

## A medium density microsatellite map of BTA10: reassignment of *INRA69*

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### Summary

We have developed a genetic map of BTA10 based on 8952 informative meioses for 13 microsatellite markers and the erythrocyte antigen Z. With the exception of *OarAE64*, the support for the order of all loci in the map exceeded a LOD > 3.0. The length of the BTA10 genetic map was 87.0 centimorgans (cM). The 14-marker, sex-average map in Kosambi cM was: *CSSM38*–8.9–*BM1237*–5.2–*HH8A*–2.6–*INRA69*–10.6–*TGLA378*–0.8–*BM6305*–17.2–*TGLA102*–17.9–*INRA96*–0.3–*CSRM60*–9.2–*DIK20*–3.0–*EAZ*–6.7–*CSSM46*–3.7–*SRCRSP3*–1.0–*OarAE64* with an average interval of 6.70 cM. The microsatellite *INRA69* was recently assigned to the pseudoautosomal region of the bovine X chromosome by linkage analysis. However, we found that twopoint support for linkage between *INRA69* and 15 X-linked bovine microsatellites was LOD < 0.50 in 529 reciprocal backcross and F<sub>2</sub> fullsib progeny. We performed twopoint analyses of *INRA69* against 275 markers distributed throughout the bovine genome and found significant associations with a LOD > 3.0 only between *INRA69* and eight BTA10 microsatellite loci. Consequently, we excluded *INRA69* from the genetic map of the X chromosome and reassign this microsatellite to BTA10.

**Keywords:** bovine, BTA10, genetic linkage, microsatellites

A weakness of the published livestock genetic maps is that each is based upon a relatively small number of coinformative meioses and this limits both the capacity to resolve marker order and the precision with which the map distance between markers can be estimated. For the purpose of localizing quantitative trait loci (QTL), it is critical that the order of loci assigned to a chromosome be correct. To overcome these limitations, chromosome workshops, which integrate data from several mapping populations, have recently been held for bovine

chromosome 23 (BTA23) (Beever *et al.* 1996) and bovine chromosome 1 (BTA1) (ISAG XXV, Tours, July 21–25 1996). Genotypes from the Texas A&M University's three-generation Angleton mapping population were contributed to both workshops. The Angleton families include 529 fullsib progeny from 39 backcross families and two F<sub>2</sub> families produced by embryo transfer from 80 Brahman, Angus and F<sub>1</sub> parents and their grandparents. These families were constructed for the primary purpose of localizing QTLs associated with growth and carcass merit traits. These families have been scored for 275 markers, and sex-specific and sex-average maps of the bovine chromosomes have been constructed (Yeh *et al.* 1995; Beever *et al.* 1996; Brenneman *et al.* 1996) according to standard procedures (Green *et al.* 1990; Barendse *et al.* 1997; Kappes *et al.* 1997).

A medium resolution genetic map of the bovine genome has recently been published (Barendse *et al.* 1997). This map localizes the microsatellite *INRA69* to the X chromosome distal to *INRA30*. We have physically mapped *INRA30* to the distal end of the long arm of the X chromosome at q42-ter and to the short arm of the Y chromosome at p13-ter (Yeh *et al.* 1995). We scored *INRA69* in the Angleton mapping population in order to extend our map of the pseudoautosomal region of the bovine X and Y chromosomes (Yeh *et al.* 1995; Barendse *et al.* 1997). However, the twopoint associations between 15 X-linked microsatellites and *INRA69* were all LOD < 0.50, excluding the localization of this locus to the X chromosome. We then ran twopoint analyses between *INRA69* and all 275 scored loci, using CRI-MAP version 2.4 (Green *et al.* 1990), in order to facilitate the integration of this locus into the appropriate chromosome framework map. Eight of 275 twopoint associations involving *INRA69* were LOD > 3.0 (Table 1), and all involved marker loci that had previously been assigned to BTA10 (Barendse *et al.* 1997; Kappes *et al.* 1997). As five of these associations were LOD > 50.0, there is conclusive evidence for the localization of *INRA69* to BTA10. Including *INRA69*, 13 microsatellite loci and the erythrocyte antigen Z on BTA10 have been scored in the Angleton

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pedigrees. Locus description and the number of informative meioses for each marker are presented in Table 1. The LOD > 3.0 framework map includes all loci except *OarAE64* and is presented in Fig. 1. The male and female maps did not differ in length ( $\chi^2_{14} = 16.88$ ;  $P > 0.25$ ) and the sex-average map, which is based on 8952 informative meioses, has a total length of 87.0 cM with an average interval size of 6.70 cM.

The bovine linkage map of Barendse *et al.* (1997) includes 746 loci integrated into 31 framework chromosome maps with a support of LOD > 6.0 for linkage and LOD > 3.0 for gene order. The localization of *INRA69* to the X chromosome map was supported by a LOD = 14.98 for linkage to *INRA30*; however, linkage to several BTA10 loci was also detected (W Barendse, personal communication). In general, the type I error rate for the published bovine maps (Barendse *et al.* 1997; Kappes *et al.* 1997) is

likely to be extremely low. Exceptions are most likely to be for the most proximal or distal markers in a linkage group, where genotyping errors that would lead to spurious double recombinants for internal markers are not revealed. Even a single genotyping error, such as the incorrect determination of a grandparental genotype, can result in a locus being forced to the end of a linkage group in order to minimize the number of double recombination events. A gross inflation in map length is also characteristic of this type of genotyping error. The map of the pseudoautosomal region of the X chromosome in Barendse *et al.* (1997) is suspicious in view of the dramatic inflation of the distance between *INRA30* and *MAF45* – 32 cM in comparison to the distance of 3.3 cM reported by Yeh *et al.* (1995) and 2.2 cM by Sonstegard *et al.* (1997). The pseudoautosomal region of the X chromosome is believed to be a

**Table 1.** Twopoint recombination fractions, LOD  $\geq$  3.0 scores and number of informative meioses for 14 bovine chromosome 10 marker loci

Locus	BM1237	HH8A	INRA69	TGLA378	BM6305	TGLA102	INRA96	CSRM60	DIK20	EAZ	CSSM46	SRCRSP3	OarAE64	N‡
<i>CSSM38</i> §	0.09*	0.11	0.14	0.23	0.23	0.39								660
	78.96†	36.58	58.08	23.26	24.16	4.86								
<i>BM1237</i> ¶		0.04	0.08	0.19	0.17	0.32								850
		62.35	117.03	48.73	47.62	18.83								
<i>HH8A</i> **			0.02	0.12	0.10	0.30								380
			73.76	27.01	36.41	7.30								
<i>INRA69</i> §				0.10	0.10	0.27	0.39	0.41						896
				81.46	88.00	29.99	5.19	4.03						
<i>TGLA378</i> §					0.01	0.17	0.31	0.31	0.39		0.41			674
					96.91	55.75	13.11	15.05	3.92		3.50			
<i>BM6305</i> ¶						0.17	0.29	0.30	0.38					654
						55.20	15.55	16.60	3.92					
<i>TGLA102</i> §							0.16	0.17	0.24		0.31	0.36		886
							65.89	69.95	35.34		23.59	4.20		
<i>INRA96</i> §								0.00	0.09	0.09	0.17	0.23	0.22	776
								193.95	93.25	8.95	71.01	16.33	4.83	
<i>CSRM60</i> §									0.09	0.11	0.17	0.21	0.21	876
									108.62	8.77	78.66	18.39	7.11	
<i>DIK20</i> §										0.03	0.09	0.14	0.19	769
										12.97	109.01	27.32	4.17	
<i>EAZ</i> ¶											0.08	0.08		81
											11.62	8.48		
<i>CSSM46</i> §												0.04	0.04	983
												68.47	28.14	
<i>SRCRSP3</i> ††													0.00	320
													4.21	
<i>OarAE64</i> ¶														147

\*Recombination fraction.

†LOD score.

‡No. informative meioses.

§Barendse *et al.* (1997).

¶Kappes *et al.* (1997).

\*\*Entrez Accession Number L25257.

††Arevalo *et al.* (1994).

recombination hot-spot, but its physical size is small and the total genetic length was estimated by Yeh *et al.* (1995) to be only 13.0 cM.

Our assignment of *INRA69* to BTA10 by linkage analysis is important for the purpose of localizing QTL to the correct chromosomal region and serves as a warning that other loci are likely to have been misassigned in the published maps. Our map of BTA10 otherwise agrees with the marker orders of Ma *et al.* (1996), Barendse *et al.* (1997) and Kappes *et al.* (1997), but is shorter in all intervals except *TGLA102-*INRA96** and *CSRM60-DIK20*, compared with the map of Barendse *et al.* (1997), and shorter in the interval *CSSM38-BM1237*, compared with the map of Ma *et al.* (1996).

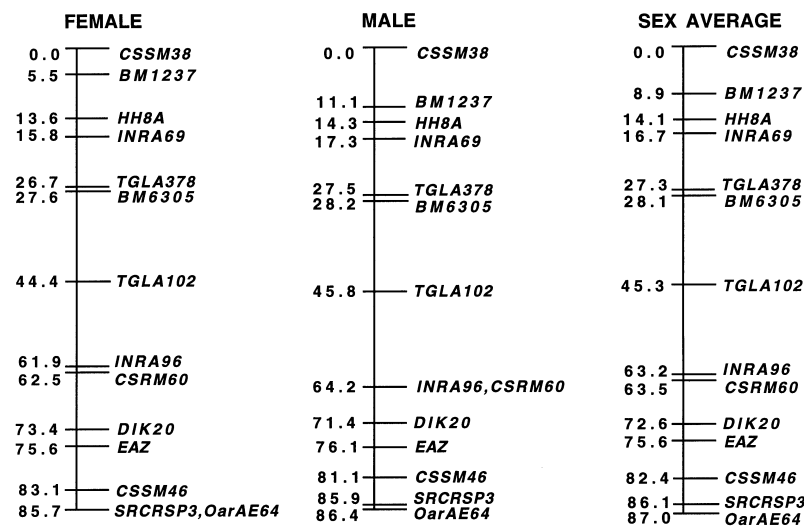


Fig. 1. Sex average and sex specific genetic maps of bovine chromosome 10 oriented at the centromere. All loci except *OarAE64* are ordered with a likelihood ratio > 1000:1 vs alternative orders.

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