1. Primers and conditions for amplification reactions.

Gene	Upstream primer	Downstream primer	Annealing temp (°C)	Size (bp)	Reference
CYM	5'-CCAGGGCTTCTGTACCAGTGGCTTC-3'	5'-TGAGAATCATCTGTCTGGAAACCTC-3'	67	253	Hidaka et al. 1986
CGA	5'-TCAACTTTCAGGATGTTGTGTATAA-3'	5'-GATCACAGACCACAGTTTTGCAGAC-3'	60	559	Goodwin et al. 1983
LDLR	5'-TGAGCTGCTGCCTTGAGTCCTCTCC-3'	5'-GCAGGCTTGCCTGGCAGAAGTAAAC-3'	65	519	Hobbs et al. 1985
F10	5'-TGTCCAGCAGCTTCACCATTACGCC-3'	5'-GCCTTCATGATCTTGTCGATCCACT-3'	70	229	Fung et al. 1984
CHGA	5'-ACACAGGCAGCCTTCCAAAGTTTGC-3'	5-'CACAATATAGTCAGGAGTCCTCAGC-3'	66	100	Iacangelo et al. 1986
COXP	5'-GAATGATGGCACAGATTTGCTCTGG-3'	5'-TACACACAGCGCTTCTCCCAGGTGA-3'	67	582	Bachman et al. 1987
OXT	5'-GCCATTAGCCGACATAACCTTGACC-3'	5'-ACGGTGTCTAAGAGGGCAGCCGCAT-3'	70	160	Rupert et al. 1984
ARVP	5'-TTCCTCAGCCTGCTGGCCTTCACCT-3'	5'-TGAAGGGGATTTCGGACGGAGAGGG-3'	67	206	Rupert et al. 1984

Bachman et al. *Gene 55:* 219–229, 1987; Fung et al. *Nucleic Acids Res 12:* 4481–4482, 1984; Goodwin et al. *Nucleic Acids Res 11:* 6873–6882, 1983; Hidaka et al. *Gene 43:* 197–203, 1986; Hobbs et al. *Proc Natl Acad Sci USA 82:* 7651–7655, 1985; Iacangelo et al. *Nature 323:* 82–86, 1986; Rupert et al. *Nature 308:* 554–557, 1984.

cycles in a Perkin-Elmer Cetus thermocycler. The primer pairs were optimized for amplification at the highest temperature possible. This temperature allowed preferential amplification of the bovine target sequence with little or no amplification of the rodent sequence. The subsequent reaction products were electrophoresed on a 3% Nuseive, 1% Seakem Me (FMC, Rockland, Me.) agarose gel containing ethidium bromide and were photographed.

Presence or absence of bovine-specific PCR amplification product was tested in 20 clones from a well-characterized, bovine-rodent somatic cell panel. Segregation profiles of bovine-specific PCR products were compared with those of previously assigned markers for each of the 31 bovine syntenic groups. Statistical analysis based on correlation (Chevalet and Corpet 1986) was performed between the tested locus and each of the representative markers ($p < 0.02$). This test determines whether the locus is syntenic, asyntenic, or undeterminable with each of the syntenic groups.

Results

Partial sequencing of the amplified DNA products by modified PCR sequencing (Allard et al. 1991) of *F10* and *CYM* was used to confirm gene specificity of the amplification reactions (data not shown). The amplified product of both of these primer sets corresponded to published sequence data. The amplification of the predicted fragment was used as evidence of successful targeting of amplification (Fig. 1).

Eight loci were assigned to bovine syntenic groups by use of PCR in bovine × hamster and bovine × mouse hybrid cells. Each hybrid clone from the somatic cell panel was tested for its ability to amplify a predicted size fragment by PCR with primers designed from published bovine sequences. The amplified fragment represents the presence of the bovine template. The presence or absence of this bovine template in each of the 20 hybrid clones determined the syntenic assignment for each gene. Statistical analysis of data corresponding to the retention or loss of bovine-specific PCR products demonstrated that *CYM, CHGA, CGA, F10, LDLR, OXT, ARVP,* and *COXP,* mapped to syntenic groups U6, U4, U2, U27, U22, U11, U11, and U3, respectively (Table 2).

CGA and *LDLR* have previously been mapped in mouse and human (Naylor et al. 1983; Francke et al. 1984; Lindgren et al. 1985; Wang et al. 1988). *CYM, CHGA, OXT, ARVP,* and *F10* have been mapped only in humans (Kolmer et al. 1991; Modi et al. 1989; Murray et al. 1987; Sausville et al. 1985; Riddell et al. 1985; Rocchi et al. 1986; de Grouchy et al. 1984). *COXP* is a pseudogene that has no demonstrated homolog in either human or mouse. *COXP* and *CYM* were assigned gene symbols according to previously determined rules for human gene nomenclature (Shows et al. 1979). By aligning the assigned human loci with their corresponding locations in cow and mouse, a three-way comparative map can be established (Fig. 2). (For detailed descriptions of other loci found on the comparative map, see Human Gene Mapping 10, 1989; Womack et al. 1989, 1991).

Discussion

Using PCR in combination with a well-characterized hybrid somatic cell panel, we have assigned eight genes to bovine syntenic groups and have used seven of these assignments to further extend the bovine–human or the bovine–human–mouse comparative map.

This is the first description of a PCR, somatic cell-based mapping study in cattle, and a few observations about the technique are in order. A critical factor in this technique is the ability to selectively amplify the bovine DNA without amplifying the corresponding rodent gene in the hybrid cells. In our hands, optimization of annealing temperature was the most efficient way of achieving preferential amplification. PCR gene mapping was very useful with primers designed from all regions of bovine sequences (exons as well as noncoding regions) when amplifying relatively short fragments (up to 600 bp) with the annealing portion of the reaction run at the highest temperature allowable.

PCR gene mapping was used to extend the bovine–human and the bovine–human–mouse comparative maps. The mapping of *LDLR* to U22 and of *CGA* to U2 further defines regions of syntenic conservation among bovine, human, and mouse. *LDLR* identifies a homologous region of bovine U22, a portion of the p arm of HSA 19 (Francke et al. 1984), and MMU 9. An evolutionary breakpoint is observed between *LDLR* and *INSR*. However, this breakpoint is not observed in cattle, since both *LDLR* and *INSR* are located on U22. Assuming a most parsimonious model, the syntenic configuration of the portion of HSA 19p, extending from *AMH* to *LDLR*, defines the mammalian ancestral synteny.

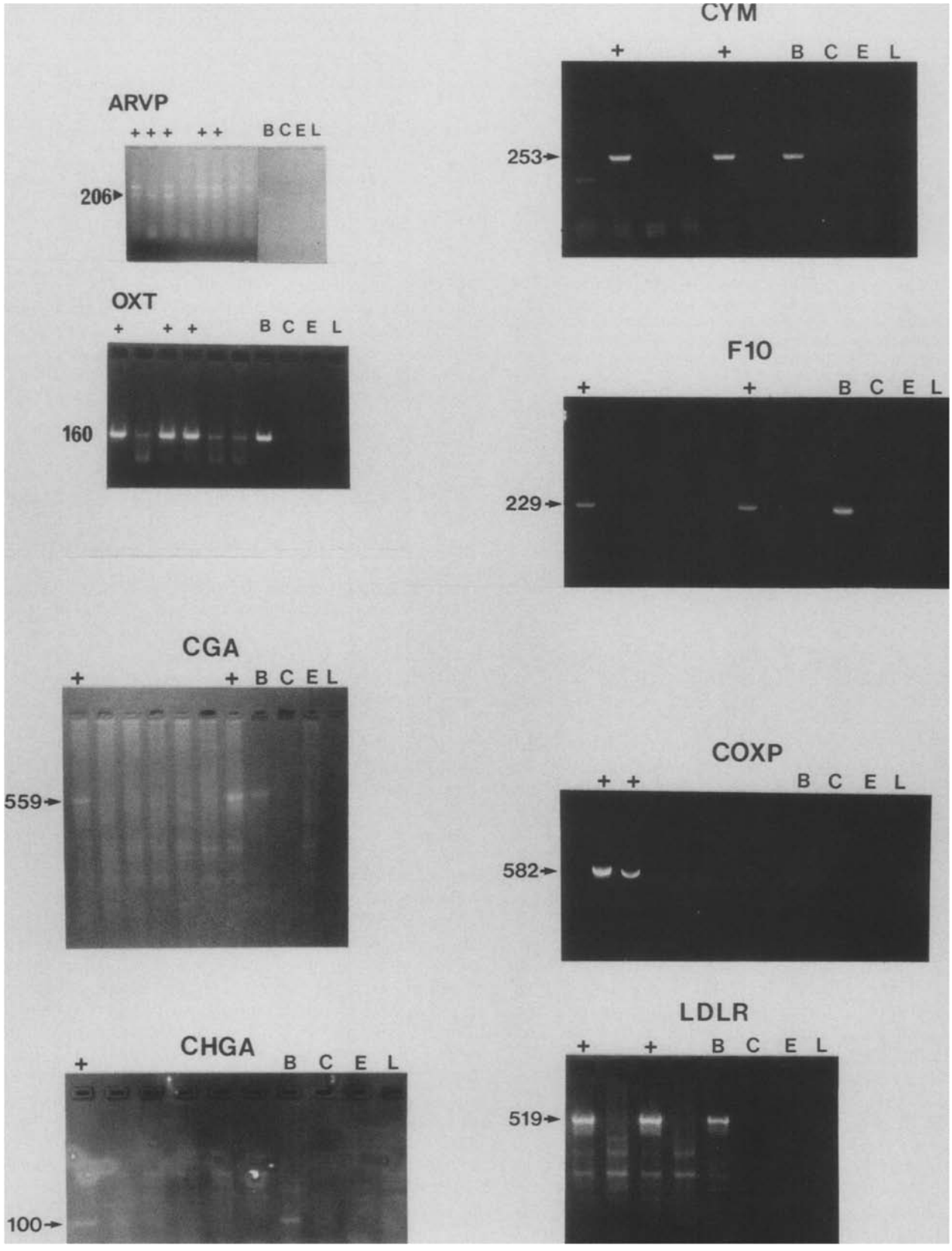

Fig. 1. Representative ethidium bromide-stained gels of amplified PCR products representing the genes in this study. Bovine control **(B)**, cell line chinese hamster ovary **(C)**, cell line E36 **(E)**, cell line $LMTK^-$ **(L)**, positive hybrid clones (+), and the amplified fragment size **(in bp)** are indicated.

Table 2. Concordancy and statistical analysis.[a]

	COXP		*ARVP*		*OXT*		*CYM*		*CGA*		*F10*		*CHGA*		*LDLR*	
Syntenic Group	ψ[b]	Con[c]	ψ	Con	ψ	Con	ψ	Con	ψ	Con	ψ	Con	ψ	Con	ψ	Con
1	0.13	60	0.47	75	0.36	70	0.04	55	0.20	60	0.36	70	0.47	75	−0.24	45
2	0.42	68	0.33	63	0.33	63	−0.59	21	**1.0**	**100**	0.19	58	0.29	63	−0.39	32
3	**1.0**	**100**	0.38	75	0.29	70	−0.25	45	0.44	70	0.52	80	−0.02	55	0.13	55
4	0.05	60	−0.10	55	−0.19	50	−0.02	55	0.44	70	0.05	60	**0.89**	**95**	−0.38	45
5	0.09	50	0.47	65	0.53	70	0.17	55	−0.20	40	−0.13	40	−0.68	15	0.24	55
6	−0.30	45	−0.20	50	−0.25	45	**1.0**	**100**	−0.52	25	−0.02	55	−0.10	50	0.54	80
7	0.00	50	0.22	55	0.00	50	0.31	65	−0.40	30	0.00	50	0.52	25	0.35	65
8	0.31	60	−0.02	35	−0.36	30	0.39	65	0.20	60	0.09	50	0.17	55	0.24	55
9	−0.30	50	0.22	75	0.15	69	−0.22	63	0.38	63	−0.22	63	0.22	75	−0.22	63
10	−0.10	45	−0.02	40	−0.29	35	0.45	70	0.10	55	0.15	55	0.45	70	0.52	70
11	0.29	70	**0.88**	**95**	**1.0**	**100**	−0.25	45	0.22	60	0.29	70	−0.25	45	−0.13	55
12	0.43	75	0.54	80	0.43	75	−0.32	40	0.52	75	0.43	75	0.12	60	−0.18	50
13	0.21	65	0.30	70	0.21	60	0.34	70	0.10	55	0.21	64	0.34	70	−0.18	50
14	0.15	58	−0.10	47	−0.19	42	−0.07	47	−0.06	47	−0.09	47	−0.07	47	0.29	63
15	−0.20	40	−0.10	45	−0.22	40	0.73	85	−0.40	30	0.00	50	−0.10	45	0.35	65
16	−0.10	55	0.20	70	0.38	75	−0.18	50	−0.12	45	0.13	65	0.06	60	−0.07	60
17	0.21	65	0.30	70	0.21	60	0.34	70	0.10	55	0.21	65	0.34	70	−0.18	50
18	0.51	80	0.58	85	0.51	80	−0.24	55	0.33	60	0.15	70	0.1	65	−0.19	65
19	0.05	60	0.13	65	0.05	60	0.66	85	−0.44	30	0.05	60	−0.48	35	0.63	85
20	0.13	65	−0.10	60	−0.13	55	0.06	60	0.35	65	0.38	75	0.3	70	0.20	70
21	−0.20	35	−0.3	30	−0.43	25	0.32	60	−0.10	45	0.02	45	0.54	70	0.42	60
22	−0.10	55	−0.10	60	−0.13	55	0.54	80	−0.35	35	0.13	65	−0.42	40	**1.0**	**100**
23	−0.10	40	0.00	45	0.09	50	0.39	65	0.00	50	0.09	50	0.17	55	0.24	55
24	−0.30	35	0.06	50	−0.07	45	0.45	70	−0.10	45	−0.07	45	0.24	60	0.29	60
25[d]	−0.30	33	0.50	67	0.71	83	−0.63	17	0.71	83	0.00	33	0.32	50	0.00	33
26	−0.20	50	−0.10	55	−0.19	50	0.21	65	−0.22	40	−0.19	50	−0.48	35	0.63	85
27	0.43	75	0.30	70	0.43	75	−0.10	50	0.10	55	**0.89**	**95**	−0.10	50	0.06	60
28	−0.10	40	−0.20	35	−0.13	40	0.17	55	0.20	60	0.31	60	0.17	55	0.24	55
29	−0.20	40	0.35	65	0.22	60	0.52	75	0.00	50	0.00	50	0.10	55	0.35	65
X	0.07	55	0.41	70	0.50	75	−0.66	20	0.10	55	−0.15	45	−0.24	40	−0.52	30

[a] Each locus was tested against each syntenic group with statistically significant values for synteny in **bold typeface**, asyntenic groups in **plain text**, and **underlined** values representing undetermined relationships between the tested locus and that syntenic group (error rate Q = 0.025, and probability for correct decision P = 0.91).
[b] Correlation coefficient.
[c] Percent concordancy.
[d] A limited number of clones were tested for syntenic Group U25.

CGA defines a conserved segment consisting of bovine U2, most of the q arm of HSA 6, and MMU 4. *CGA* extends the known bovine U2–HSA 6 homology to include the MMU 4 region. *CGA* is another example of disruption of ancestral syntenies in the mouse with remaining conservation of these syntenies between human and cow. HSA 6 is the only known location for homologs to the genes in syntenic group U2 and U20. The location of *CGA* on HSA 6 is defined as either p23-p21.1 or q12-q21. The comparative map is not sufficiently defined to enable the determination of the correct locality. BF and C4 both map to HSA 6p21.3 and *Bos taurus* 23 (bovine syntenic group U20). Therefore, it is more likely that *CGA* would be sublocalized to the q arm of human 6; however, the data are still unclear.

F10, CYM, OXT, ARVP, and *CHGA* extend the human–bovine comparative map only, since they are not yet mapped in the mouse. *OXT* and *VAS* map to HSA 20. The loci that have been assigned to the human–mouse–bovine comparative map extend along the entire region of HSA 20, indicating extensive evolutionary conservation for this human syntenic group. *OXT* and *ARVP* have not been assigned in mouse; however, on the basis of the demonstrated conservation seen in the comparative map (Lalley and Diaz 1984), we predict the physical location of *OXT* and *ARVP* will be MMU 2.

F10 demonstrates a new region of conservation between bovine U27 and HSA 13. *ESD* is the only other gene on the comparative map of HSA 13 and has been found to be syntenic with bovine syntenic group U13 (BTA 2) and mapped to MMU 14. *F10* has been sublocalized to 13q34, making *F10* a good distal marker to help determine the comparative map in this region of the genome. It is interesting to note that the human–mouse comparative map suggests that HSA 13 is highly conserved between these species. *F10* may then be a good subject for further investigation into the human–mouse comparative map for this region.

CHGA is found to be on an evolutionarily conserved segment with *IGH* on bovine U4 (BTA 21) (Threadgill et al. 1990b). The homologous human region has been located on 14q32. The homologous region of telomeric HSA 14 has been mapped to MMU 12. On the three-way comparative map, this also include *FOS*. However, *FOS* is located on BTA 10, revealing a region that has been conserved between mouse and human and disrupted in cattle. The conserved region surrounding *CHGA* and represented by *IGH* on the comparative map also contains five loci that have been mapped to both mouse and human, but not yet assigned in cattle. The mouse–human comparative map for this region is highly conserved, with all five of these loci mapping to MMU 12. Therefore, we predict the mouse homolog of *CHGA* is likely to map to MMU 12.

CYM was found to map to bovine syntenic group U6. It has recently been demonstrated that *CYM* maps to HSA 1; however, it has not been sublocalized

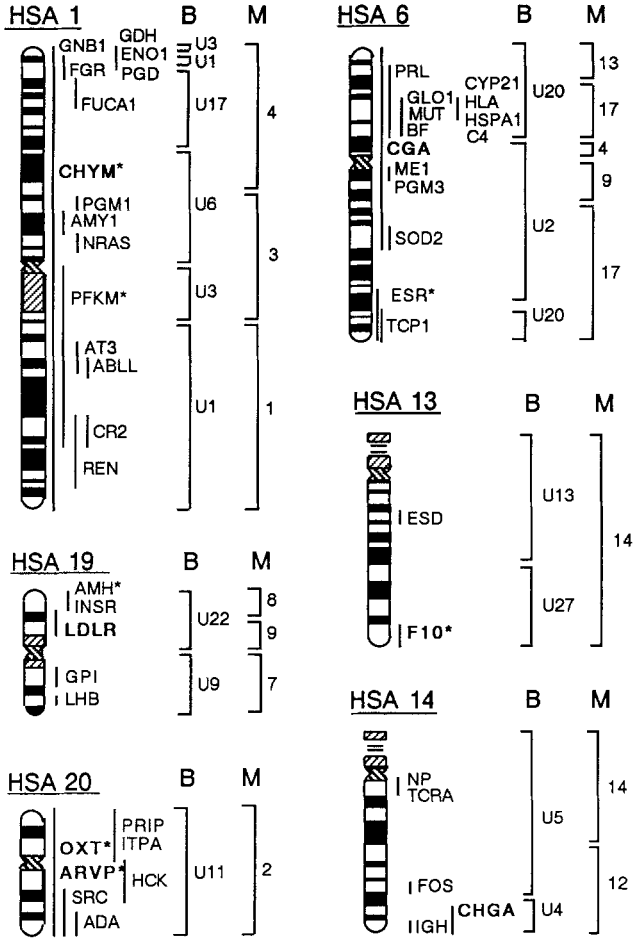

Fig. 2. Comparative maps based on the human idiogram with the bovine syntenic group (**B**) and the mouse chromosome (**M**) location indicated to the **right.** All loci indicated have been mapped in human and bovine. Loci that have not been mapped in the mouse are indicated (*). **Brackets** are generalized localizations used for clarity.

(Kolmer et al. 1991). The human bovine comparative map consists of five defined regions of conservation. Four of the regions are derived from syntenic groups U1 and U3. There is only one region of HSA 1 that is defined by bovine syntenic group U6. The region is defined by *PGM1* at HSA 1p22 that maps to bovine syntenic group U1, and *SPTA1* at HSA 1q21 that maps to bovine U1. This region contains three genes—*PGM1, AMY1,* and *NGFB*—that map to bovine U6. Since this is the only region defined by U6, we sublocalize *CYM* to the boundaries of the comparative map HSA 1p32-q21.

PCR in combination with somatic cell genetics is very useful for assigning bovine genes to bovine syntenic groups. We have mapped eight genes by this technology, two that define new regions of chromosomal conservation between mouse, human, and cow, and five that define regions between human and cow. It should also be noted that, through the development of PCR assays for these eight genes, we have developed the bovine equivalent of expressed sequence tags (ESTs; Adams et al. 1991). Expressed sequence tags and nonexpressed sequence-tagged sites (STSs; Olson et al. 1989) are becoming standard markers for physical mapping in the human genome. The primers designed in this study can be used by other investigators interested in either the individual locus or in the physical regions represented by the loci. This process can occur without the time and expense involved with transfer of biological materials. The development of bovine ESTs will capitalize on the current technology to gain rapid and detailed development of the bovine gene map. These eight ESTs map to seven bovine syntenic groups, resulting in a panel of PCR-based assays that will also function as rapid sources for the future characterization of hybrid somatic cell panels.

The continued development of a three-species comparative map will aid in the further localization of homologous segments across species and will provide for an efficient basis for the generation of linkage maps in this and other economically important species.

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References

Adams, M.D., Kelly, J.M., Gocayne, J.D., Dubnick, M., Polymeropoulos, M.H., Xiao, H., Merril, C.R., Wu, A., Olde, B., Moreno, R.F., Kerlavage, A.R., McCombie, W.R., and Venter, J.C.: Complementary DNA sequencing: expressed sequence tags and the human genome project. *Science 252:* 1651–1656, 1991.

Allard, M.W., Ellsworth, D.L., and Honeycutt, R.L.: The production of single-stranded DNA suitable for sequencing using the polymerase chain reaction. *BioTechniques 10:* 24–26, 1991.

Blinn, N. and Stafford, D.W.: A general method for isolation of high molecular weight DNA from eukaryotes. *Nucleic Acids Res 3:* 2303–2308, 1976.

Brubacher, M.G., Siewertsen, M.A., Billingsley, G.D., Benger, J.C., and Cox, D.W.: A genetic linkage map of human Chromosome 14 and homology with the mouse. *Am J Hum Genet 47 Suppl.:* A175, 1990 (Abstract).

Chevalet, C. and Corpet, F.: Statistical decision rules concerning synteny or independence between markers. *Cytogenet Cell Genet 43:* 132–139, 1986.

Copeland, N.G. and Jenkins, N.A.: Development and applications of a molecular genetic linkage map of the mouse genome. *Trends Genet 7:* 113–118, 1991.

Cornall, R.J., Aitman, T.J., Hearne, C.M., and Todd, J.A.: The generation of a library of PCR-analyzed microsatellite variants for genetic mapping of the mouse genome. *Genomics 10:* 874–881, 1991.

de Grouchy, J., Dautzenberg, M.-D., Turleau, C., Beguin, S., and Chavin-Colin, F.: Regional mapping of clotting factors *VII* and *X* to 13q34. Expression of factor *VII* through Chromosome 8. *Hum Genet 66:* 230–233, 1984.

Dionne, C.A., Kaplan, R., Seuanez, H., O'Brien, S.J., and Jaye, M.: Chromosome assignment by polymerase chain reaction techniques: assignment of the oncogene *FGF-5* to human chromosome 4. *BioTechniques 8:* 190–194, 1990.

Francke, U., Brown, M.S., and Goldstein, J.L.: Assignment of the human gene for the low density lipoprotein receptor to Chromosome 19: synteny of a receptor, a ligand, and a genetic disease. *Proc Natl Acad Sci USA 81:* 2826–2830, 1984.

Human Gene Mapping 10 (1989): Tenth International Workshop on Human Gene Mapping. *Cytogenet Cell Genet 51:* 1–1148, 1989.

Iggo, R., Gough, A., Xu, W., Lane, D.P., and Spurr, N.K.: Chromosome mapping of the human gene encoding the 68-kDa nuclear

antigen (p68) by using the polymerase chain reaction. *Proc Natl Acad Sci USA 86:* 6211–6214, 1989.

Kolmer, M., Ord, T., Alhonen, L., Hyttinen, J.-M., Saarma, M., Villems, R., and Janne, J.: Assignment of human prochymosin pseudogene to Chromosome 1. *Genomics 10:* 496–498, 1991.

Lalley, P.A. and Diaz, J.A.: Comparative gene mapping in the mouse involving genes assigned to human Chromosomes 7 and 20. *Cytogenet Cell Genet 37:* 515, 1984 (Abstract).

Levan, G., Szpirer, J., Szpirer, C., Klinga, K., Hanson, C., and Islam, M.Q.: The gene map of the Norway rat (*Rattus norvegicus*) and comparative mapping with mouse and man. *Genomics 10:* 699–718, 1991.

Lindgren, V., Luskey, K.L., Russell, D.W., and Francke, U.: Human genes involved in cholesterol metabolism: chromosomal mapping of the loci for the low density lipoprotein receptor and 3-hydroxy-3-methylglutaryl-coenzyme A reductase with cDNA probes. *Proc Natl Acad Sci USA 82:* 8567–8571, 1985.

Modi, W.S., Levine, M.A., Dean, M., Seuanez, H., and O'Brien, S.J.: The chromogranin A gene: chromosome assignment and RFLP analysis. *Cytogenet Cell Genet 51:* 1046, 1989 (Abstract).

Murray, S.S., Deaven, L.L., Burton, D.W., O'Connor, D.T., Mellon, P.L., and Deftos, L.J.: The gene for human chromogranin A (CgA) is located on chromosome 14. *Biochem Biophys Res Commun 142:* 141–146, 1987.

Nadeau, J.H.: Maps of linkage and synteny homologies between mouse and man. *Trends Genet 5:* 81–86, 1989.

Naylor, S.L., Chin, W.W., Goodman, H.M., Lalley, P.A., Grzeschik, K.-H., and Sakaguchi, A.Y.: Chromosome assignment of genes encoding the α and β subunits of glycoprotein hormones in man and mouse. *Somatic Cell Genet 9:* 757–770, 1983.

Olson, M., Hood, L., Cantor, C., and Botstein, D.: A common language for physical mapping of the human genome. *Science 245:* 1434–1435, 1989.

Riddell, D.C., Mallonee, R., Phillips, J.A., Parkes, J.S., Sexton, L.A., and Hamerton, J.L.: Chromosomal assignment of human sequences encoding arginine vasopressin-neurophysin II and growth hormone releasing factor. *Somatic Cell Mol Genet 11:* 189–195, 1985.

Rocchi, M., Roncuzzi, L., Santamaria, R., Archidiacono, N., Dente, L., and Romeo, G.: Mapping through somatic cell hybrids and cDNA probes of protein C to Chromosome 2, factor X to chromosome 13, and α1-acid glycoprotein to Chromosome 9. *Hum Genet 74:* 30–33, 1986.

Rose, E.A.: Applications of the polymerase chain reaction to genome analysis. *FASEB J 5:* 46–53, 1991.

Sausville, E., Carney, D., and Battey, J.: The human vasopressin gene is linked to the oxytocin gene and is selectively expressed in a cultured lung cancer cell line. *J Biol Chem 260:* 10236–10241, 1985.

Shows, T.B., Alper, C.A., Bootsma, D., Dorf, M., Douglas, T., Huisman, T., Kit, S., Klinger, H.P., Kozak, C., Lalley, P.A., Lindsley, D., McAlpine, P.J., McDougall, J.K., Meera Khan, P., Meisler, M., Morton, N.E., Opitz, J.M., Partridge, C.W., Payne, R., Roderick, T.H., Rubinstein, P., Ruddle, F.H., Shaw, M., Spranger, J.W., and Weiss, K.: International system for human gene nomenclature (1979) ISGN (1979). *Cytogenet Cell Genet 25:* 96–116, 1979.

Skow, L.C., Womack, J.E., Petresh, J.M., and Miller, W.L.: Synteny mapping of the genes for 21 steroid hydroxylase, alpha a-crystallin, and class I bovine leukocyte antigen in cattle. *DNA 7:* 153–159 1988.

Threadgill, D.W. and Womack, J.E.: Syntenic conservation between humans and cattle I. Human chromosome 9. *Genomics 8:* 22–28, 1990.

Threadgill, D.W., Adkison, L.R., and Womack, J.E.: Syntenic conservation between humans and cattle II. Human chromosome 12. *Genomics 8:* 29–34, 1990a.

Threadgill, D.W., Fries, R., Faber, L.K., Vassart, G., Gunawardana, A., Stranzinger, G., and Womack, J.E.: The thyroglobulin gene is syntenic with the *MYC* and *MOS* protooncogenes and carbonic anhydrase II and maps to chromosome 14 in cattle. *Cytogenet Cell Genet 53:* 32–36, 1990b.

Threadgill, D.W., Kraus, J.P., Krawetz, S.A., and Womack, J.E.: Evidence for the evolutionary origin of human Chromosome 21 from comparative gene mapping in the cow and mouse. *Proc Natl Acad Sci USA 88:* 154–158, 1991.

Trapani, J.A., Kwon, B.S., Kozak, C.A., Chintamaneni, C., Young, J.D., and Dupont, B.: Genomic organization of the mouse pore-forming protein (perforin) gene and localization to chromosome 10. Similarities to and differences from C9. *J Exp Med 171:* 545–557, 1990.

Wang, L.-M., Killary, A.M., Fang, X.-E., Parriott, S.K., Lalley, P.A., Bell, G.I., and Sakaguchi, A.Y.: Chromosome assignment of mouse insulin, colony stimulating factor 1, and low-density lipoprotein receptors. *Genomics 3:* 172–175, 1988.

Womack, J.E.: Gene mapping in the cow. *In* R.A. McFeely (ed.); *Advances in Veterinary Science and Comparative Medicine: Domestic Animal Cytogenetics,* pp 251–271, San Diego, Academic Press, Inc., 1990.

Womack, J.E. and Moll, Y.D.: Gene map of the cow: conservation of linkage with mouse and man. *J Hered 77:* 2–7, 1986.

Womack, J.E., Threadgill, D.W., Moll, Y.D., Faber, L.K., Foreman, M.L., Dietz, A.B., Tobin, T.C., Skow, L.C., Zneimer, S.M., Gallagher, D.S., and Rogers, D.S.: Syntenic mapping of 37 loci in cattle. Chromosomal conservation with mouse and man. *Cytogenet Cell Genet 51:* 1109, 1989 (Abstract).

Womack, J.E., Dietz, A.B., Gallagher, D.S., Li, L., Nan, Z., Neibergs, H.L., Moll, Y.D., and Ryan, A.M.: Assignment of 47 additional comparative anchor loci to the bovine synteny map. *Cytogenet Cell Genet,* in press, 1991.